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(54) Title: NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

(57) Abstract

The invention provides proteins from Neisseria meningitidis, including the amino acid sequences and the corresponding nucleotide sequences. The proteins are predicted to be useful antigens for vaccines and/or diagnostics.

919 (46 kDa)

A) PURIFICATION



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NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

This application is a continuation-in-part of the following U.S. Provisional Patent applications, from each of which priority is claimed, and each of which is incorporated by reference in its entirety: 60/083,758 (filed May 1, 1998); 60/094,869 (filed July 31, 1998); 60/098,994 (filed September 2, 1998); 60/099,062 (filed September 2, 1998); 60/103,749 (filed October 9, 1998); 60/103,794 (filed October 9, 1998); 60/103,796 (filed October 9, 1998); and 60/121,528 (filed February 25, 1999).

This invention relates to antigens from the bacterial species: *Neisseria meningitidis* and *Neisseria gonorrhoeae*.

BACKGROUND

Neisseria meningitidis is a non-motile, gram negative diplococcus human pathogen. It colonizes the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. It is closely related to *N. gonorrhoea*, although one feature that clearly differentiates meningococcus from gonococcus is the presence of a polysaccharide capsule that is present in all pathogenic meningococci.

N. meningitidis causes both endemic and epidemic disease. In the United States the attack rate is 0.6-1 per 100,000 persons per year, and it can be much greater during outbreaks. (see Lieberman *et al.* (1996) Safety and Immunogenicity of a Serogroups A/C *Neisseria meningitidis* Oligosaccharide-Protein Conjugate Vaccine in Young Children. *JAMA* 275(19):1499-1503; Schuchat *et al* (1997) Bacterial Meningitis in the United States in 1995. *N Engl J Med* 337(14):970-976). In developing countries, endemic disease rates are much higher and during epidemics incidence rates can reach 500 cases per 100,000 persons per year. Mortality is extremely high, at 10-20% in the United States, and much higher in developing countries. Following the introduction of the conjugate vaccine against *Haemophilus influenzae*, *N. meningitidis* is the major cause of bacterial meningitis at all ages in the United States (Schuchat *et al* (1997) *supra*).

Based on the organism's capsular polysaccharide, 12 serogroups of *N. meningitidis* have been identified. Group A is the pathogen most often implicated in epidemic disease in sub-Saharan Africa. Serogroups B and C are responsible for the vast majority of cases in the

United States and in most developed countries. Serogroups W135 and Y are responsible for the rest of the cases in the United States and developed countries. The meningococcal vaccine currently in use is a tetravalent polysaccharide vaccine composed of serogroups A, C, Y and W135. Although efficacious in adolescents and adults, it induces a poor immune response and short duration of protection, and cannot be used in infants [eg. Morbidity and Mortality weekly report, Vol.46, No. RR-5 (1997)]. This is because polysaccharides are T-cell independent antigens that induce a weak immune response that cannot be boosted by repeated immunization. Following the success of the vaccination against *H.influenzae*, conjugate vaccines against serogroups A and C have been developed and are at the final stage of clinical testing (Zollinger WD "New and Improved Vaccines Against Meningococcal Disease". In: *New Generation Vaccines, supra*, pp. 469-488; Lieberman *et al* (1996) *supra*; Costantino *et al* (1992) Development and phase I clinical testing of a conjugate vaccine against meningococcus A and C. *Vaccine* 10:691-698).

Meningococcus B (menB) remains a problem, however. This serotype currently is responsible for approximately 50% of total meningitis in the United States, Europe, and South America. The polysaccharide approach cannot be used because the menB capsular polysaccharide is a polymer of $\alpha(2-8)$ -linked *N*-acetyl neuraminic acid that is also present in mammalian tissue. This results in tolerance to the antigen; indeed, if an immune response were elicited, it would be anti-self, and therefore undesirable. In order to avoid induction of autoimmunity and to induce a protective immune response, the capsular polysaccharide has, for instance, been chemically modified substituting the *N*-acetyl groups with *N*-propionyl groups, leaving the specific antigenicity unaltered (Romero & Outschoorn (1994) Current status of Meningococcal group B vaccine candidates: capsular or non-capsular? *Clin Microbiol Rev* 7(4):559-575).

Alternative approaches to menB vaccines have used complex mixtures of outer membrane proteins (OMPs), containing either the OMPs alone, or OMPs enriched in porins, or deleted of the class 4 OMPs that are believed to induce antibodies that block bactericidal activity. This approach produces vaccines that are not well characterized. They are able to protect against the homologous strain, but are not effective at large where there are many antigenic variants of the outer membrane proteins. To overcome the antigenic variability, multivalent vaccines containing up to nine different porins have been constructed (eg. Poolman JT (1992) Development of a meningococcal vaccine. *Infect. Agents Dis.* 4:13-28).

Additional proteins to be used in outer membrane vaccines have been the opa and opc proteins, but none of these approaches have been able to overcome the antigenic variability (eg. Ala'Aldeen & Borriello (1996) The meningococcal transferrin-binding proteins 1 and 2 are both surface exposed and generate bactericidal antibodies capable of killing homologous and heterologous strains. *Vaccine* 14(1):49-53).

A certain amount of sequence data is available for meningococcal and gonococcal genes and proteins (e.g. EP-A-0467714, WO96/29412), but this is by no means complete. Other men B proteins may include those listed in WO 97/28273, WO 96/29412, WO 95/03413, US 5,439,808, and US 5,879,686.

The provision of further sequences could provide an opportunity to identify secreted or surface-exposed proteins that are presumed targets for the immune system and which are not antigenically variable. For instance, some of the identified proteins could be components of efficacious vaccines against meningococcus B, some could be components of vaccines against all meningococcal serotypes, and others could be components of vaccines against all pathogenic *Neisseriae* including *Neisseria meningitidis* or *Neisseria gonorrhoeae*. Those sequences specific to *N. meningitidis* or *N. gonorrhoeae* that are more highly conserved are further preferred sequences.

It is thus an object of the invention is to provide Neisserial DNA sequences which encode proteins that are antigenic or immunogenic.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 illustrates the products of protein expression and purification of the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 2 illustrates the products of protein expression and purification of the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 3 illustrates the products of protein expression and purification of the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 4 illustrates the products of protein expression and purification of the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 5 illustrates the products of protein expression and purification of the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 6 illustrates the products of protein expression and purification of the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 7 illustrates the products of protein expression and purification of the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 8 illustrates the products of protein expression and purification of the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 9 illustrates the products of protein expression and purification of the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 10 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 11 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 12 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 13 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 14 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 15 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 16 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 17 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 18 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 19 shows an alignment comparison of amino acid sequences for ORF 225 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 20 shows an alignment comparison of amino acid sequences for ORF 235 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 21 shows an alignment comparison of amino acid sequences for ORF 287 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 22 shows an alignment comparison of amino acid sequences for ORF 519 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 23 shows an alignment comparison of amino acid sequences for ORF 919 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

THE INVENTION

The invention provides proteins comprising the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples.

It also provides proteins comprising sequences homologous (i.e., those having sequence identity) to the *N. meningitidis* amino acid sequences disclosed in the examples. Depending on the particular sequence, the degree of homology (sequence identity) is preferably greater than 50% (eg. 60%, 70%, 80%, 90%, 95%, 99% or more). These proteins include mutants and allelic variants of the sequences disclosed in the examples. Typically, 50% identity or more between two proteins is considered to be an indication of functional equivalence. Identity between proteins is preferably determined by the Smith-Waterman

homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with parameters: gap penalty 12, gap extension penalty 1.

The invention further provides proteins comprising fragments of the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples. The fragments should comprise at least n consecutive amino acids from the sequences and, depending on the particular sequence, n is 7 or more (eg. 8, 10, 12, 14, 16, 18, 20 or more). Preferably the fragments comprise an epitope from the sequence.

The proteins of the invention can, of course, be prepared by various means (eg. recombinant expression, purification from cell culture, chemical synthesis *etc.*) and in various forms (eg. native, fusions *etc.*). They are preferably prepared in substantially pure or isolated form (*ie.* substantially free from other *N. meningitidis* or *N. gonorrhoeae* host cell proteins)

According to a further aspect, the invention provides antibodies which bind to these proteins. These may be polyclonal or monoclonal and may be produced by any suitable means.

According to a further aspect, the invention provides nucleic acid comprising the *N. meningitidis* nucleotide sequences and *N. gonorrhoeae* nucleotide sequences disclosed in the examples.

According to a further aspect, the invention comprises nucleic acids having sequence identity of greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) to the nucleic acid sequences herein. Sequence identity is determined as above-discussed.

According to a further aspect, the invention comprises nucleic acid that hybridizes to the sequences provided herein. Conditions for hybridization are set forth herein.

Nucleic acid comprising fragments of these sequences are also provided. These should comprise at least n consecutive nucleotides from the *N. meningitidis* sequences or *N. gonorrhoeae* sequences and depending on the particular sequence, n is 10 or more (eg 12, 14, 15, 18, 20, 25, 30, 35, 40 or more).

According to a further aspect, the invention provides nucleic acid encoding the proteins and protein fragments of the invention.

It should also be appreciated that the invention provides nucleic acid comprising sequences complementary to those described above (eg. for antisense or probing purposes).

Nucleic acid according to the invention can, of course, be prepared in many ways (eg. by chemical synthesis, in part or in whole, from genomic or cDNA libraries, from the

organism itself *etc.*) and can take various forms (*eg.* single stranded, double stranded, vectors, probes *etc.*).

In addition, the term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones, and also protein nucleic acids (PNA) *etc.*

According to a further aspect, the invention provides vectors comprising nucleotide sequences of the invention (*eg.* expression vectors) and host cells transformed with such vectors.

According to a further aspect, the invention provides compositions comprising protein, antibody, and/or nucleic acid according to the invention. These compositions may be suitable as vaccines, for instance, or as diagnostic reagents or as immunogenic compositions.

The invention also provides nucleic acid, protein, or antibody according to the invention for use as medicaments (*eg.* as vaccines) or as diagnostic reagents. It also provides the use of nucleic acid, protein, or antibody according to the invention in the manufacture of (I) a medicament for treating or preventing infection due to Neisserial bacteria (ii) a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria or (iii) for raising antibodies. Said Neisserial bacteria may be any species or strain (such as *N. gonorrhoeae*) but are preferably *N. meningitidis*, especially strain B or strain C.

The invention also provides a method of treating a patient, comprising administering to the patient a therapeutically effective amount of nucleic acid, protein, and/or antibody according to the invention.

According to further aspects, the invention provides various processes.

A process for producing proteins of the invention is provided, comprising the step of culturing a host cell according to the invention under conditions which induce protein expression.

A process for detecting polynucleotides of the invention is provided, comprising the steps of: (a) contacting a nucleic probe according to the invention with a biological sample under hybridizing conditions to form duplexes; and (b) detecting said duplexes.

A process for detecting proteins of the invention is provided, comprising the steps of: (a) contacting an antibody according to the invention with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

Methodology - Summary of standard procedures and techniques.

General

This invention provides *Neisseria meningitidis* menB nucleotide sequences, amino acid sequences encoded therein. With these disclosed sequences, nucleic acid probe assays and expression cassettes and vectors can be produced. The expression vectors can be transformed into host cells to produce proteins. The purified or isolated polypeptides (which may also be chemically synthesized) can be used to produce antibodies to detect menB proteins. Also, the host cells or extracts can be utilized for biological assays to isolate agonists or antagonists. In addition, with these sequences one can search to identify open reading frames and identify amino acid sequences. The proteins may also be used in immunogenic compositions, antigenic compositions and as vaccine components.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature e.g., Sambrook *Molecular Cloning; A Laboratory Manual, Second Edition* (1989); *DNA Cloning, Volumes I and ii* (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); *Transcription and Translation* (B.D. Hames & S.J. Higgins eds. 1984); *Animal Cell Culture* (R.I. Freshney ed. 1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide to Molecular Cloning* (1984); the *Methods in Enzymology* series (Academic Press, Inc.), especially volumes 154 & 155; *Gene Transfer Vectors for Mammalian Cells* (J.H. Miller and M.P. Calos eds. 1987, Cold Spring Harbor Laboratory); Mayer and Walker, eds. (1987), *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); Scopes, (1987) *Protein Purification: Principles and Practice*, Second Edition (Springer-Verlag, N.Y.), and *Handbook of Experimental Immunology, Volumes I-IV* (D.M. Weir and C.C. Blackwell eds 1986).

Standard abbreviations for nucleotides and amino acids are used in this specification.

All publications, patents, and patent applications cited herein are incorporated in full by reference.

Expression systems

The *Neisseria menB* nucleotide sequences can be expressed in a variety of different expression systems; for example those used with mammalian cells, plant cells, baculoviruses, bacteria, and yeast.

i. Mammalian Systems

Mammalian expression systems are known in the art. A mammalian promoter is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiating region, which is usually placed proximal to the 5' end of the coding sequence, and a TATA box, usually located 25-30 base pairs (bp) upstream of the transcription initiation site. The TATA box is thought to direct RNA polymerase II to begin RNA synthesis at the correct site. A mammalian promoter will also contain an upstream promoter element, usually located within 100 to 200 bp upstream of the TATA box. An upstream promoter element determines the rate at which transcription is initiated and can act in either orientation (Sambrook et al. (1989) "Expression of Cloned Genes in Mammalian Cells." In *Molecular Cloning: A Laboratory Manual*, 2nd ed.).

Mammalian viral genes are often highly expressed and have a broad host range; therefore sequences encoding mammalian viral genes provide particularly useful promoter sequences. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter (Ad MLP), and herpes simplex virus promoter. In addition, sequences derived from non-viral genes, such as the murine metallothionein gene, also provide useful promoter sequences. Expression may be either constitutive or regulated (inducible). Depending on the promoter selected, many promoters may be inducible using known substrates, such as the use of the mouse mammary tumor virus (MMTV) promoter with the glucocorticoid responsive element (GRE) that is induced by glucocorticoid in hormone-responsive transformed cells (see for example, U.S. Patent 5,783,681).

The presence of an enhancer element (enhancer), combined with the promoter elements described above, will usually increase expression levels. An enhancer is a

regulatory DNA sequence that can stimulate transcription up to 1000-fold when linked to homologous or heterologous promoters, with synthesis beginning at the normal RNA start site. Enhancers are also active when they are placed upstream or downstream from the transcription initiation site, in either normal or flipped orientation, or at a distance of more than 1000 nucleotides from the promoter (Maniatis et al. (1987) *Science* 236:1237; Alberts et al. (1989) *Molecular Biology of the Cell*, 2nd ed.). Enhancer elements derived from viruses may be particularly useful, because they usually have a broader host range. Examples include the SV40 early gene enhancer (Dijkema et al (1985) *EMBO J.* 4:761) and the enhancer/promoters derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus (Gorman et al. (1982b) *Proc. Natl. Acad. Sci.* 79:6777) and from human cytomegalovirus (Boshart et al. (1985) *Cell* 41:521). Additionally, some enhancers are regulatable and become active only in the presence of an inducer, such as a hormone or metal ion (Sassone-Corsi and Borelli (1986) *Trends Genet.* 2:215; Maniatis et al. (1987) *Science* 236:1237).

A DNA molecule may be expressed intracellularly in mammalian cells. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in mammalian cells. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The adenovirus tripartite leader is an example of a leader sequence that provides for secretion of a foreign protein in mammalian cells.

Usually, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. The 3' terminus of the mature mRNA is formed by site-specific post-transcriptional cleavage and polyadenylation (Birnstiel et al. (1985) *Cell* 41:349; Proudfoot and Whitelaw (1988) "Termination and 3' end processing of eukaryotic RNA. In *Transcription and splicing* (ed. B.D. Hames and D.M.

Glover); Proudfoot (1989) *Trends Biochem. Sci.* 14:105). These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator/polyadenylation signals include those derived from SV40 (Sambrook et al (1989) "Expression of cloned genes in cultured mammalian cells." In *Molecular Cloning: A Laboratory Manual*).

Usually, the above described components, comprising a promoter, polyadenylation signal, and transcription termination sequence are put together into expression constructs. Enhancers, introns with functional splice donor and acceptor sites, and leader sequences may also be included in an expression construct, if desired. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as mammalian cells or bacteria. Mammalian replication systems include those derived from animal viruses, which require trans-acting factors to replicate. For example, plasmids containing the replication systems of papovaviruses, such as SV40 (Gluzman (1981) *Cell* 23:175) or polyomavirus, replicate to extremely high copy number in the presence of the appropriate viral T antigen. Additional examples of mammalian replicons include those derived from bovine papillomavirus and Epstein-Barr virus. Additionally, the replicon may have two replication systems, thus allowing it to be maintained, for example, in mammalian cells for expression and in a prokaryotic host for cloning and amplification. Examples of such mammalian-bacteria shuttle vectors include pMT2 (Kaufman et al. (1989) *Mol. Cell. Biol.* 9:946) and pHEBO (Shimizu et al. (1986) *Mol. Cell. Biol.* 6:1074).

The transformation procedure used depends upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (e.g., Hep G2), and a number of other cell lines.

ii. Plant Cellular Expression Systems

There are many plant cell culture and whole plant genetic expression systems known in the art. Exemplary plant cellular genetic expression systems include those described in patents, such as: U.S. 5,693,506; US 5,659,122; and US 5,608,143. Additional examples of genetic expression in plant cell culture has been described by Zenk, *Phytochemistry* 30:3861-3863 (1991). Descriptions of plant protein signal peptides may be found in addition to the references described above in Vaulcombe et al., *Mol. Gen. Genet.* 209:33-40 (1987); Chandler et al., *Plant Molecular Biology* 3:407-418 (1984); Rogers, *J. Biol. Chem.* 260:3731-3738 (1985); Rothstein et al., *Gene* 55:353-356 (1987); Whittier et al., *Nucleic Acids Research* 15:2515-2535 (1987); Wirsal et al., *Molecular Microbiology* 3:3-14 (1989); Yu et al., *Gene* 122:247-253 (1992). A description of the regulation of plant gene expression by the phytohormone, gibberellic acid and secreted enzymes induced by gibberellic acid can be found in R.L. Jones and J. MacMillin, *Gibberellins*: in: *Advanced Plant Physiology*, Malcolm B. Wilkins, ed., 1984 Pitman Publishing Limited, London, pp. 21-52. References that describe other metabolically-regulated genes: Sheen, *Plant Cell*, 2:1027-1038(1990); Maas et al., *EMBO J.* 9:3447-3452 (1990); Benkel and Hickey, *Proc. Natl. Acad. Sci.* 84:1337-1339 (1987)

Typically, using techniques known in the art, a desired polynucleotide sequence is inserted into an expression cassette comprising genetic regulatory elements designed for operation in plants. The expression cassette is inserted into a desired expression vector with companion sequences upstream and downstream from the expression cassette suitable for expression in a plant host. The companion sequences will be of plasmid or viral origin and provide necessary characteristics to the vector to permit the vectors to move DNA from an original cloning host, such as bacteria, to the desired plant host. The basic bacterial/plant vector construct will preferably provide a broad host range prokaryote replication origin; a prokaryote selectable marker; and, for *Agrobacterium* transformations, T DNA sequences for *Agrobacterium*-mediated transfer to plant chromosomes. Where the heterologous gene is not readily amenable to detection, the construct will preferably also have a selectable marker gene suitable for determining if a plant cell has been transformed. A general review of suitable markers, for example for the members of the grass family, is found in Wilmink and Dons, 1993, *Plant Mol. Biol. Repr.* 11(2):165-185.

Sequences suitable for permitting integration of the heterologous sequence into the plant genome are also recommended. These might include transposon sequences and the like for homologous recombination as well as Ti sequences which permit random insertion of a heterologous expression cassette into a plant genome. Suitable prokaryote selectable markers include resistance toward antibiotics such as ampicillin or tetracycline. Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art.

The nucleic acid molecules of the subject invention may be included into an expression cassette for expression of the protein(s) of interest. Usually, there will be only one expression cassette, although two or more are feasible. The recombinant expression cassette will contain in addition to the heterologous protein encoding sequence the following elements, a promoter region, plant 5' untranslated sequences, initiation codon depending upon whether or not the structural gene comes equipped with one, and a transcription and translation termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette allow for easy insertion into a pre-existing vector.

A heterologous coding sequence may be for any protein relating to the present invention. The sequence encoding the protein of interest will encode a signal peptide which allows processing and translocation of the protein, as appropriate, and will usually lack any sequence which might result in the binding of the desired protein of the invention to a membrane. Since, for the most part, the transcriptional initiation region will be for a gene which is expressed and translocated during germination, by employing the signal peptide which provides for translocation, one may also provide for translocation of the protein of interest. In this way, the protein(s) of interest will be translocated from the cells in which they are expressed and may be efficiently harvested. Typically secretion in seeds are across the aleurone or scutellar epithelium layer into the endosperm of the seed. While it is not required that the protein be secreted from the cells in which the protein is produced, this facilitates the isolation and purification of the recombinant protein.

Since the ultimate expression of the desired gene product will be in a eucaryotic cell it is desirable to determine whether any portion of the cloned gene contains sequences which will be processed out as introns by the host's splicosome machinery. If so, site-directed mutagenesis of the "intron" region may be conducted to prevent losing a portion of the genetic message as a false intron code, Reed and Maniatis, *Cell* 41:95-105, 1985.

The vector can be microinjected directly into plant cells by use of micropipettes to mechanically transfer the recombinant DNA. Crossway, *Mol. Gen. Genet.*, 202:179-185, 1985. The genetic material may also be transferred into the plant cell by using polyethylene glycol, Krens, et al., *Nature*, 296, 72-74, 1982. Another method of introduction of nucleic acid segments is high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface, Klein, et al., *Nature*, 327, 70-73, 1987 and Knudsen and Muller, 1991, *Planta*, 185:330-336 teaching particle bombardment of barley endosperm to create transgenic barley. Yet another method of introduction would be fusion of protoplasts with other entities, either minicells, cells, lysosomes or other fusible lipid-surfaced bodies, Fraley, et al., *Proc. Natl. Acad. Sci. USA*, 79, 1859-1863, 1982.

The vector may also be introduced into the plant cells by electroporation. (Fromm et al., *Proc. Natl. Acad. Sci. USA* 82:5824, 1985). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the gene construct. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and form plant callus.

All plants from which protoplasts can be isolated and cultured to give whole regenerated plants can be transformed by the present invention so that whole plants are recovered which contain the transferred gene. It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to all major species of sugarcane, sugar beet, cotton, fruit and other trees, legumes and vegetables. Some suitable plants include, for example, species from the genera *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersion*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Cichorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Hererocallis*, *Nemesia*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Glycine*, *Lolium*, *Zea*, *Triticum*, *Sorghum*, and *Datura*.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts containing copies of the heterologous gene is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced from the protoplast suspension.

These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Shoots and roots normally develop simultaneously. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is fully reproducible and repeatable.

In some plant cell culture systems, the desired protein of the invention may be excreted or alternatively, the protein may be extracted from the whole plant. Where the desired protein of the invention is secreted into the medium, it may be collected. Alternatively, the embryos and embryoless-half seeds or other plant tissue may be mechanically disrupted to release any secreted protein between cells and tissues. The mixture may be suspended in a buffer solution to retrieve soluble proteins. Conventional protein isolation and purification methods will be then used to purify the recombinant protein. Parameters of time, temperature pH, oxygen, and volumes will be adjusted through routine methods to optimize expression and recovery of heterologous protein.

iii. Baculovirus Systems

The polynucleotide encoding the protein can also be inserted into a suitable insect expression vector, and is operably linked to the control elements within that vector. Vector construction employs techniques which are known in the art. Generally, the components of the expression system include a transfer vector, usually a bacterial plasmid, which contains both a fragment of the baculovirus genome, and a convenient restriction site for insertion of the heterologous gene or genes to be expressed; a wild type baculovirus with a sequence homologous to the baculovirus-specific fragment in the transfer vector (this allows for the homologous recombination of the heterologous gene in to the baculovirus genome); and appropriate insect host cells and growth media.

After inserting the DNA sequence encoding the protein into the transfer vector, the vector and the wild type viral genome are transfected into an insect host cell where the vector and viral genome are allowed to recombine. The packaged recombinant virus is expressed and recombinant plaques are identified and purified. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *inter alia*, Invitrogen, San Diego CA ("MaxBac" kit). These techniques are generally known to

those skilled in the art and fully described in Summers and Smith, *Texas Agricultural Experiment Station Bulletin No. 1555* (1987) (hereinafter "Summers and Smith").

Prior to inserting the DNA sequence encoding the protein into the baculovirus genome, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are usually assembled into an intermediate transplacement construct (transfer vector). This construct may contain a single gene and operably linked regulatory elements; multiple genes, each with its own set of operably linked regulatory elements; or multiple genes, regulated by the same set of regulatory elements. Intermediate transplacement constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as a bacterium. The replicon will have a replication system, thus allowing it to be maintained in a suitable host for cloning and amplification.

Currently, the most commonly used transfer vector for introducing foreign genes into AcNPV is pAc373. Many other vectors, known to those of skill in the art, have also been designed. These include, for example, pVL985 (which alters the polyhedrin start codon from ATG to ATT, and which introduces a BamHI cloning site 32 basepairs downstream from the ATT; see Luckow and Summers, *Virology* (1989) 17:31).

The plasmid usually also contains the polyhedrin polyadenylation signal (Miller et al. (1988) *Ann. Rev. Microbiol.*, 42:177) and a prokaryotic ampicillin-resistance (*amp*) gene and origin of replication for selection and propagation in *E. coli*.

Baculovirus transfer vectors usually contain a baculovirus promoter. A baculovirus promoter is any DNA sequence capable of binding a baculovirus RNA polymerase and initiating the downstream (5' to 3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A baculovirus transfer vector may also have a second domain called an enhancer, which, if present, is usually distal to the structural gene. Expression may be either regulated or constitutive.

Structural genes, abundantly transcribed at late times in a viral infection cycle, provide particularly useful promoter sequences. Examples include sequences derived from the gene encoding the viral polyhedron protein, Friesen et al., (1986) "The Regulation of Baculovirus Gene Expression," in: *The Molecular Biology of Baculoviruses* (ed. Walter Doerfler); EPO

Publ. Nos. 127 839 and 155 476; and the gene encoding the p10 protein, Vlcek et al., (1988), *J. Gen. Virol.* 69:765.

DNA encoding suitable signal sequences can be derived from genes for secreted insect or baculovirus proteins, such as the baculovirus polyhedrin gene (Carbonell et al. (1988) *Gene*, 73:409). Alternatively, since the signals for mammalian cell posttranslational modifications (such as signal peptide cleavage, proteolytic cleavage, and phosphorylation) appear to be recognized by insect cells, and the signals required for secretion and nuclear accumulation also appear to be conserved between the invertebrate cells and vertebrate cells, leaders of non-insect origin, such as those derived from genes encoding human (α -interferon, Maeda et al., (1985), *Nature* 315:592; human gastrin-releasing peptide, Lebacqz-Verheyden et al., (1988), *Molec. Cell. Biol.* 8:3129; human IL-2, Smith et al., (1985) *Proc. Nat'l Acad. Sci. USA*, 82:8404; mouse IL-3, (Miyajima et al., (1987) *Gene* 58:273; and human glucocerebrosidase, Martin et al. (1988) *DNA*, 7:99, can also be used to provide for secretion in insects.

A recombinant polypeptide or polyprotein may be expressed intracellularly or, if it is expressed with the proper regulatory sequences, it can be secreted. Good intracellular expression of nonfused foreign proteins usually requires heterologous genes that ideally have a short leader sequence containing suitable translation initiation signals preceding an ATG start signal. If desired, methionine at the N-terminus may be cleaved from the mature protein by *in vitro* incubation with cyanogen bromide.

Alternatively, recombinant polyproteins or proteins which are not naturally secreted can be secreted from the insect cell by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in insects. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the translocation of the protein into the endoplasmic reticulum.

After insertion of the DNA sequence and/or the gene encoding the expression product precursor of the protein, an insect cell host is co-transformed with the heterologous DNA of the transfer vector and the genomic DNA of wild type baculovirus -- usually by co-transfection. The promoter and transcription termination sequence of the construct will usually comprise a 2-5kb section of the baculovirus genome. Methods for introducing heterologous DNA into the desired site in the baculovirus virus are known in the art. (See

Summers and Smith *supra*; Ju et al. (1987); Smith et al., *Mol. Cell. Biol.* (1983) 3:2156; and Luckow and Summers (1989)). For example, the insertion can be into a gene such as the polyhedrin gene, by homologous double crossover recombination; insertion can also be into a restriction enzyme site engineered into the desired baculovirus gene. Miller et al., (1989), *Bioessays* 4:91. The DNA sequence, when cloned in place of the polyhedrin gene in the expression vector, is flanked both 5' and 3' by polyhedrin-specific sequences and is positioned downstream of the polyhedrin promoter.

The newly formed baculovirus expression vector is subsequently packaged into an infectious recombinant baculovirus. Homologous recombination occurs at low frequency (between about 1% and about 5%); thus, the majority of the virus produced after cotransfection is still wild-type virus. Therefore, a method is necessary to identify recombinant viruses. An advantage of the expression system is a visual screen allowing recombinant viruses to be distinguished. The polyhedrin protein, which is produced by the native virus, is produced at very high levels in the nuclei of infected cells at late times after viral infection. Accumulated polyhedrin protein forms occlusion bodies that also contain embedded particles. These occlusion bodies, up to 15 μm in size, are highly refractile, giving them a bright shiny appearance that is readily visualized under the light microscope. Cells infected with recombinant viruses lack occlusion bodies. To distinguish recombinant virus from wild-type virus, the transfection supernatant is plaqued onto a monolayer of insect cells by techniques known to those skilled in the art. Namely, the plaques are screened under the light microscope for the presence (indicative of wild-type virus) or absence (indicative of recombinant virus) of occlusion bodies. *Current Protocols in Microbiology* Vol. 2 (Ausubel et al. eds) at 16.8 (Supp. 10, 1990); Summers and Smith, *supra*; Miller et al. (1989).

Recombinant baculovirus expression vectors have been developed for infection into several insect cells. For example, recombinant baculoviruses have been developed for, *inter alia*: *Aedes aegypti*, *Autographa californica*, *Bombyx mori*, *Drosophila melanogaster*, *Spodoptera frugiperda*, and *Trichoplusia ni* (PCT Pub. No. WO 89/046699; Carbonell et al., (1985) *J. Virol.* 56:153; Wright (1986) *Nature* 321:718; Smith et al., (1983) *Mol. Cell. Biol.* 3:2156; and see generally, Fraser, et al. (1989) *In Vitro Cell. Dev. Biol.* 25:225).

Cells and cell culture media are commercially available for both direct and fusion expression of heterologous polypeptides in a baculovirus/expression system; cell culture technology is generally known to those skilled in the art. See, e.g., Summers and Smith *supra*.

The modified insect cells may then be grown in an appropriate nutrient medium, which allows for stable maintenance of the plasmid(s) present in the modified insect host. Where the expression product gene is under inducible control, the host may be grown to high density, and expression induced. Alternatively, where expression is constitutive, the product will be continuously expressed into the medium and the nutrient medium must be continuously circulated, while removing the product of interest and augmenting depleted nutrients. The product may be purified by such techniques as chromatography, e.g., HPLC, affinity chromatography, ion exchange chromatography, etc.; electrophoresis; density gradient centrifugation; solvent extraction, or the like. As appropriate, the product may be further purified, as required, so as to remove substantially any insect proteins which are also secreted in the medium or result from lysis of insect cells, so as to provide a product which is at least substantially free of host debris, e.g., proteins, lipids and polysaccharides.

In order to obtain protein expression, recombinant host cells derived from the transformants are incubated under conditions which allow expression of the recombinant protein encoding sequence. These conditions will vary, dependent upon the host cell selected. However, the conditions are readily ascertainable to those of ordinary skill in the art, based upon what is known in the art.

iv. Bacterial Systems

Bacterial expression techniques are known in the art. A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, that may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if present is usually proximal (5') to the RNA polymerase binding sequence. An example of a gene activator protein is the catabolite activator protein (CAP), which helps

initiate transcription of the lac operon in *Escherichia coli* (*E. coli*) (Raibaud *et al.* (1984) *Annu. Rev. Genet.* 18:173). Regulated expression may therefore be either positive or negative, thereby either enhancing or reducing transcription.

Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (*lac*) (Chang *et al.* (1977) *Nature* 198:1056), and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (*trp*) (Goeddel *et al.* (1980) *Nuc. Acids Res.* 8:4057; Yelverton *et al.* (1981) *Nucl. Acids Res.* 9:731; U.S. Patent 4,738,921; EPO Publ. Nos. 036 776 and 121 775). The beta-lactamase (*bla*) promoter system (Weissmann (1981) "The cloning of interferon and other mistakes." In *Interferon 3* (ed. I. Gresser)), bacteriophage lambda PL (Shimatake *et al.* (1981) *Nature* 292:128) and T5 (U.S. Patent 4,689,406) promoter systems also provide useful promoter sequences.

In addition, synthetic promoters which do not occur in nature also function as bacterial promoters. For example, transcription activation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequences of another bacterial or bacteriophage promoter, creating a synthetic hybrid promoter (U.S. Patent 4,551,433). For example, the *tac* promoter is a hybrid *trp-lac* promoter comprised of both *trp* promoter and *lac* operon sequences that is regulated by the *lac* repressor (Amann *et al.* (1983) *Gene* 25:167; de Boer *et al.* (1983) *Proc. Natl. Acad. Sci.* 80:21). Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system (Studier *et al.* (1986) *J. Mol. Biol.* 189:113; Tabor *et al.* (1985) *Proc Natl. Acad. Sci.* 82:1074). In addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EPO Publ. No. 267 851).

In addition to a functioning promoter sequence, an efficient ribosome binding site is also useful for the expression of foreign genes in prokaryotes. In *E. coli*, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon

(Shine *et al.* (1975) *Nature* 254:34). The SD sequence is thought to promote binding of mRNA to the ribosome by the pairing of bases between the SD sequence and the 3' end of *E. coli* 16S rRNA (Steitz *et al.* (1979) "Genetic signals and nucleotide sequences in messenger RNA." In *Biological Regulation and Development: Gene Expression* (ed. R.F. Goldberger)). To express eukaryotic genes and prokaryotic genes with weak ribosome-binding site, it is often necessary to optimize the distance between the SD sequence and the ATG of the eukaryotic gene (Sambrook *et al.* (1989) "Expression of cloned genes in *Escherichia coli*." In *Molecular Cloning: A Laboratory Manual*).

A DNA molecule may be expressed intracellularly. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide or by either *in vivo* or *in vitro* incubation with a bacterial methionine N-terminal peptidase (EPO Publ. No. 219 237).

Fusion proteins provide an alternative to direct expression. Usually, a DNA sequence encoding the N-terminal portion of an endogenous bacterial protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the bacteriophage lambda cell gene can be linked at the 5' terminus of a foreign gene and expressed in bacteria. The resulting fusion protein preferably retains a site for a processing enzyme (factor Xa) to cleave the bacteriophage protein from the foreign gene (Nagai *et al.* (1984) *Nature* 309:810). Fusion proteins can also be made with sequences from the *lacZ* (Jia *et al.* (1987) *Gene* 60:197), *trpE* (Allen *et al.* (1987) *J. Biotechnol.* 5:93; Makoff *et al.* (1989) *J. Gen. Microbiol.* 135:11), and *Chey* (EPO Publ. No. 324 647) genes. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin specific processing-protease) to cleave the ubiquitin from the foreign protein. Through this method, native foreign protein can be isolated (Miller *et al.* (1989) *Bio/Technology* 7:698).

Alternatively, foreign proteins can also be secreted from the cell by creating chimeric DNA molecules that encode a fusion protein comprised of a signal peptide sequence fragment that provides for secretion of the foreign protein in bacteria (U.S. Patent 4,336,336). The

signal sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). Preferably there are processing sites, which can be cleaved either *in vivo* or *in vitro* encoded between the signal peptide fragment and the foreign gene.

DNA encoding suitable signal sequences can be derived from genes for secreted bacterial proteins, such as the *E. coli* outer membrane protein gene (*ompA*) (Masui *et al.* (1983), in: *Experimental Manipulation of Gene Expression*; Ghayeb *et al.* (1984) *EMBO J.* 3:2437) and the *E. coli* alkaline phosphatase signal sequence (*phoA*) (Oka *et al.* (1985) *Proc. Natl. Acad. Sci.* 82:7212). As an additional example, the signal sequence of the alpha-amylase gene from various *Bacillus* strains can be used to secrete heterologous proteins from *B. subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. No. 244 042).

Usually, transcription termination sequences recognized by bacteria are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Transcription termination sequences frequently include DNA sequences of about 50 nucleotides capable of forming stem loop structures that aid in terminating transcription. Examples include transcription termination sequences derived from genes with strong promoters, such as the *trp* gene in *E. coli* as well as other biosynthetic genes.

Usually, the above described components, comprising a promoter, signal sequence (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as bacteria. The replicon will have a replication system, thus allowing it to be maintained in a prokaryotic host either for expression or for cloning and amplification. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably contain at least about 10, and more preferably at least about 20 plasmids. Either a high or low copy number

vector may be selected, depending upon the effect of the vector and the foreign protein on the host.

Alternatively, the expression constructs can be integrated into the bacterial genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to the bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various *Bacillus* strains integrate into the *Bacillus* chromosome (EPO Publ. No. 127 328). Integrating vectors may also be comprised of bacteriophage or transposon sequences.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of bacterial strains that have been transformed. Selectable markers can be expressed in the bacterial host and may include genes which render bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin (neomycin), and tetracycline (Davies *et al.* (1978) *Annu. Rev. Microbiol.* 32:469). Selectable markers may also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways.

Alternatively, some of the above described components can be put together in transformation vectors. Transformation vectors are usually comprised of a selectable market that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extra-chromosomal replicons or integrating vectors, have been developed for transformation into many bacteria. For example, expression vectors have been developed for, *inter alia*, the following bacteria: *Bacillus subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541), *Escherichia coli* (Shimatake *et al.* (1981) *Nature* 292:128; Amann *et al.* (1985) *Gene* 40:183; Studier *et al.* (1986) *J. Mol. Biol.* 189:113; EPO Publ. Nos. 036 776, 136 829 and 136 907), *Streptococcus cremoris* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655); *Streptococcus lividans* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655), *Streptomyces lividans* (U.S. Patent 4,745,056).

Methods of introducing exogenous DNA into bacterial hosts are well-known in the art, and usually include either the transformation of bacteria treated with CaCl_2 or other agents, such as divalent cations and DMSO. DNA can also be introduced into bacterial cells by

electroporation. Transformation procedures usually vary with the bacterial species to be transformed. (See e.g., use of *Bacillus*: Masson *et al.* (1989) *FEMS Microbiol. Lett.* 60:273; Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541; use of *Campylobacter*: Miller *et al.* (1988) *Proc. Natl. Acad. Sci.* 85:856; and Wang *et al.* (1990) *J. Bacteriol.* 172:949; use of *Escherichia coli*: Cohen *et al.* (1973) *Proc. Natl. Acad. Sci.* 69:2110; Dower *et al.* (1988) *Nucleic Acids Res.* 16:6127; Kushner (1978) "An improved method for transformation of *Escherichia coli* with ColE1-derived plasmids. In *Genetic Engineering: Proceedings of the International Symposium on Genetic Engineering* (eds. H.W. Boyer and S. Nicosia); Mandel *et al.* (1970) *J. Mol. Biol.* 53:159; Taketo (1988) *Biochim. Biophys. Acta* 949:318; use of *Lactobacillus*: Chassy *et al.* (1987) *FEMS Microbiol. Lett.* 44:173; use of *Pseudomonas*: Fiedler *et al.* (1988) *Anal. Biochem* 170:38; use of *Staphylococcus*: Augustin *et al.* (1990) *FEMS Microbiol. Lett.* 66:203; use of *Streptococcus*: Barany *et al.* (1980) *J. Bacteriol.* 144:698; Harlander (1987) "Transformation of *Streptococcus lactis* by electroporation, in: *Streptococcal Genetics* (ed. J. Ferretti and R. Curtiss III); Perry *et al.* (1981) *Infect. Immun.* 32:1295; Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655; Somkuti *et al.* (1987) *Proc. 4th Eur. Cong. Biotechnology* 1:412.

v. Yeast Expression

Yeast expression systems are also known to one of ordinary skill in the art. A yeast promoter is any DNA sequence capable of binding yeast RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site (the "TATA Box") and a transcription initiation site. A yeast promoter may also have a second domain called an upstream activator sequence (UAS), which, if present, is usually distal to the structural gene. The UAS permits regulated (inducible) expression. Constitutive expression occurs in the absence of a UAS. Regulated expression may be either positive or negative, thereby either enhancing or reducing transcription.

Yeast is a fermenting organism with an active metabolic pathway, therefore sequences encoding enzymes in the metabolic pathway provide particularly useful promoter sequences.

Examples include alcohol dehydrogenase (ADH) (EPO Publ. No. 284 044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EPO Publ. No. 329 203). The yeast *PHO5* gene, encoding acid phosphatase, also provides useful promoter sequences (Myanohara *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:1).

In addition, synthetic promoters which do not occur in nature also function as yeast promoters. For example, UAS sequences of one yeast promoter may be joined with the transcription activation region of another yeast promoter, creating a synthetic hybrid promoter. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (U.S. Patent Nos. 4,876,197 and 4,880,734). Other examples of hybrid promoters include promoters which consist of the regulatory sequences of either the *ADH2*, *GAL4*, *GAL10*, OR *PHO5* genes, combined with the transcriptional activation region of a glycolytic enzyme gene such as GAP or PyK (EPO Publ. No. 164 556). Furthermore, a yeast promoter can include naturally occurring promoters of non-yeast origin that have the ability to bind yeast RNA polymerase and initiate transcription. Examples of such promoters include, *inter alia*, (Cohen *et al.* (1980) *Proc. Natl. Acad. Sci. USA* 77:1078; Henikoff *et al.* (1981) *Nature* 283:835; Hollenberg *et al.* (1981) *Curr. Topics Microbiol. Immunol.* 96:119; Hollenberg *et al.* (1979) "The Expression of Bacterial Antibiotic Resistance Genes in the Yeast *Saccharomyces cerevisiae*," in: *Plasmids of Medical, Environmental and Commercial Importance* (eds. K.N. Timmis and A. Puhler); Mercerau-Puigalon *et al.* (1980) *Gene* 11:163; Panthier *et al.* (1980) *Curr. Genet.* 2:109;).

A DNA molecule may be expressed intracellularly in yeast. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Fusion proteins provide an alternative for yeast expression systems, as well as in mammalian, plant, baculovirus, and bacterial expression systems. Usually, a DNA sequence encoding the N-terminal portion of an endogenous yeast protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the yeast or human

superoxide dismutase (SOD) gene, can be linked at the 5' terminus of a foreign gene and expressed in yeast. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. See e.g., EPO Publ. No. 196056. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin-specific processing protease) to cleave the ubiquitin from the foreign protein. Through this method, therefore, native foreign protein can be isolated (e.g., WO88/024066).

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provide for secretion in yeast of the foreign protein. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell.

DNA encoding suitable signal sequences can be derived from genes for secreted yeast proteins, such as the yeast invertase gene (EPO Publ. No. 012 873; JPO Publ. No. 62:096,086) and the A-factor gene (U.S. Patent 4,588,684). Alternatively, leaders of non-yeast origin, such as an interferon leader, exist that also provide for secretion in yeast (EPO Publ. No. 060 057).

A preferred class of secretion leaders are those that employ a fragment of the yeast alpha-factor gene, which contains both a "pre" signal sequence, and a "pro" region. The types of alpha-factor fragments that can be employed include the full-length pre-pro alpha factor leader (about 83 amino acid residues) as well as truncated alpha-factor leaders (usually about 25 to about 50 amino acid residues) (U.S. Patent Nos. 4,546,083 and 4,870,008; EPO Publ. No. 324 274). Additional leaders employing an alpha-factor leader fragment that provides for secretion include hybrid alpha-factor leaders made with a presequence of a first yeast, but a pro-region from a second yeast alphafactor. (See e.g., PCT Publ. No. WO 89/02463.)

Usually, transcription termination sequences recognized by yeast are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator

sequence and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes.

Usually, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for example, in yeast for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEp24 (Botstein *et al.* (1979) *Gene* 8:17-24), pCl/1 (Brake *et al.* (1984) *Proc. Natl. Acad. Sci USA* 81:4642-4646), and YRp17 (Stinchcomb *et al.* (1982) *J. Mol. Biol.* 158:157). In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably have at least about 10, and more preferably at least about 20. Either a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host. See e.g., Brake *et al.*, *supra*.

Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to a yeast chromosome that allows the vector to integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome (Orr-Weaver *et al.* (1983) *Methods in Enzymol.* 101:228-245). An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver *et al.*, *supra*. One or more expression construct may integrate, possibly affecting levels of recombinant protein produced (Rine *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:6750). The chromosomal sequences included in the vector can occur either as a single segment in the vector, which results in the integration of the entire vector, or two segments homologous to adjacent segments in the chromosome and flanking the expression construct in the vector, which can result in the stable integration of only the expression construct.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of yeast strains that have been transformed. Selectable markers may include biosynthetic genes that can be expressed in the yeast host, such as *ADE2*, *HIS4*, *LEU2*, *TRP1*, and *ALG7*, and the G418 resistance gene, which confer resistance in yeast cells to tunicamycin and G418, respectively. In addition, a suitable selectable marker may also provide yeast with the ability to grow in the presence of toxic compounds, such as metal. For example, the presence of *CUP1* allows yeast to grow in the presence of copper ions (Butt *et al.* (1987) *Microbiol. Rev.* 51:351).

Alternatively, some of the above described components can be put together into transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extrachromosomal replicons or integrating vectors, have been developed for transformation into many yeasts. For example, expression vectors and methods of introducing exogenous DNA into yeast hosts have been developed for, *inter alia*, the following yeasts: *Candida albicans* (Kurtz, *et al.* (1986) *Mol. Cell. Biol.* 6:142); *Candida maltosa* (Kunze, *et al.* (1985) *J. Basic Microbiol.* 25:141); *Hansenula polymorpha* (Gleeson, *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302); *Kluyveromyces fragilis* (Das, *et al.* (1984) *J. Bacteriol.* 158:1165); *Kluyveromyces lactis* (De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:737; Van den Berg *et al.* (1990) *Bio/Technology* 8:135); *Pichia guillerimondii* (Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141); *Pichia pastoris* (Cregg, *et al.* (1985) *Mol. Cell. Biol.* 5:3376; U.S. Patent Nos. 4,837,148 and 4,929,555); *Saccharomyces cerevisiae* (Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163); *Schizosaccharomyces pombe* (Beach and Nurse (1981) *Nature* 300:706); and *Yarrowia lipolytica* (Davidow, *et al.* (1985) *Curr. Genet.* 10:380471 Gaillardin, *et al.* (1985) *Curr. Genet.* 10:49).

Methods of introducing exogenous DNA into yeast hosts are well-known in the art, and usually include either the transformation of spheroplasts or of intact yeast cells treated with alkali cations. Transformation procedures usually vary with the yeast species to be transformed. See e.g., [Kurtz *et al.* (1986) *Mol. Cell. Biol.* 6:142; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; *Candida*]; [Gleeson *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302; *Hansenula*]; [Das *et al.* (1984) *J.*

Bacteriol. 158:1165; De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:1165; Van den Berg *et al.* (1990) *Bio/Technology* 8:135; Kluyveromyces]; [Cregg *et al.* (1985) *Mol. Cell. Biol.* 5:3376; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; U.S. Patent Nos. 4,837,148 and 4,929,555; *Pichia*]; [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163 *Saccharomyces*]; [Beach and Nurse (1981) *Nature* 300:706; *Schizosaccharomyces*]; [Davidow *et al.* (1985) *Curr. Genet.* 10:39; Gaillardin *et al.* (1985) *Curr. Genet.* 10:49; *Yarrowia*].

Definitions

A composition containing X is "substantially free of" Y when at least 85% by weight of the total X+Y in the composition is X. Preferably, X comprises at least about 90% by weight of the total of X+Y in the composition, more preferably at least about 95% or even 99% by weight.

A "conserved" *Neisseria* amino acid fragment or protein is one that is present in a particular *Neisseria* protein in at least x% of *Neisseria*. The value of x may be 50% or more, e.g., 66%, 75%, 80%, 90%, 95% or even 100% (i.e. the amino acid is found in the protein in question in all *Neisseria*). In order to determine whether an amino acid is "conserved" in a particular *Neisseria* protein, it is necessary to compare that amino acid residue in the sequences of the protein in question from a plurality of different *Neisseria* (a reference population). The reference population may include a number of different *Neisseria* species or may include a single species. The reference population may include a number of different serogroups of a particular species or a single serogroup. A preferred reference population consists of the 5 most common *Neisseria* strains.

The term "heterologous" refers to two biological components that are not found together in nature. The components may be host cells, genes, or regulatory regions, such as promoters. Although the heterologous components are not found together in nature, they can function together, as when a promoter heterologous to a gene is operably linked to the gene. Another example is where a *Neisseria* sequence is heterologous to a mouse host cell.

"Epitope" means antigenic determinant, and may elicit a cellular and/or humoral response.

Conditions for "high stringency" are 65 degrees C in 0.1 xSSC 0.5% SDS solution.

An "origin of replication" is a polynucleotide sequence that initiates and regulates replication of polynucleotides, such as an expression vector. The origin of replication behaves as an autonomous unit of polynucleotide replication within a cell, capable of replication under its own control. An origin of replication may be needed for a vector to replicate in a particular host cell. With certain origins of replication, an expression vector can be reproduced at a high copy number in the presence of the appropriate proteins within the cell. Examples of origins are the autonomously replicating sequences, which are effective in yeast; and the viral T-antigen, effective in COS-7 cells.

A "mutant" sequence is defined as a DNA, RNA or amino acid sequence differing from but having homology with the native or disclosed sequence. Depending on the particular sequence, the degree of homology (sequence identity) between the native or disclosed sequence and the mutant sequence is preferably greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) which is calculated as described above. As used herein, an "allelic variant" of a nucleic acid molecule, or region, for which nucleic acid sequence is provided herein is a nucleic acid molecule, or region, that occurs at essentially the same locus in the genome of another or second isolate, and that, due to natural variation caused by, for example, mutation or recombination, has a similar but not identical nucleic acid sequence. A coding region allelic variant typically encodes a protein having similar activity to that of the protein encoded by the gene to which it is being compared. An allelic variant can also comprise an alteration in the 5' or 3' untranslated regions of the gene, such as in regulatory control regions. (see, for example, U.S. Patent 5,753,235).

Antibodies

As used herein, the term "antibody" refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An "antibody combining site" is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows a binding of the antibody with the antigen. "Antibody" includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanized antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies.

Antibodies against the proteins of the invention are useful for affinity chromatography, immunoassays, and distinguishing/identifying *Neisseria menB* proteins.

Antibodies elicited against the proteins of the present invention bind to antigenic polypeptides or proteins or protein fragments that are present and specifically associated with strains of *Neisseria meningitidis* menB. In some instances, these antigens may be associated with specific strains, such as those antigens specific for the menB strains. The antibodies of the invention may be immobilized to a matrix and utilized in an immunoassay or on an affinity chromatography column, to enable the detection and/or separation of polypeptides, proteins or protein fragments or cells comprising such polypeptides, proteins or protein fragments. Alternatively, such polypeptides, proteins or protein fragments may be immobilized so as to detect antibodies bindably specific thereto.

Antibodies to the proteins of the invention, both polyclonal and monoclonal, may be prepared by conventional methods. In general, the protein is first used to immunize a suitable animal, preferably a mouse, rat, rabbit or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 50-200 µg/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by *in vitro* immunization using methods known in the art, which for the purposes of this invention is considered equivalent to *in vivo* immunization. Polyclonal antisera is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25°C for one hour, followed by incubating at 4°C for 2-18 hours. The serum is recovered by centrifugation (e.g., 1,000g for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.

Monoclonal antibodies are prepared using the standard method of Kohler & Milstein (*Nature* (1975) 256:495-96), or a modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells may be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate or well coated with the protein antigen. B-cells that express membrane-bound immunoglobulin specific for the antigen bind to the plate, and

are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective medium (e.g., hypoxanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are assayed for the production of antibodies which bind specifically to the immunizing antigen (and which do not bind to unrelated antigens). The selected MAb-secreting hybridomas are then cultured either *in vitro* (e.g., in tissue culture bottles or hollow fiber reactors), or *in vivo* (as ascites in mice).

If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques. Suitable labels include fluorophores, chromophores, radioactive atoms (particularly ^{32}P and ^{125}I), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to convert 3,3',5,5'-tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific therefor. Other specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct classes, as the same label may serve in several different modes. For example, ^{125}I may serve as a radioactive label or as an electron-dense reagent. HRP may serve as enzyme or as antigen for a MAb. Further, one may combine various labels for desired effect. For example, MAbs and avidin also require labels in the practice of this invention: thus, one might label a MAb with biotin, and detect its presence with avidin labeled with ^{125}I , or with an anti-biotin MAb labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

Antigens, immunogens, polypeptides, proteins or protein fragments of the present invention elicit formation of specific binding partner antibodies. These antigens, immunogens, polypeptides, proteins or protein fragments of the present invention comprise immunogenic compositions of the present invention. Such immunogenic compositions may further comprise or include adjuvants, carriers, or other compositions that promote or enhance

or stabilize the antigens, polypeptides, proteins or protein fragments of the present invention. Such adjuvants and carriers will be readily apparent to those of ordinary skill in the art.

Pharmaceutical Compositions

Pharmaceutical compositions can comprise (include) either polypeptides, antibodies, or nucleic acid of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature, when given to a patient that is febrile. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgment of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of

organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

Delivery Methods

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal and transcutaneous applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Vaccines

Vaccines according to the invention may either be prophylactic (i.e., to prevent infection) or therapeutic (i.e., to treat disease after infection).

Such vaccines comprise immunizing antigen(s) or immunogen(s), immunogenic polypeptide, protein(s) or protein fragments, or nucleic acids (e.g., ribonucleic acid or deoxyribonucleic acid), usually in combination with "pharmaceutically acceptable carriers," which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or

liposomes), and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the immunogen or antigen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, etc. pathogens.

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59 (PCT Publ. No. WO 90/14837), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalane, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) RibiTM adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (DetoxTM); (3) saponin adjuvants, such as StimulonTM (Cambridge Bioscience, Worcester, MA) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (e.g., IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (e.g., gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc; (6) detoxified mutants of a bacterial ADP-ribosylating toxin such as a cholera toxin (CT), a pertussis toxin (PT), or an *E. coli* heat-labile toxin (LT), particularly LT-K63, LT-R72, CT-S109, PT-K9/G129; see, e.g., WO 93/13302 and WO 92/19265; and (7) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59 are preferred.

As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-*sn*-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), etc.

The vaccine compositions comprising immunogenic compositions (e.g., which may include the antigen, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Alternatively, vaccine compositions comprising immunogenic compositions may comprise an antigen, polypeptide, protein, protein fragment or nucleic acid in a pharmaceutically acceptable carrier.

More specifically, vaccines comprising immunogenic compositions comprise an immunologically effective amount of the immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (e.g., nonhuman primate, primate, *etc.*), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

Typically, the vaccine compositions or immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

The immunogenic compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal and transcutaneous applications. Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.

As an alternative to protein-based vaccines, DNA vaccination may be employed (e.g., Robinson & Torres (1997) *Seminars in Immunology* 9:271-283; Donnelly *et al.* (1997) *Annu Rev Immunol* 15:617-648).

Gene Delivery Vehicles

Gene therapy vehicles for delivery of constructs, including a coding sequence of a therapeutic of the invention, to be delivered to the mammal for expression in the mammal, can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches in *in vivo* or *ex vivo* modality. Expression of such coding sequence can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence *in vivo* can be either constitutive or regulated.

The invention includes gene delivery vehicles capable of expressing the contemplated nucleic acid sequences. The gene delivery vehicle is preferably a viral vector and, more preferably, a retroviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vector. The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, or togavirus viral vector. See generally, Jolly (1994) *Cancer Gene Therapy* 1:51-64; Kimura (1994) *Human Gene Therapy* 5:845-852; Connelly (1995) *Human Gene Therapy* 6:185-193; and Kaplitt (1994) *Nature Genetics* 6:148-153.

Retroviral vectors are well known in the art, including B, C and D type retroviruses, xenotropic retroviruses (for example, NZB-X1, NZB-X2 and NZB9-1 (see O'Neill (1985) *J. Virol.* 53:160) polytropic retroviruses e.g., MCF and MCF-MLV (see Kelly (1983) *J. Virol.* 45:291), spumaviruses and lentiviruses. See RNA Tumor Viruses, Second Edition, Cold Spring Harbor Laboratory, 1985.

Portions of the retroviral gene therapy vector may be derived from different retroviruses. For example, retrovector LTRs may be derived from a Murine Sarcoma Virus, a tRNA binding site from a Rous Sarcoma Virus, a packaging signal from a Murine Leukemia Virus, and an origin of second strand synthesis from an Avian Leukosis Virus.

These recombinant retroviral vectors may be used to generate transduction competent retroviral vector particles by introducing them into appropriate packaging cell lines (see US patent 5,591,624). Retrovirus vectors can be constructed for site-specific integration into host cell DNA by incorporation of a chimeric integrase enzyme into the retroviral particle (see WO96/37626). It is preferable that the recombinant viral vector is a replication defective recombinant virus.

Packaging cell lines suitable for use with the above-described retrovirus vectors are well known in the art, are readily prepared (see WO95/30763 and WO92/05266), and can be used to create producer cell lines (also termed vector cell lines or "VCLs") for the production of recombinant vector particles. Preferably, the packaging cell lines are made from human parent cells (e.g., HT1080 cells) or mink parent cell lines, which eliminates inactivation in human serum.

Preferred retroviruses for the construction of retroviral gene therapy vectors include Avian Leukosis Virus, Bovine Leukemia Virus, Murine Leukemia Virus, Mink-Cell Focus-Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis Virus and Rous Sarcoma Virus. Particularly preferred Murine Leukemia Viruses include 4070A and 1504A (Hartley and Rowe (1976) *J Virol* 19:19-25), Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi, Gross (ATCC No. VR-590), Kirsten, Harvey Sarcoma Virus and Rauscher (ATCC No. VR-998) and Moloney Murine Leukemia Virus (ATCC No. VR-190). Such retroviruses may be obtained from depositories or collections such as the American Type Culture Collection ("ATCC") in Rockville, Maryland or isolated from known sources using commonly available techniques.

Exemplary known retroviral gene therapy vectors employable in this invention include those described in patent applications GB2200651, EP0415731, EP0345242, EP0334301, WO89/02468; WO89/05349, WO89/09271, WO90/02806, WO90/07936, WO94/03622, WO93/25698, WO93/25234, WO93/11230, WO93/10218, WO91/02805, WO91/02825, WO95/07994, US 5,219,740, US 4,405,712, US 4,861,719, US 4,980,289, US 4,777,127, US 5,591,624. See also Vile (1993) *Cancer Res* 53:3860-3864; Vile (1993) *Cancer Res* 53:962-967; Ram (1993) *Cancer Res* 53 (1993) 83-88; Takamiya (1992) *J Neurosci Res* 33:493-503; Baba (1993) *J Neurosurg* 79:729-735; Mann (1983) *Cell* 33:153; Cane (1984) *Proc Natl Acad Sci* 81:6349; and Miller (1990) *Human Gene Therapy* 1.

Human adenoviral gene therapy vectors are also known in the art and employable in this invention. See, for example, Berkner (1988) *Biotechniques* 6:616 and Rosenfeld (1991) *Science* 252:431, and WO93/07283, WO93/06223, and WO93/07282. Exemplary known adenoviral gene therapy vectors employable in this invention include those described in the above referenced documents and in WO94/12649, WO93/03769, WO93/19191, WO94/28938, WO95/11984, WO95/00655, WO95/27071, WO95/29993, WO95/34671, WO96/05320, WO94/08026, WO94/11506, WO93/06223, WO94/24299, WO95/14102,

WO95/24297, WO95/02697, WO94/28152, WO94/24299, WO95/09241, WO95/25807, WO95/05835, WO94/18922 and WO95/09654. Alternatively, administration of DNA linked to killed adenovirus as described in Curiel (1992) *Hum. Gene Ther.* 3:147-154 may be employed. The gene delivery vehicles of the invention also include adenovirus associated virus (AAV) vectors. Leading and preferred examples of such vectors for use in this invention are the AAV-2 based vectors disclosed in Srivastava, WO93/09239. Most preferred AAV vectors comprise the two AAV inverted terminal repeats in which the native D-sequences are modified by substitution of nucleotides, such that at least 5 native nucleotides and up to 18 native nucleotides, preferably at least 10 native nucleotides up to 18 native nucleotides, most preferably 10 native nucleotides are retained and the remaining nucleotides of the D-sequence are deleted or replaced with non-native nucleotides. The native D-sequences of the AAV inverted terminal repeats are sequences of 20 consecutive nucleotides in each AAV inverted terminal repeat (i.e., there is one sequence at each end) which are not involved in HP formation. The non-native replacement nucleotide may be any nucleotide other than the nucleotide found in the native D-sequence in the same position. Other employable exemplary AAV vectors are pWP-19, pWN-1, both of which are disclosed in Nahreini (1993) *Gene* 124:257-262. Another example of such an AAV vector is psub201 (see Samulski (1987) *J. Virol.* 61:3096). Another exemplary AAV vector is the Double-D ITR vector. Construction of the Double-D ITR vector is disclosed in US Patent 5,478,745. Still other vectors are those disclosed in Carter US Patent 4,797,368 and Muzyczka US Patent 5,139,941, Chartejee US Patent 5,474,935, and Kotin WO94/288157. Yet a further example of an AAV vector employable in this invention is SSV9AFABTKneo, which contains the AFP enhancer and albumin promoter and directs expression predominantly in the liver. Its structure and construction are disclosed in Su (1996) *Human Gene Therapy* 7:463-470. Additional AAV gene therapy vectors are described in US 5,354,678, US 5,173,414, US 5,139,941, and US 5,252,479.

The gene therapy vectors comprising sequences of the invention also include herpes vectors. Leading and preferred examples are herpes simplex virus vectors containing a sequence encoding a thymidine kinase polypeptide such as those disclosed in US 5,288,641 and EP0176170 (Roizman). Additional exemplary herpes simplex virus vectors include HFEM/ICP6-LacZ disclosed in WO95/04139 (Wistar Institute), pHSVlac described in Geller (1988) *Science* 241:1667-1669 and in WO90/09441 and WO92/07945, HSV Us3::pgC-lacZ

described in Fink (1992) *Human Gene Therapy* 3:11-19 and HSV 7134, 2 RH 105 and GAL4 described in EP 0453242 (Breakefield), and those deposited with the ATCC as accession numbers ATCC VR-977 and ATCC VR-260.

Also contemplated are alpha virus gene therapy vectors that can be employed in this invention. Preferred alpha virus vectors are Sindbis viruses vectors. Togaviruses, Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC VR-1250; ATCC VR-1249; ATCC VR-532), and those described in US patents 5,091,309, 5,217,879, and WO92/10578. More particularly, those alpha virus vectors described in U.S. Serial No. 08/405,627, filed March 15, 1995, WO94/21792, WO92/10578, WO95/07994, US 5,091,309 and US 5,217,879 are employable. Such alpha viruses may be obtained from depositories or collections such as the ATCC in Rockville, Maryland or isolated from known sources using commonly available techniques. Preferably, alphavirus vectors with reduced cytotoxicity are used (see USSN 08/679640).

DNA vector systems such as eukaryotic layered expression systems are also useful for expressing the nucleic acids of the invention. See WO95/07994 for a detailed description of eukaryotic layered expression systems. Preferably, the eukaryotic layered expression systems of the invention are derived from alphavirus vectors and most preferably from Sindbis viral vectors.

Other viral vectors suitable for use in the present invention include those derived from poliovirus, for example ATCC VR-58 and those described in Evans, *Nature* 339 (1989) 385 and Sabin (1973) *J. Biol. Standardization* 1:115; rhinovirus, for example ATCC VR-1110 and those described in Arnold (1990) *J Cell Biochem* L401; pox viruses such as canary pox virus or vaccinia virus, for example ATCC VR-111 and ATCC VR-2010 and those described in Fisher-Hoch (1989) *Proc Natl Acad Sci* 86:317; Flexner (1989) *Ann NY Acad Sci* 569:86, Flexner (1990) *Vaccine* 8:17; in US 4,603,112 and US 4,769,330 and WO89/01973; SV40 virus, for example ATCC VR-305 and those described in Mulligan (1979) *Nature* 277:108 and Madzak (1992) *J Gen Virol* 73:1533; influenza virus, for example ATCC VR-797 and recombinant influenza viruses made employing reverse genetics techniques as described in US 5,166,057 and in Enami (1990) *Proc Natl Acad Sci* 87:3802-3805; Enami & Palese (1991) *J Virol* 65:2711-2713 and Luytjes (1989) *Cell* 59:110, (see also McMichael (1983) *NEJ Med* 309:13, and Yap (1978) *Nature* 273:238 and *Nature* (1979) 277:108); human

immunodeficiency virus as described in EP-0386882 and in Buchschacher (1992) *J. Virol.* 66:2731; measles virus, for example ATCC VR-67 and VR-1247 and those described in EP-0440219; Aura virus, for example ATCC VR-368; Bebaru virus, for example ATCC VR-600 and ATCC VR-1240; Cabassou virus, for example ATCC VR-922; Chikungunya virus, for example ATCC VR-64 and ATCC VR-1241; Fort Morgan Virus, for example ATCC VR-924; Getah virus, for example ATCC VR-369 and ATCC VR-1243; Kyzylagach virus, for example ATCC VR-927; Mayaro virus, for example ATCC VR-66; Mucambo virus, for example ATCC VR-580 and ATCC VR-1244; Ndumu virus, for example ATCC VR-371; Pixuna virus, for example ATCC VR-372 and ATCC VR-1245; Tonate virus, for example ATCC VR-925; Trinita virus, for example ATCC VR-469; Una virus, for example ATCC VR-374; Whataroa virus, for example ATCC VR-926; Y-62-33 virus, for example ATCC VR-375; O'Nyong virus, Eastern encephalitis virus, for example ATCC VR-65 and ATCC VR-1242; Western encephalitis virus, for example ATCC VR-70, ATCC VR-1251, ATCC VR-622 and ATCC VR-1252; and coronavirus, for example ATCC VR-740 and those described in Hamre (1966) *Proc Soc Exp Biol Med* 121:190.

Delivery of the compositions of this invention into cells is not limited to the above mentioned viral vectors. Other delivery methods and media may be employed such as, for example, nucleic acid expression vectors, polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example see US Serial No. 08/366,787, filed December 30, 1994 and Curiel (1992) *Hum Gene Ther* 3:147-154 ligand linked DNA, for example see Wu (1989) *J Biol Chem* 264:16985-16987, eucaryotic cell delivery vehicles cells, for example see US Serial No.08/240,030, filed May 9, 1994, and US Serial No. 08/404,796, deposition of photopolymerized hydrogel materials, hand-held gene transfer particle gun, as described in US Patent 5,149,655, ionizing radiation as described in US5,206,152 and in WO92/11033, nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip (1994) *Mol Cell Biol* 14:2411-2418 and in Woffendin (1994) *Proc Natl Acad Sci* 91:1581-1585.

Particle mediated gene transfer may be employed, for example see US Serial No. 60/023,867. Briefly, the sequence can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, as described in Wu &

Wu (1987) *J. Biol. Chem.* 262:4429-4432, insulin as described in Hucked (1990) *Biochem Pharmacol* 40:253-263, galactose as described in Plank (1992) *Bioconjugate Chem* 3:533-539, lactose or transferrin.

Naked DNA may also be employed to transform a host cell. Exemplary naked DNA introduction methods are described in WO 90/11092 and US 5,580,859. Uptake efficiency may be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm.

Liposomes that can act as gene delivery vehicles are described in U.S. 5,422,120, WO95/13796, WO94/23697, WO91/14445 and EP-524,968. As described in USSN. 60/023,867, on non-viral delivery, the nucleic acid sequences encoding a polypeptide can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then be incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, insulin, galactose, lactose, or transferrin. Other delivery systems include the use of liposomes to encapsulate DNA comprising the gene under the control of a variety of tissue-specific or ubiquitously-active promoters. Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al* (1994) *Proc. Natl. Acad. Sci. USA* 91(24):11581-11585. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in U.S. 5,149,655; use of ionizing radiation for activating transferred gene, as described in U.S. 5,206,152 and WO92/11033.

Exemplary liposome and polycationic gene delivery vehicles are those described in US 5,422,120 and 4,762,915; in WO 95/13796; WO94/23697; and WO91/14445; in EP-0524968; and in Stryer, *Biochemistry*, pages 236-240 (1975) W.H. Freeman, San Francisco; Szoka (1980) *Biochem Biophys Acta* 600:1; Bayer (1979) *Biochem Biophys Acta* 550:464; Rivnay (1987) *Meth Enzymol* 149:119; Wang (1987) *Proc Natl Acad Sci* 84:7851; Plant (1989) *Anal Biochem* 176:420.

A polynucleotide composition can comprises therapeutically effective amount of a gene therapy vehicle, as the term is defined above. For purposes of the present invention, an effective dose will be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

Delivery Methods

Once formulated, the polynucleotide compositions of the invention can be administered (1) directly to the subject; (2) delivered *ex vivo*, to cells derived from the subject; or (3) *in vitro* for expression of recombinant proteins. The subjects to be treated can be mammals or birds. Also, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a tumor or lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in *eg.* WO93/14778. Examples of cells useful in *ex vivo* applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells.

Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by the following procedures, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Polynucleotide and polypeptide pharmaceutical compositions

In addition to the pharmaceutically acceptable carriers and salts described above, the following additional agents can be used with polynucleotide and/or polypeptide compositions.

A. Polypeptides

One example are polypeptides which include, without limitation: asioloorosomucoid (ASOR); transferrin; asialoglycoproteins; antibodies; antibody fragments; ferritin; interleukins; interferons, granulocyte, macrophage colony stimulating factor (GM-CSF),

granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), stem cell factor and erythropoietin. Viral antigens, such as envelope proteins, can also be used. Also, proteins from other invasive organisms, such as the 17 amino acid peptide from the circumsporozoite protein of plasmodium falciparum known as RII.

B.Hormones, Vitamins, Etc.

Other groups that can be included are, for example: hormones, steroids, androgens, estrogens, thyroid hormone, or vitamins, folic acid.

C.Polyalkylenes, Polysaccharides, etc.

Also, polyalkylene glycol can be included with the desired polynucleotides or polypeptides. In a preferred embodiment, the polyalkylene glycol is polyethylene glycol. In addition, mono-, di-, or polysaccharides can be included. In a preferred embodiment of this aspect, the polysaccharide is dextran or DEAE-dextran. Also, chitosan and poly(lactide-co-glycolide)

D.Lipids, and Liposomes

The desired polynucleotide or polypeptide can also be encapsulated in lipids or packaged in liposomes prior to delivery to the subject or to cells derived therefrom.

Lipid encapsulation is generally accomplished using liposomes which are able to stably bind or entrap and retain nucleic acid. The ratio of condensed polynucleotide or polypeptide to lipid preparation can vary but will generally be around 1:1 (mg DNA:micromoles lipid), or more of lipid. For a review of the use of liposomes as carriers for delivery of nucleic acids, see, Hug and Sleight (1991) *Biochim. Biophys. Acta.* 1097:1-17; Straubinger (1983) *Meth. Enzymol.* 101:512-527.

Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner (1987) *Proc. Natl. Acad. Sci. USA* 84:7413-7416); mRNA (Malone (1989) *Proc. Natl. Acad. Sci. USA* 86:6077-6081); and purified transcription factors (Debs (1990) *J. Biol. Chem.* 265:10189-10192), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. (See, also, Felgner *supra*). Other commercially available liposomes include transfectace (DDAB/DOPE) and

DOTAP/DOPE (Boehringer). Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, eg. Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; WO90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilammellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. See eg. Straubinger (1983) *Meth. Immunol.* 101:512-527; Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; Papahadjopoulos (1975) *Biochim. Biophys. Acta* 394:483; Wilson (1979) *Cell* 17:77; Deamer & Bangham (1976) *Biochim. Biophys. Acta* 443:629; Ostro (1977) *Biochem. Biophys. Res. Commun.* 76:836; Fraley (1979) *Proc. Natl. Acad. Sci. USA* 76:3348; Enoch & Strittmatter (1979) *Proc. Natl. Acad. Sci. USA* 76:145; Fraley (1980) *J. Biol. Chem.* (1980) 255:10431; Szoka & Papahadjopoulos (1978) *Proc. Natl. Acad. Sci. USA* 75:145; and Schaefer-Ridder (1982) *Science* 215:166.

E.Lipoproteins

In addition, lipoproteins can be included with the polynucleotide or polypeptide to be delivered. Examples of lipoproteins to be utilized include: chylomicrons, HDL, IDL, LDL, and VLDL. Mutants, fragments, or fusions of these proteins can also be used. Also, modifications of naturally occurring lipoproteins can be used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are including with the polynucleotide to be delivered, no other targeting ligand is included in the composition.

Naturally occurring lipoproteins comprise a lipid and a protein portion. The protein portion are known as apoproteins. At the present, apoproteins A, B, C, D, and E have been

isolated and identified. At least two of these contain several proteins, designated by Roman numerals, AI, AII, AIV; CI, CII, CIII.

A lipoprotein can comprise more than one apoprotein. For example, naturally occurring chylomicrons comprises of A, B, C, and E, over time these lipoproteins lose A and acquire C and E apoproteins. VLDL comprises A, B, C, and E apoproteins, LDL comprises apoprotein B; and HDL comprises apoproteins A, C, and E.

The amino acid of these apoproteins are known and are described in, for example, Breslow (1985) *Annu Rev. Biochem* 54:699; Law (1986) *Adv. Exp Med. Biol.* 151:162; Chen (1986) *J Biol Chem* 261:12918; Kane (1980) *Proc Natl Acad Sci USA* 77:2465; and Utermann (1984) *Hum Genet* 65:232.

Lipoproteins contain a variety of lipids including, triglycerides, cholesterol (free and esters), and phospholipids. The composition of the lipids varies in naturally occurring lipoproteins. For example, chylomicrons comprise mainly triglycerides. A more detailed description of the lipid content of naturally occurring lipoproteins can be found, for example, in *Meth. Enzymol.* 128 (1986). The composition of the lipids are chosen to aid in conformation of the apoprotein for receptor binding activity. The composition of lipids can also be chosen to facilitate hydrophobic interaction and association with the polynucleotide binding molecule.

Naturally occurring lipoproteins can be isolated from serum by ultracentrifugation, for instance. Such methods are described in *Meth. Enzymol. (supra)*; Pitas (1980) *J. Biochem.* 255:5454-5460 and Mahey (1979) *J Clin. Invest* 64:743-750.

Lipoproteins can also be produced by *in vitro* or recombinant methods by expression of the apoprotein genes in a desired host cell. See, for example, Atkinson (1986) *Annu Rev Biophys Chem* 15:403 and Radding (1958) *Biochim Biophys Acta* 30: 443.

Lipoproteins can also be purchased from commercial suppliers, such as Biomedical Technologies, Inc., Stoughton, Massachusetts, USA.

Further description of lipoproteins can be found in Zuckermann et al., PCT. Appln. No. US97/14465.

F. Polycationic Agents

Polycationic agents can be included, with or without lipoprotein, in a composition with the desired polynucleotide or polypeptide to be delivered.

Polycationic agents, typically, exhibit a net positive charge at physiological relevant pH and are capable of neutralizing the electrical charge of nucleic acids to facilitate delivery to a desired location. These agents have both in vitro, ex vivo, and in vivo applications. Polycationic agents can be used to deliver nucleic acids to a living subject either intramuscularly, subcutaneously, etc.

The following are examples of useful polypeptides as polycationic agents: polylysine, polyarginine, polyornithine, and protamine. Other examples include histones, protamines, human serum albumin, DNA binding proteins, non-histone chromosomal proteins, coat proteins from DNA viruses, such as (X174, transcriptional factors also contain domains that bind DNA and therefore may be useful as nucleic acid condensing agents. Briefly, transcriptional factors such as C/CEBP, c-jun, c-fos, AP-1, AP-2, AP-3, CPF, Prot-1, Sp-1, Oct-1, Oct-2, CREP, and TFIID contain basic domains that bind DNA sequences.

Organic polycationic agents include: spermine, spermidine, and putrescine.

The dimensions and of the physical properties of a polycationic agent can be extrapolated from the list above, to construct other polypeptide polycationic agents or to produce synthetic polycationic agents.

Synthetic Polycationic Agents

Synthetic polycationic agents which are useful include, for example, DEAE-dextran, polybrene. Lipofectin[®], and lipofectAMINE[®] are monomers that form polycationic complexes when combined with polynucleotides or polypeptides.

Immunodiagnostic Assays

Neisserial antigens of the invention can be used in immunoassays to detect antibody levels (or, conversely, anti-Neisserial antibodies can be used to detect antigen levels). Immunoassays based on well defined, recombinant antigens can be developed to replace invasive diagnostics methods. Antibodies to Neisserial proteins within biological samples, including for example, blood or serum samples, can be detected. Design of the immunoassays is subject to a great deal of variation, and a variety of these are known in the art. Protocols for the immunoassay may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the signals from the probe are also known; examples of which are

assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays.

Kits suitable for immunodiagnosis and containing the appropriate labeled reagents are constructed by packaging the appropriate materials, including the compositions of the invention, in suitable containers, along with the remaining reagents and materials (for example, suitable buffers, salt solutions, *etc.*) required for the conduct of the assay, as well as suitable set of assay instructions.

Nucleic Acid Hybridisation

“Hybridization” refers to the association of two nucleic acid sequences to one another by hydrogen bonding. Typically, one sequence will be fixed to a solid support and the other will be free in solution. Then, the two sequences will be placed in contact with one another under conditions that favor hydrogen bonding. Factors that affect this bonding include: the type and volume of solvent; reaction temperature; time of hybridization; agitation; agents to block the non-specific attachment of the liquid phase sequence to the solid support (Denhardt's reagent or BLOTTO); concentration of the sequences; use of compounds to increase the rate of association of sequences (dextran sulfate or polyethylene glycol); and the stringency of the washing conditions following hybridization. See Sambrook *et al.* [*supra*] Volume 2, chapter 9, pages 9.47 to 9.57.

“Stringency” refers to conditions in a hybridization reaction that favor association of very similar sequences over sequences that differ. For example, the combination of temperature and salt concentration should be chosen that is approximately 120 to 200°C below the calculated T_m of the hybrid under study. The temperature and salt conditions can often be determined empirically in preliminary experiments in which samples of genomic DNA immobilized on filters are hybridized to the sequence of interest and then washed under conditions of different stringencies. See Sambrook *et al.* at page 9.50.

Variables to consider when performing, for example, a Southern blot are (1) the complexity of the DNA being blotted and (2) the homology between the probe and the sequences being detected. The total amount of the fragment(s) to be studied can vary a magnitude of 10, from 0.1 to 1 µg for a plasmid or phage digest to 10^{-9} to 10^{-8} g for a single copy gene in a highly complex eukaryotic genome. For lower complexity polynucleotides, substantially shorter blotting, hybridization, and exposure times, a smaller amount of starting polynucleotides, and lower specific activity of probes can be used. For example, a single-copy

yeast gene can be detected with an exposure time of only 1 hour starting with 1 μg of yeast DNA, blotting for two hours, and hybridizing for 4-8 hours with a probe of 10^8 cpm/ μg . For a single-copy mammalian gene a conservative approach would start with 10 μg of DNA, blot overnight, and hybridize overnight in the presence of 10% dextran sulfate using a probe of greater than 10^8 cpm/ μg , resulting in an exposure time of ~24 hours.

Several factors can affect the melting temperature (T_m) of a DNA-DNA hybrid between the probe and the fragment of interest, and consequently, the appropriate conditions for hybridization and washing. In many cases the probe is not 100% homologous to the fragment. Other commonly encountered variables include the length and total G+C content of the hybridizing sequences and the ionic strength and formamide content of the hybridization buffer. The effects of all of these factors can be approximated by a single equation:

$$T_m = 81 + 16.6(\log_{10} C_i) + 0.4[\%(G + C)] - 0.6(\%\text{formamide}) - 600/n - 1.5(\%\text{mismatch}).$$

where C_i is the salt concentration (monovalent ions) and n is the length of the hybrid in base pairs (slightly modified from Meinkoth & Wahl (1984) *Anal. Biochem.* 138: 267-284).

In designing a hybridization experiment, some factors affecting nucleic acid hybridization can be conveniently altered. The temperature of the hybridization and washes and the salt concentration during the washes are the simplest to adjust. As the temperature of the hybridization increases (*ie.* stringency), it becomes less likely for hybridization to occur between strands that are nonhomologous, and as a result, background decreases. If the radiolabeled probe is not completely homologous with the immobilized fragment (as is frequently the case in gene family and interspecies hybridization experiments), the hybridization temperature must be reduced, and background will increase. The temperature of the washes affects the intensity of the hybridizing band and the degree of background in a similar manner. The stringency of the washes is also increased with decreasing salt concentrations.

In general, convenient hybridization temperatures in the presence of 50% formamide are 42°C for a probe with is 95% to 100% homologous to the target fragment, 37°C for 90% to 95% homology, and 32°C for 85% to 90% homology. For lower homologies, formamide content should be lowered and temperature adjusted accordingly, using the equation above. If the homology between the probe and the target fragment are not known, the simplest approach is to start with both hybridization and wash conditions which are nonstringent. If non-specific bands or high background are observed after autoradiography, the filter can be

washed at high stringency and reexposed. If the time required for exposure makes this approach impractical, several hybridization and/or washing stringencies should be tested in parallel.

Nucleic Acid Probe Assays

Methods such as PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes according to the invention can determine the presence of cDNA or mRNA. A probe is said to "hybridize" with a sequence of the invention if it can form a duplex or double stranded complex, which is stable enough to be detected.

The nucleic acid probes will hybridize to the Neisserial nucleotide sequences of the invention (including both sense and antisense strands). Though many different nucleotide sequences will encode the amino acid sequence, the native Neisserial sequence is preferred because it is the actual sequence present in cells. mRNA represents a coding sequence and so a probe should be complementary to the coding sequence; single-stranded cDNA is complementary to mRNA, and so a cDNA probe should be complementary to the non-coding sequence.

The probe sequence need not be identical to the Neisserial sequence (or its complement) — some variation in the sequence and length can lead to increased assay sensitivity if the nucleic acid probe can form a duplex with target nucleotides, which can be detected. Also, the nucleic acid probe can include additional nucleotides to stabilize the formed duplex. Additional Neisserial sequence may also be helpful as a label to detect the formed duplex. For example, a non-complementary nucleotide sequence may be attached to the 5' end of the probe, with the remainder of the probe sequence being complementary to a Neisserial sequence. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the a Neisserial sequence in order to hybridize therewith and thereby form a duplex which can be detected.

The exact length and sequence of the probe will depend on the hybridization conditions, such as temperature, salt condition and the like. For example, for diagnostic applications, depending on the complexity of the analyte sequence, the nucleic acid probe typically contains at least 10-20 nucleotides, preferably 15-25, and more preferably at least 30 nucleotides, although it may be shorter than this. Short primers generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

Probes may be produced by synthetic procedures, such as the triester method of Matteucci *et al.* [*J. Am. Chem. Soc.* (1981) 103:3185], or according to Urdea *et al.* [*Proc. Natl. Acad. Sci. USA* (1983) 80: 7461], or using commercially available automated oligonucleotide synthesizers.

The chemical nature of the probe can be selected according to preference. For certain applications, DNA or RNA are appropriate. For other applications, modifications may be incorporated *eg.* backbone modifications, such as phosphorothioates or methylphosphonates, can be used to increase *in vivo* half-life, alter RNA affinity, increase nuclease resistance *etc.* [*eg.* see Agrawal & Iyer (1995) *Curr Opin Biotechnol* 6:12-19; Agrawal (1996) *TIBTECH* 14:376-387]; analogues such as peptide nucleic acids may also be used [*eg.* see Corey (1997) *TIBTECH* 15:224-229; Buchardt *et al.* (1993) *TIBTECH* 11:384-386].

One example of a nucleotide hybridization assay is described by Urdea *et al.* in international patent application WO92/02526 [see also US patent 5,124,246].

Alternatively, the polymerase chain reaction (PCR) is another well-known means for detecting small amounts of target nucleic acids. The assay is described in: Mullis *et al.* [*Meth. Enzymol.* (1987) 155: 335-350]; US patent 4,683,195; and US patent 4,683,202. Two "primer" nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can comprise sequence that does not hybridize to the sequence of the amplification target (or its complement) to aid with duplex stability or, for example, to incorporate a convenient restriction site. Typically, such sequence will flank the desired Neisserial sequence.

A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a threshold amount of target nucleic acids are generated by the polymerase, they can be detected by more traditional methods, such as Southern blots. When using the Southern blot method, the labelled probe will hybridize to the Neisserial sequence (or its complement).

Also, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al* [*supra*]. mRNA, or cDNA generated from mRNA using a polymerase enzyme, can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labelled probe and then washed to remove any unhybridized probe. Next, the duplexes

containing the labeled probe are detected. Typically, the probe is labelled with a radioactive moiety.

EXAMPLES

The examples describe nucleic acid sequences which have been identified in *N. meningitidis*, and *N. gonorrhoeae* along with their respective and putative translation products. Not all of the nucleic acid sequences are complete *ie.* they encode less than the full-length wild-type protein.

The examples are generally in the following format:

- a nucleotide sequence which has been identified in *N. meningitidis*
- the putative translation product of said *N. meningitidis* sequence
- a computer analysis of said translation product based on database comparisons
- a corresponding nucleotide sequence identified from *N. gonorrhoeae*
- the putative translation product of said *N. gonorrhoeae* sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a corresponding nucleotide sequence identified from strain A of *N. meningitidis*
- the putative translation product of said *N. meningitidis* strain A sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a description of the characteristics of the protein which indicates that it might be suitably antigenic or immunogenic.

Sequence comparisons were performed at NCBI (<http://www.ncbi.nlm.nih.gov>) using the algorithms BLAST, BLAST2, BLASTn, BLASTp, tBLASTn, BLASTx, & tBLASTx [eg. see also Altschul *et al.* (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research* 25:2289-3402]. Searches were performed against the following databases: non-redundant GenBank+EMBL+DDBJ+PDB sequences and non-redundant GenBank CDS translations+PDB+SwissProt+SPupdate+PIR sequences.

Dots within nucleotide sequences represent nucleotides which have been arbitrarily introduced in order to maintain a reading frame. In the same way, double-underlined nucleotides were removed. Lower case letters represent ambiguities which arose during

alignment of independent sequencing reactions (some of the nucleotide sequences in the examples are derived from combining the results of two or more experiments).

Nucleotide sequences were scanned in all six reading frames to predict the presence of hydrophobic domains using an algorithm based on the statistical studies of Esposti *et al.* [Critical evaluation of the hydropathy of membrane proteins (1990) *Eur J Biochem* 190:207-219]. These domains represent potential transmembrane regions or hydrophobic leader sequences.

Open reading frames were predicted from fragmented nucleotide sequences using the program ORFFINDER (NCBI).

Underlined amino acid sequences indicate possible transmembrane domains or leader sequences in the ORFs, as predicted by the PSORT algorithm (<http://www.psort.nibb.ac.jp>). Functional domains were also predicted using the MOTIFS program (GCG Wisconsin & PROSITE).

For each of the following examples: based on the presence of a putative leader sequence and/or several putative transmembrane domains (single-underlined) in the gonococcal protein, it is predicted that the proteins from *N. meningitidis* and *N. gonorrhoeae*, and their respective epitopes, could be useful antigens or immunogenic compositions for vaccines or diagnostics.

The standard techniques and procedures which may be employed in order to perform the invention (*e.g.* to utilize the disclosed sequences for vaccination or diagnostic purposes) were summarized above. This summary is not a limitation on the invention but, rather, gives examples that may be used, but are not required.

In particular, the following methods were used to express, purify and biochemically characterize the proteins of the invention.

Chromosomal DNA Preparation

N.meningitidis strain 2996 was grown to exponential phase in 100ml of GC medium, harvested by centrifugation, and resuspended in 5ml buffer (20%(w/v) Sucrose, 50mM Tris-HCl, 50mM EDTA, pH8). After 10 minutes incubation on ice, the bacteria were lysed by adding 10ml of lysis solution (50mM NaCl, 1% Na-Sarkosyl, 50µg/ml Proteinase K), and the suspension incubated at 37°C for 2 hours. Two phenol extractions (equilibrated to pH 8) and one CHCl₃/isoamylalcohol (24:1) extraction were performed. DNA was precipitated by addition of 0.3M sodium acetate and 2 volumes of ethanol, and collected by centrifugation.

The pellet was washed once with 70%(v/v) ethanol and redissolved in 4.0ml TE buffer (10mM Tris-HCl, 1mM EDTA, pH 8.0). The DNA concentration was measured by reading the OD at 260 nm.

Oligonucleotide design

Synthetic oligonucleotide primers were designed on the basis of the coding sequence of each ORF, using (a) the meningococcus B sequence when available, or (b) the gonococcus/meningococcus A sequence, adapted to the codon preference usage of meningococcus as necessary. Any predicted signal peptides were omitted, by designing the 5' primers to sequence immediately downstream from the predicted leader sequence.

For most ORFs, the 5' primers included two restriction enzyme recognition sites (*Bam*HI-*Nde*I, *Bam*HI-*Nhe*I, *Eco*RI-*Nde*I or *Eco*RI-*Nhe*I), depending on the restriction pattern of the gene of interest. The 3' primers included a *Xho*I or a *Hind*III restriction site (table 1). This procedure was established in order to direct the cloning of each amplification product (corresponding to each ORF) into two different expression systems: pGEX-KG (using *Bam*HI-*Xho*I, *Bam*HI-*Hind*III, *Eco*RI-*Xho*I or *Eco*RI-*Hind*III), and pET21b+ (using *Nde*I-*Xho*I, *Nhe*I-*Xho*I, *Nde*I-*Hind*III or *Nhe*I-*Hind*III).

5'-end primer tail:	<u>CGCGGATCCCATATG</u>	(<i>Bam</i> HI- <i>Nde</i> I)
	<u>CGCGGATCCGCTAGC</u>	(<i>Bam</i> HI- <i>Nhe</i> I)
	<u>CCGGAATTCTACATATG</u>	(<i>Eco</i> RI- <i>Nde</i> I)
	<u>CCGGAATTCTAGCTAGC</u>	(<i>Eco</i> RI- <i>Nhe</i> I)
3'-end primer tail:	<u>CCCGCTCGAG</u>	(<i>Xho</i> I)
	<u>CCCGCTCGAG</u>	(<i>Hind</i> III)

For cloning ORFs into the pGEX-His vector, the 5' and 3' primers contained only one restriction enzyme site (*Eco*RI, *Kpn*I or *Sal*I for the 5' primers and *Pst*I, *Xba*I, *Sph*I or *Sal*I for the 3' primers). Again restriction sites were chosen according to the particular restriction pattern of the gene (table 1).

5'-end primer tail:	(AAA) <u>AAAGAATTC</u>	(<i>Eco</i> RI)
	(AAA) <u>AAAGGTACC</u>	(<i>Kpn</i> I)
3'-end primer tail:	(AAA) <u>AAACTGCAG</u>	(<i>Pst</i> I)
	(AAA) <u>AAATCTAGA</u>	(<i>Xba</i> I)

5' or 3'-end primer tail: AAAGCATGC (*Sph*I)
AAAAAAGTCGAC (*Sal*I)

As well as containing the restriction enzyme recognition sequences, the primers included nucleotides which hybridized to the sequence to be amplified. The melting temperature depended on the number and type of hybridising nucleotides in the whole primer, and was determined for each primer using the formulae:

$$T_m = 4 (G+C) + 2 (A+T) \quad (\text{tail excluded})$$

$$T_m = 64.9 + 0.41 (\% \text{ GC}) - 600/N \quad (\text{whole primer})$$

The melting temperatures of the selected oligonucleotides were usually 65-70°C for the whole oligo and 50-55°C for the hybridising region alone.

Table 1 shows the forward and reverse primers used for each amplification. In certain cases, the sequence of the primer does not exactly match the sequence of the predicted ORF. This is because when initial amplifications were performed, the complete 5' and/or 3' sequences for some meningococcal B ORFs were not known. However the corresponding sequences had been identified in *Gonococcus* or in *Meningococcus A*. Hence, when the *Meningococcus B* sequence was incomplete or uncertain, *Gonococcal* or *Meningococcal A* sequences were used as the basis for primer design. These sequences were altered to take account of codon preference. It can be appreciated that, once the complete sequence is identified, this approach will no longer be necessary.

Oligonucleotides were synthesized using a Perkin Elmer 394 DNA/RNA Synthesizer, eluted from the columns in 2.0ml NH₄OH, and deprotected by 5 hours incubation at 56°C. The oligos were precipitated by addition of 0.3M Na-Acetate and 2 volumes ethanol. The samples were centrifuged and the pellets resuspended in either 100µl or 1.0ml of water. The OD₂₆₀ was determined using a Perkin Elmer Lambda Bio spectrophotometer and the concentration adjusted to 2-10pmol/µl.

Amplification

The standard PCR protocol was as follows: 50-200ng of genomic DNA was used as a template in the presence of 20-40μM of each oligonucleotide primer, 400-800μM dNTPs solution, 1x PCR buffer (including 1.5mM MgCl₂), 2.5 units *TaqI* DNA polymerase (using

Perkin-Elmer AmpliTaq, GIBCO Platinum, Pwo DNA polymerase, or Tahara Shuzo Taq polymerase). In some cases, PCR was optimised by the addition of 10µl DMSO or 50µl 2M Betaine.

After a hot start (adding the polymerase during a preliminary 3 minute incubation of the whole mix at 95°C), each sample underwent a two-step amplification. The first 5 cycles were performed using the hybridization temperature that excluded the restriction enzyme tail of the primer (see above). This was followed by 30 cycles using the hybridization temperature calculated for the whole length oligos. The cycles were completed with a 10 minute extension step at 72°C. The standard cycles were as follows:

	Denaturation	Hybridisation	Elongation
First 5 cycles	30 seconds 95°C	30 seconds 50-55°C	30-60 seconds 72°C
Last 30 cycles	30 seconds 95°C	30 seconds 65-70°C	30-60 seconds 72°C

Elongation times varied according to the length of the ORF to be amplified. Amplifications were performed using either a 9600 or a 2400 Perkin Elmer GeneAmp PCR System. To check the results, 1/10 of the amplification volume was loaded onto a 1-1.5% (w/v) agarose gel and the size of each amplified fragment compared with a DNA molecular weight marker.

The amplified DNA was either loaded directly on a 1% agarose gel or first precipitated with ethanol and resuspended in a volume suitable to be loaded on a 1.0% agarose gel. The DNA fragment corresponding to the band of correct size was purified using the Qiagen Gel Extraction Kit, following the manufacturer's protocol. DNA fragments were eluted in a volume of 30µl or 50µl with either H₂O or 10mM Tris, pH 8.5.

Digestion of PCR fragments

The purified DNA corresponding to the amplified fragment was doubly-digested with the appropriate restriction enzymes for; cloning into pET-21b+ and expressing the protein as a C-terminus His-tagged fusion, for cloning into pGEX-KG and expressing the protein as a N-

terminus GST-fusion, and for cloning into pGEX-His and expressing the protein as a N-terminus GST-His tagged fusion.

Each purified DNA fragment was incubated at 37°C for 3 hours to overnight with 20 units of appropriate restriction enzyme (New England Biolabs) in a volume of either 30 or 40 µl in the presence of suitable digestion buffer. Digested fragments were purified using the QIAquick PCR purification kit (following the manufacturer's instructions) and eluted in a volume of 30 µl or 50 µl with either H₂O or 10 mM Tris, pH 8.5. The DNA concentration was determined by quantitative agarose gel electrophoresis (1.0% gel) in the presence of a titrated molecular weight marker.

Digestion of the cloning vectors (pET22B, pGEX-KG, pTRC-His A, pET21b+, pGEX-KG, and pGEX-His)

The vector pGEX-His is a modified pGEX-2T vector carrying a region encoding six histidine residues upstream of the thrombin cleavage site and containing the multiple cloning site of the vector pTRC99 (Pharmacia). 10 µg plasmid was double-digested with 50 units of each restriction enzyme in 200 µl reaction volume in the presence of appropriate buffer by overnight incubation at 37°C. After loading the whole digestion on a 1% agarose gel, the band corresponding to the digested vector was purified from the gel using the Qiagen QIAquick Gel Extraction Kit and the DNA was eluted in 50 µl of 10 mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD₂₆₀ of the sample, and adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

10 µg of plasmid vector was doubly-digested with 50 units of each restriction enzyme in a volume of 200 µl with the appropriate buffer overnight at 37°C. The digest was loaded onto a 1.0% agarose gel and the band corresponding to the digested vector purified using the Qiagen QIAquick Gel Extraction Kit. DNA was eluted in 50 µl of 10 mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD_{260nm} and the concentration adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

Cloning

For some ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated in both pET22b and pGEX-KG. In a final volume of 20 µl, a molar

ratio of 3:1 fragment/vector was ligated using 0.5 μ l of NEB T4 DNA ligase (400 units/ μ l), in the presence of the buffer supplied by the manufacturer. The reaction was incubated at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit", following the manufacturer's instructions.

In order to introduce the recombinant plasmid in a suitable strain, 100 μ l *E. coli* DH5 competent cells were incubated with the ligase reaction solution for 40 minutes on ice, then at 37°C for 3 minutes, then, after adding 800 μ l LB broth, again at 37°C for 20 minutes. The cells were then centrifuged at maximum speed in an Eppendorf microfuge and resuspended in approximately 200 μ l of the supernatant. The suspension was then plated on LB ampicillin (100 mg/ml).

The screening of the recombinant clones was performed by growing 5 randomly-chosen colonies overnight at 37 °C in either 2 ml (pGEX or pTC clones) or 5ml (pET clones) LB broth + 100 μ g/ml ampicillin. The cells were then pelleted and the DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions, to a final volume of 30 μ l. 5 μ l of each individual miniprep (approximately 1g) were digested with either *NdeI/XhoI* or *BamHI/XhoI* and the whole digestion loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1Kb DNA Ladder, GIBCO). The screening of the positive clones was made on the base of the correct insert size.

For other ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated into both pET21b+ and pGEX-KG. A molar ratio of of 3:1 fragment/vector was used in a final volume of 20 μ l, that included 0.5 μ l T4 DNA ligase (400 units/ μ l, NEB) and ligation buffer supplied by the manufacturer. The reaction was performed at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit" and the manufacturer's protocol.

Recombinant plasmid was transformed into 100 μ l of competent *E. coli* DH5 or HB101 by incubating the ligase reaction solution and bacteria for 40 minutes on ice then at 37°C for 3 minutes. This was followed by the addition of 800 μ l LB broth and incubation at 37°C for 20 minutes. The cells were centrifuged at maximum speed in an Eppendorf microfuge, resuspended in approximately 200 μ l of the supernatant and plated onto LB ampicillin (100mg/ml) agar.

Screening for recombinant clones was performed by growing 5 randomly selected colonies overnight at 37°C in either 2.0ml (pGEX-KG clones) or 5.0ml (pET clones) LB broth + 100µg/ml ampicillin. Cells were pelleted and plasmid DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions. Approximately 1µg of each individual miniprep was digested with the appropriate restriction enzymes and the digest loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1kb DNA Ladder, GIBCO). Positive clones were selected on the basis of the size of insert.

ORFs were cloned into PGEX-His, by doubly-digesting the PCR product and ligating into similarly digested vector. After cloning, recombinant plasmids were transformed into the *E.coli* host W3110. Individual clones were grown overnight at 37°C in LB broth with 50µg/ml ampicillin.

Certain ORFs may be cloned into the pGEX-HIS vector using *EcoRI-PstI* cloning sites, or *EcoRI-SalI*, or *SalI-PstI*. After cloning, the recombinant plasmids may be introduced in the *E.coli* host W3110.

Expression

Each ORF cloned into the expression vector may then be transformed into the strain suitable for expression of the recombinant protein product. 1 µl of each construct was used to transform 30 µl of *E.coli* BL21 (pGEX vector), *E.coli* TOP 10 (pTRC vector) or *E.coli* BL21-DE3 (pET vector), as described above. In the case of the pGEX-His vector, the same *E.coli* strain (W3110) was used for initial cloning and expression. Single recombinant colonies were inoculated into 2ml LB+Amp (100 µg/ml), incubated at 37°C overnight, then diluted 1:30 in 20 ml of LB+Amp (100 µg/ml) in 100 ml flasks, making sure that the OD₆₀₀ ranged between 0.1 and 0.15. The flasks were incubated at 30°C into gyratory water bath shakers until OD indicated exponential growth suitable for induction of expression (0.4-0.8 OD for pET and pTRC vectors; 0.8-1 OD for pGEX and pGEX-His vectors). For the pET, pTRC and pGEX-His vectors, the protein expression was induced by addition of 1mM IPTG, whereas in the case of pGEX system the final concentration of IPTG was 0.2 mM. After 3 hours incubation at 30°C, the final concentration of the sample was checked by OD. In order to check expression, 1ml of each sample was removed, centrifuged in a microfuge, the pellet

resuspended in PBS, and analysed by 12% SDS-PAGE with Coomassie Blue staining. The whole sample was centrifuged at 6000g and the pellet resuspended in PBS for further use.

GST-fusion proteins large-scale purification.

For some ORFs, a single colony was grown overnight at 37°C on LB+Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600 ml of fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD₅₅₀ 0.8-1. Protein expression was induced with 0.2mM IPTG followed by three hours incubation. The culture was centrifuged at 8000 rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml cold PBS. The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia) (previously washed with PBS) and incubated at room temperature for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold PBS for 10 minutes, resuspended in 1ml cold PBS, and loaded on a disposable column. The resin was washed twice with 2ml cold PBS until the flow-through reached OD₂₈₀ of 0.02-0.06. The GST-fusion protein was eluted by addition of 700µl cold Glutathione elution buffer 10mM reduced glutathione, 50mM Tris-HCl) and fractions collected until the OD₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel using either Biorad SDS-PAGE Molecular weight standard broad range (M1) (200, 116.25, 97.4, 66.2, 45, 31, 21.5, 14.4, 6.5 kDa) or Amersham Rainbow Marker (M'') (220, 66, 46, 30, 21.5, 14.3 kDa) as standards. As the MW of GST is 26kDa, this value must be added to the MW of each GST-fusion protein.

For other ORFs, for each clone to be purified as a GST-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp. (100µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD_{550nm} reached 0.6-0.8. Recombinant protein expression was induced by addition of IPTG (final concentration 0.2mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml cold PBS. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia), previously equilibrated with PBS, and incubated at room temperature with gentle agitation for 30 min. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batchwise) with 10ml cold PBS for 10 min, resuspended in 1ml cold PBS, and loaded onto a disposable column. The resin continued to be washed with cold PBS, until the OD_{280nm} of the flow-through reached 0.02-0.01. The GST-fusion protein was eluted by addition of 700µl cold glutathione elution buffer (10mM reduced glutathione, 50mM Tris-HCl pH 8.0) and fractions collected, until the OD_{280nm} of the eluate indicated all the recombinant protein was obtained. 20µl aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. The molecular mass of the purified proteins was determined using either the Bio-Rad broad range molecular weight standard (M1) (200, 116, 97.4, 66.2, 45.0, 31.0, 21.5, 14.4, 6.5 kDa) or the Amersham Rainbow Marker (M2) (220, 66.2, 46.0, 30.0, 21.5, 14.3 kDa). The molecular weights of GST-fusion proteins are a combination of the 26 kDa GST protein and its fusion partner. Protein concentrations were estimated using the Bradford assay.

His-fusion soluble proteins large-scale purification.

For some ORFs, a single colony was grown overnight at 37°C on a LB + Amp agar plate. The bacteria were inoculated into 20ml of LB+Amp liquid culture and incubated overnight in a water bath shaker. Bacteria were diluted 1:30 into 600ml fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD₅₅₀ 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000 rpm at 4°C, the supernatant was discarded and the bacterial pellet was resuspended in 7.5ml cold 10mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 10 mM imidazole, pH 8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Ni²⁺-resin (Pharmacia) (previously washed with 10mM imidazole buffer) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold 10mM imidazole buffer for 10 minutes,

resuspended in 1ml cold 10mM imidazole buffer and loaded on a disposable column. The resin was washed at 4°C with 2ml cold 10mM imidazole buffer until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The resin was washed with 2ml cold 20mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 20 mM imidazole, pH 8) until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl cold 250mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 250 mM imidazole, pH 8) and fractions collected until the O.D₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

His-fusion insoluble proteins large-scale purification.

A single colony was grown overnight at 37 °C on a LB + Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600ml fresh medium and let to grow at the optimal temperature (37°C) to O.D₅₅₀ 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml buffer B (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed twice and centrifuged again. The supernatant was stored at -20°C, while the pellets were resuspended in 2 ml guanidine buffer (6M guanidine hydrochloride, 100mM phosphate buffer, 10 mM Tris-HCl, pH 7.5) and treated in a homogenizer for 10 cycles. The product was centrifuged at 13000 rpm for 40 minutes. The supernatant was mixed with 150µl Ni²⁺-resin (Pharmacia) (previously washed with buffer B) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700 g for 5 minutes at 4°C. The resin was washed twice with 10 ml buffer B for 10 minutes, resuspended in 1ml buffer B, and loaded on a disposable column. The resin was washed at room temperature with 2ml buffer B until the flow-through reached the OD₂₈₀ of 0.02-0.06. The resin was washed with 2ml buffer C (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl elution buffer (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions collected until the OD₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

Purification of His-fusion proteins.

For each clone to be purified as a His-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp (100 µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100 µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD_{550nm} reached 0.6-0.8. Expression of recombinant protein was induced by addition of IPTG (final concentration 1.0mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml of either (i) cold buffer A (300mM NaCl, 50mM phosphate buffer, 10mM imidazole, pH 8.0) for soluble proteins or (ii) buffer B (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8) for insoluble proteins. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. For insoluble proteins, pellets were resuspended in 2.0 ml buffer C (6M guanidine hydrochloride, 100mM phosphate buffer, 10mM Tris-HCl, pH 7.5) and treated with a Dounce homogenizer for 10 cycles. The homogenate was centrifuged at 13 000xg for 40 min and the supernatant retained.

Supernatants for both soluble and insoluble preparations were mixed with 150µl Ni²⁺-resin (previously equilibrated with either buffer A or buffer B, as appropriate) and incubated at room temperature with gentle agitation for 30 min. The resin was Chelating Sepharose Fast Flow (Pharmacia), prepared according to manufacturers protocol. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batch-wise) with 10ml buffer A or B for 10 min, resuspended in 1.0 ml buffer A or B and loaded onto a disposable column. The resin continued to be washed with either (i) buffer A at 4°C or (ii) buffer B at room temperature, until the OD_{280nm} of the flow-through reached 0.02-0.01. The resin was further washed with either (i) cold buffer C (300mM NaCl, 50mM phosphate buffer, 20mM imidazole, pH 8.0) or (ii) buffer D (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the the OD_{280nm} of the flow-through reached 0.02-0.01. The His-fusion protein was eluted by addition of 700µl of either (i) cold elution buffer A (300mM NaCl, 50mM phosphate buffer, 250mM imidazole, pH 8.0) or (ii) elution buffer B (8 M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions

collected until the $O.D_{280nm}$ indicated all the recombinant protein was obtained. 20 μ l aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. Protein concentrations were estimated using the Bradford assay.

His-fusion proteins renaturation

In the cases where denaturation was required to solubilize proteins, a renaturation step was employed prior to immunization. Glycerol was added to the denatured fractions obtained above to give a final concentration of 10%(v/v). The proteins were diluted to 200 μ g/ml using dialysis buffer I (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, 2.0M urea, pH 8.8) and dialysed against the same buffer for 12-14 hours at 4°C. Further dialysis was performed with buffer II (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Alternatively, 10% glycerol was added to the denatured proteins. The proteins were then diluted to 20 μ g/ml using dialysis buffer I (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, 2M urea, pH 8.8) and dialysed against the same buffer at 4°C for 12-14 hours. The protein was further dialysed against dialysis buffer II (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Protein concentration was evaluated using the formula:

$$\text{Protein (mg/ml)} = (1.55 \times OD_{280}) - (0.76 \times OD_{260})$$

Purification of proteins

To analyse the solubility, pellets obtained from 3.0ml cultures were resuspended in 500 μ l buffer M1 (PBS pH 7.2). 25 μ l of lysozyme (10mg/ml) was added and the bacteria incubated for 15 min at 4°C. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and the pellet resuspended in buffer M2 [8M urea, 0.5M NaCl, 20mM imidazole and 0.1M NaH_2PO_4] and incubated for 3 to 4 hours at 4°C. After centrifugation, the supernatant was collected and the pellet resuspended in buffer M3 [6M guanidinium-HCl, 0.5M NaCl, 20mM imidazole and 0.1M NaH_2PO_4] overnight at 4°C. The

supernatants from all steps were analysed by SDS-PAGE. Some proteins were found to be soluble in PBS, others need urea or guanidium-HCl for solubilization.

For preparative scale purifications, 500ml cultures were induced and fusion proteins solubilized in either buffer M1, M2 or M3 using the procedure described above. Crude extracts were loaded onto a Ni-NTA superflow column (Quiagen) equilibrated with buffer M1, M2 or M3 depending on the solubilization buffer employed. Unbound material was eluted by washing the column with the same buffer. The recombinant fusion protein was eluted with the corresponding buffer containing 500mM imidazole then dialysed against the same buffer in the absence of imidazole.

Mice immunisations

20µg of each purified protein are used to immunise mice intraperitoneally. In the case of some ORFs, Balb-C mice were immunised with Al(OH)₃ as adjuvant on days 1, 21 and 42, and immune response was monitored in samples taken on day 56. For other ORFs, CD1 mice could be immunised using the same protocol. For ORFs 25 and 40, CD1 mice were immunised using Freund's adjuvant, and the same immunisation protocol was used, except that the immune response was measured on day 42, rather than 56. Similarly, for still other ORFs, CD1 mice were immunised with Freund's adjuvant, but the immune response was measured on day 49. Alternatively, 20µg of each purified protein was mixed with Freund's adjuvant and used to immunise CD1 mice intraperitoneally. For many of the proteins, the immunization was performed on days 1, 21 and 35, and immune response was monitored in samples taken on days 34 and 49. For some proteins, the third immunization was performed on day 28, rather than 35, and the immune response was measured on days 20 and 42, rather than 34 and 49.

ELISA assay (sera analysis)

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 7ml of Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10000 rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated

for 2 hours at room temperature and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200 µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200 µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN₃ in PBS) were added to each well and the plates incubated for 90 minutes at 37°C. Wells were washed three times with PBT. 100 µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100 µl of substrate buffer for HRP (25 ml of citrate buffer pH5, 10 mg of O-phenildiamine and 10 µl of H₂O) were added to each well and the plates were left at room temperature for 20 minutes. 100 µl H₂SO₄ was added to each well and OD₄₉₀ was followed. The ELISA was considered positive when OD₄₉₀ was 2.5 times the respective pre-immune sera.

Alternatively, The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10 000rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated for 1 hour at 37°C and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN₃ in PBS) were added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 100µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100µl of substrate buffer for HRP (25ml of citrate buffer pH5, 10mg of O-

phenildiamine and 10 μ l of H₂O₂) were added to each well and the plates were left at room temperature for 20 minutes. 100 μ l of 12.5% H₂SO₄ was added to each well and OD₄₉₀ was followed. The ELISA titers were calculated arbitrarily as the dilution of sera which gave an OD₄₉₀ value of 0.4 above the level of preimmune sera. The ELISA was considered positive when the dilution of sera with OD₄₉₀ of 0.4 was higher than 1:400.

FACScan bacteria Binding Assay procedure.

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 4 tubes containing 8ml each Mueller-Hinton Broth (Difco) containing 0.25% glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.35-0.5. The culture was centrifuged for 10 minutes at 4000rpm. The supernatant was discarded and the pellet was resuspended in blocking buffer (1% BSA in PBS, 0.4% NaN₃) and centrifuged for 5 minutes at 4000rpm. Cells were resuspended in blocking buffer to reach OD₆₂₀ of 0.07. 100 μ l bacterial cells were added to each well of a Costar 96 well plate. 100 μ l of diluted (1:100, 1:200, 1:400) sera (in blocking buffer) were added to each well and plates incubated for 2 hours at 4°C. Cells were centrifuged for 5 minutes at 4000rpm, the supernatant aspirated and cells washed by addition of 200 μ l/well of blocking buffer in each well. 100 μ l of R-Phicoerytrin conjugated F(ab)₂ goat anti-mouse, diluted 1:100, was added to each well and plates incubated for 1 hour at 4°C. Cells were spun down by centrifugation at 4000rpm for 5 minutes and washed by addition of 200 μ l/well of blocking buffer. The supernatant was aspirated and cells resuspended in 200 μ l/well of PBS, 0.25% formaldehyde. Samples were transferred to FACScan tubes and read. The condition for FACScan (Laser Power 15mW) setting were: FL2 on; FSC-H threshold:92; FSC PMT Voltage: E 01; SSC PMT: 474; Amp. Gains 6.1; FL-2 PMT: 586; compensation values: 0.

OMV preparations

Bacteria were grown overnight on 5 GC plates, harvested with a loop and resuspended in 10 ml 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30 minutes and the bacteria disrupted by sonication for 10' on ice (50% duty cycle, 50% output). Unbroken cells were removed by centrifugation at 5000g for 10 minutes and the total cell envelope

fraction recovered by centrifugation at 50000g at 4°C for 75 minutes. To extract cytoplasmic membrane proteins from the crude outer membranes, the whole fraction was resuspended in 2% sarkosyl (Sigma) and incubated at room temperature for 20 minutes. The suspension was centrifuged at 10000g for 10 minutes to remove aggregates, and the supernatant further ultracentrifuged at 50000g for 75 minutes to pellet the outer membranes. The outer membranes were resuspended in 10mM Tris-HCl, pH8 and the protein concentration measured by the Bio-Rad Protein assay, using BSA as a standard.

Whole Extracts preparation

Bacteria were grown overnight on a GC plate, harvested with a loop and resuspended in 1ml of 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30' minutes.

Western blotting

Purified proteins (500ng/lane), outer membrane vesicles (5µg) and total cell extracts (25µg) derived from MenB strain 2996 were loaded onto a 12% SDS-polyacrylamide gel and transferred to a nitrocellulose membrane. The transfer was performed for 2 hours at 150mA at 4°C, using transfer buffer (0.3 % Tris base, 1.44 % glycine, 20% (v/v) methanol). The membrane was saturated by overnight incubation at 4°C in saturation buffer (10% skimmed milk, 0.1% Triton X100 in PBS). The membrane was washed twice with washing buffer (3% skimmed milk, 0.1% Triton X100 in PBS) and incubated for 2 hours at 37°C with mice sera diluted 1:200 in washing buffer. The membrane was washed twice and incubated for 90 minutes with a 1:2000 dilution of horseradish peroxidase labelled anti-mouse Ig. The membrane was washed twice with 0.1% Triton X100 in PBS and developed with the Opti-4CN Substrate Kit (Bio-Rad). The reaction was stopped by adding water.

Bactericidal assay

MC58 and 2996 strains were grown overnight at 37°C on chocolate agar plates. 5-7 colonies were collected and used to inoculate 7ml Mueller-Hinton broth. The suspension was incubated at 37°C on a nutator and let to grow until OD₆₂₀ was in between 0.5-0.8. The culture was aliquoted into sterile 1.5ml Eppendorf tubes and centrifuged for 20 minutes at maximum speed in a microfuge. The pellet was washed once in Gey's buffer (Gibco) and resuspended in the same buffer to an OD₆₂₀ of 0.5, diluted 1:20000 in Gey's buffer and stored at 25°C.

50µl of Gey's buffer/1% BSA was added to each well of a 96-well tissue culture plate. 25µl of diluted (1:100) mice sera (dilution buffer: Gey's buffer/0.2% BSA) were added to each well and the plate incubated at 4°C. 25µl of the previously described bacterial suspension were added to each well. 25µl of either heat-inactivated (56°C waterbath for 30 minutes) or normal baby rabbit complement were added to each well. Immediately after the addition of the baby rabbit complement, 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 0). The 96-well plate was incubated for 1 hour at 37°C with rotation and then 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 1). After overnight incubation the colonies corresponding to time 0 and time 1h were counted.

Gene Variability

The *ORF4* and *919* genes were amplified by PCR on chromosomal DNA extracted from various *Neisseria* strains (see list of strains). The following oligonucleotides used as PCR primers were designed in the upstream and downstream regions of the genes:

orf 4.1	(forward)	CGAATCCGGACGGCAGGACTC
orf 4.3	(reverse)	GGCAGGGAATGGCGGATTAAAG
919.1	(forward)	AAAATGCCTCTCCACGGCTG or CTGCGCCCTGTGTTAAAATCCCCCT
919.6	(reverse)	CAAATAAGAAAGGAATTTTG or GGTATCGCAAACTTCGCCTTAATGCG

The PCR cycling conditions were:

1 cycle	2 min. at 94°
30 cycles	30 sec. at 94°
	30 sec. at ~ 54° or ~ 60° (in according to T _m of the primers)
	40 sec. at 72°
1 cycle	7 min. at 72°

The PCR products were purified from 1 % agarose gel and sequenced using the following primers:

orf 4.1 (forward)	CGAATCCGGACGGCAGGACTC
orf 4.2 (forward)	CGACCGCGCCTTTGGGACTG
orf 4.3 (reverse)	GGCAGGGAATGGCGGATTAAAG
orf 4.4 (reverse)	TCTTTGAGTTTGATCCAACC

- 919.1 (forward) AAAATGCCTCTCCACGGCTG or
CTGCGCCCTGTGTAAAATCCCCT
- 919.2 (forward) ATCCTTCCGCCTCGGCTGCG
- 919.3 (forward) AAAACAGCGGCACAATCGAC
- 919.4 (forward) ATAAGGGCTACCTCAAACCTC
- 919.5 (forward) GCGCGTGGATTATTTTTGGG
- 919.6 (reverse) CAAATAAGAAAGGAATTTTG or
GGTATCGCAAAACTTCGCCTTAATGCG
- 919.7 (reverse) CCCAAGGTAATGTAAGTGCCG
- 919.8 (reverse) TAAAAAAAAGTTCGACAGGG
- 919.9 (reverse) CCGTCCGCCTGTCGTCGCCC
- 919.10 (reverse) TCGTTCCGGCGGGGTCGGGG

All documents cited herein are incorporated by reference in their entireties.

The following Examples are presented to illustrate, not limit, the invention

EXAMPLE 1

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

Table 1: Oligonucleotides used for PCR for Examples 2-10

ORF	Primer	Sequence	Restriction sites
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCACGATT <SEQ ID 3021>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTAGAAGCGGGCGGCAA <SEQ ID 3022>	XhoI
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA <SEQ ID 3023>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC <SEQ ID 3024>	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT <SEQ ID 3025>	BamHI-NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTTGATGTCGAC <SEQ ID 3026>	XhoI
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC <SEQ ID 3027>	BamHI-NdeI
	Reverse	CCCGCTCGAG-CGGGCGGTATTCGGG <SEQ ID 3028>	XhoI
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT <SEQ ID 3029>	BamHI-NdeI

128	Reverse	CCCGCTCGAG-ATAATAATATCCCGCGCCC <SEQ ID 3030>	XhoI
	Forward	CGCGGATCCCATATG-ACTGACAACGCACT <SEQ ID 3031>	BamHI-NdeI
	Reverse	CCCGCTCGAG-GACCGCGTTGTCGAAA <SEQ ID 3032>	XhoI
206	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA <SEQ ID 3033>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTCTGTAAAAAAGTATGTGC <SEQ ID 3034>	XhoI
287	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG <SEQ ID 3035>	EcoRI-NheI
	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTTGCC <SEQ ID 3036>	XhoI
406	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG <SEQ ID 3037>	BamHI-NdeI
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG <SEQ ID 3038>	XhoI

Localization of the ORFs

The following DNA and amino acid sequences are identified by titles of the following form: [g, m, or a] [#].[seq or pep], where "g" means a sequence from *N. gonorrhoeae*, "m" means a sequence from *N. meningitidis B*, and "a" means a sequence from *N. meningitidis A*; "#" means the number of the sequence; "seq" means a DNA sequence, and "pep" means an amino acid sequence. For example, "g001.seq" refers to an *N. gonorrhoeae* DNA sequence, number 1. The presence of the suffix "-1" to these sequences indicates an additional sequence found for the same ORF, thus, data for an ORF having both an unsuffixed and a suffixed sequence designation applies to both such designated sequences. Further, open reading frames are identified as ORF #, where "#" means the number of the ORF, corresponding to the number of the sequence which encodes the ORF, and the ORF designations may be suffixed with ".ng" or ".a", indicating that the ORF corresponds to a *N. gonorrhoeae* sequence or a *N. meningitidis A* sequence, respectively. The word "partial" before a sequence indicates that the sequence may be a partial or a complete ORF. Computer analysis was performed for the comparisons that follow between "g", "m", and "a" peptide sequences; and therein the "pep" suffix is implied where not expressly stated. Further, in the event of a conflict between the text immediately preceding and describing which sequences are being compared, and the

designated sequences being compared, the designated sequence controls and is the actual sequence being compared.

ORF: contig:

279 gnm4.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3039>:

m279.seq

1	ATAACGCGGA	TTTGCGGGCTG	CTTGATTTC	ACGGTTTTCA	GGGCTTCGGC
51	AAGTTTGTCT	GCGGCGGGTT	TCATCAGGCT	GCAATGGGAA	GGTACGGACA
101	CGGGCAGCGG	CAGGGCGCGT	TTGGCACC	CTTCTTTGGC	GGCAGCCATG
151	GCGCGTCCGA	CGGCGGCGGC	GTTGCCTGCA	ATCACGATTT	GTCCGGGTGA
201	GTTGAAGTTG	ACGGCTTCGA	CCACTTCGCT	TTGGGCGGCT	TCGGCACAAA
251	TGGCTTTAAC	CTGCTCATCT	TCCAAGCCGA	GAATCGCCGC	CATTGCGCCC
301	ACGCCTTGCG	GTACGGCGGA	CTGCATCAGT	TCGGCGCGCA	GGCGCACGAG
351	TTTGCACCGC	TCGGCAAAAT	TCAATGCGCC	GGCGGCAACG	AGTGCGGTGT
401	ATTGCGCGAG	GCTGTGTCCG	GCAACGGCGG	CAGGCGTTTT	GCCGCCCGCT
451	TCTAAATAG				

This corresponds to the amino acid sequence <SEQ ID 3040; ORF 279>:

m279.pep

```

1  ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAQMALTCSS SKPRIAAIAP
101 TPCGTADCIS SARRRSLTA SAKFNAPAAT SAVYSPRLCP ATAAGVLPPA
151 SK*

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 3041>:

g279.seq

1	atgacgcgga	tttgcggtcg	cttgatttca	acggttttga	gtgtttcggc
51	aagtttgtcg	gcggcggggt	tcatcaggct	gcaatgggaa	ggaacggat
101	ccggcagcgg	cagggcgcg	ttggctccgg	cttctttggc	ggcagccatg
151	gtgctgccga	cggcggcggc	gttgctgca	atcacgactt	gtccgggcga
201	gttgaagt	acggcttcga	ccacttcgcc	ctgtgcggat	tcggcacaaa
251	tctgcctgac	ctgttcatct	tccaaaccca	aatggccgc	cattgcgcct
301	acgccttgcg	gtacggcgga	ctgcatcagt	tcggcgcgca	ggcggacgag
351	tttgacggca	tcggcaaaat	ccaatgcttc	ggcggcgaca	agcgcggtgt
401	attgcgcgag	gctgtgtccg	gcaacggcgg	caggcgtttt	gccgccact
451	tccaaatag				

This corresponds to the amino acid sequence <SEQ ID 3042; ORF 279.ng>:

g279.pep

```

1  MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTCSS SKPKMAAIAP
101 TPCGTADCIS SARRRTSLTA SAKSNSAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

```

          10      20      30      40      50      60
m279.pep ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRRARLAPASLAAAMARPTAAALPA
           :| ||||| |: |:||||| ||||||||| ||||||| ||||||| |||||: |||||
g279     MTRICGCLISTVLVSASLSAAGFIRLQWEGTDTGSGRRARLAPASLAAAMVRPTAAALPA
          10      20      30      40      50      60
```



```

              70          80          90          100          110          120
m279.pep      ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA
               ||| ||||| ||||| | ||| : ||||| ||| :: ||||| ||||| ||||| ||||| |||||
g279           ITTCPGELKLTASTTSPCADSAQICLTCSSSKPKMAAIAPTPCGTADCISSARRRTSLTA
               70          80          90          100          110          120

              130          140          150
m279.pep      SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX
               ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g279           SAKSNASAATSAVYSPRLCPATAAGVLPPTSKX
               130          140          150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3043>:

a279.seq

```
1 ATGACNCNGA TTTGCGGCTG CTTGATTTC ACGGTTTNA GGGCTTCGGC
51 GAGTTTGTCT GCGGCGGGTT TCATGAGGCT GCAATGGGA GGTCACGACA
101 CNGGCAGCGG CAGGGCGCGT TTGGCGCCGG CTTCTTTGGC GGCAAGCATA
151 GCGCGCTCGA CGGCGGCGGC ATTGCCTGCA ATCAGACTT GTCCGGGCGA
201 GTTGAAGTTG ACGGCTTCAA CCACTTCATC CTGTGCGGAT TCGGCGCAAA
251 TTTGTTTTAC CTGTTCACT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACCCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA NGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT CCAATGCGCC GCGGCAACN AGTGCGGTGT
401 ATTCGCCGAN GCTGTGTCG GCAACGGCGG CAGGCGTTTT GCCGCCCGT
451 TCCGAATAG
```

This corresponds to the amino acid sequence <SEQ ID 3044; ORF 279.a>:

a279.ppep

1	MTXICGCLIS	TVXRASASLS	AAGFMRLQWE	GTDTGSGRAR	LAPASLAASI
51	ARSTAAALPA	ITTCPGELKL	TASTTSSCAD	SAQICFTCSS	SKPRIAAIAP
101	TPCGTADCIS	SARXRTSLTA	SAKSNAPEAT	SAVYSEPLCP	ATAAGVLPPA
151	SE*				

m279/a279 ORFs 279 and 279.a showed a 88.2% identity in 152 aa overlap

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLOWEGTDTGSGRRARLAPASLAAAMARPTAAALPA					
a279	: : :					
	10	20	30	40	50	60
	MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRRARLAPASLAASIARSTAAALPA					
	70	80	90	100	110	120
m279.pep	ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA					
a279	:					
	70	80	90	100	110	120
	ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTPCGTADCISSARXRTSLTA					
	130	140	150			
m279.pep	SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX					
a279	:					
	130	140	150			
	SAKSNAAPAATSAVYSPXLCPATAAGVLPPASEX					

519 and 519-1 gnm7.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3045>:

m519.seq (partial)

```
1  ..TCCGTTATCG GCGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
51  AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGgCTTgGG
101 GTGTGAAGGT TTTGCGTTAT GAGATTAAAG ACTTGGTTCC GCCCAAGAA
151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAAACGCGC
201 CCGTATCGCC GAATCCGAAG GTCGTAAAAT CGAACAAATC AACCTTGCCA
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251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
351 AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA
401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTTGCCGAC ATCGGCAGCC
551 TGATTTCTGC CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

```

This corresponds to the amino acid sequence <SEQ ID 3046; ORF 519>:

```

m519.pep (partial)
  1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
  51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGQREAE IQQSEGEAQAA
 101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
 151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLISAGMK IIDSSKTAK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3047>:

```

g519.seq
  1 atggaatttt tcattatctt gttggcagcc gtcgccgttt tcggcttcaa
  51 atcctttgtc gtcattcccc agcaggaagt ccacgttgtc gaaaggctcg
 101 ggcgtttcca tcgcgccctg acggccggtt tgaatatatt gattcccttt
 151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
 201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actggtgacg
 251 gcatcatcta tttccaagta accgatccca aactcgctc atacggttcg
 301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
 351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
 401 tcaacagtac cgtcgtctcc gccctcgatg aagccgccgg ggcttggggg
 451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
 501 ctttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
 551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa cttgccaagt
 601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctcaggctgc
 651 ggtcaatgcg tccaatgccg agaaaatcgc ccgcatcaac cgcgccaag
 701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
 751 cgtcaaattg ccgccgccct tcaaacccaa agcggggcgg atgcggtcaa
 801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaag
 851 aagacaatac gcggattaag cccgccaagg ttgccgaaat cgggaaccct
 901 aattttcggc ggcatgaaaa attttcgcca gaagcaaaaa cggccaata
 951 a

```

This corresponds to the amino acid sequence <SEQ ID 3048; ORF 519.ng>:

```

g519.pep
  1 MEFFIILLAA VAVFGFSKV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
  51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGQAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAAN
 251 RQIAAALQTQ SGADAVNLKI AGQVVTAFKN LAKEDNTRIK PAKVAEIGNP
 301 NFRRHEKFSP EAKTAK*

```

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

m519/g519

```

m519.pep
          10      20      30
          SVIGRMELDKTFEERDEINSTVVAALDEAA
          |||||
g519      YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
          90      100     110     120     130     140
          40      50      60      70      80      90
m519.pep  GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLAGQREAE

```

```

|||||
g519      GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGKRIEQINLASQREAE
          150      160      170      180      190      200

          100      110      120      130      140      150
m519.pep  IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTGGADAV
          |||||
g519      IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAANRQIAAALQTQSGADAV
          210      220      230      240      250      260

          160      170      180      190      200
m519.pep  NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK
          |||||
g519      NLKIAGQYVTAFKNLAKEDNTRIKPAKVAEIGNPNFRRHEKFSPEAKTAK
          270      280      290      300      310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3049>:

```

a519.seq
1   ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGGGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGC AAGCCGAAAT CCAACAATCC GAAGCGGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3050; ORF 519.a>:

```

a519.pep
1   MEFFIILLAA VVVFgKFSFV VIPQqEVHVv ERLGRFhRAL TAGLNILIPF
51  IDRvAYRHsL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLRsVIG RMELDKTFEE RDEINSTVVS ALDEAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEg RKIEQINLAS
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519/a519 ORFs 519 and 519.a showed a 99.5% identity in 199 aa overlap

```

          10      20      30
m519.pep  SVIGRMELDKTFEERDEINSTVVAALDEAA
          |||||
a519      YFQVTDPKLASYGSSNYIMAITQLAQTTLRsVIGRMELDKTFEERDEINSTVVSALDEAA
          90      100      110      120      130      140

          40      50      60      70      80      ' 90
m519.pep  GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGKRIEQINLASQREAE
          |||||
a519      GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGKRIEQINLASQREAE
          150      160      170      180      190      200

          100      110      120      130      140      150

```

```

m519.pep      IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a519          IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
                210      220      230      240      250      260

                160      170      180      190      200
m519.pep      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a519          NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                270      280      290      300      310

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3051>:

```

m519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
101 GCGGTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC TGTGTGTGCG GCTTTGGACG AGGCGGCCGG GGCTTGGGGT
451 GTGAAGGTTT TGC GTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3052; ORF 519-1>:

```

m519-1.
1  MEFFIILLVA VAVFGKSFV VIPOQEVHVV ERLGRFHRAL TAGLNILIPF
51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3053>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51 ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGGGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG

```

851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GCATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 3054; ORF 519-1.ng>:

g519-1.pep
 1 MEFFIILLAA VAVFGFKSFV VIPQQEVHV V ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

m519-1/g519-1 ORFs 519-1 and 519-1.ng showed a 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
	130	140	150	160	170	180
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
	190	200	210	220	230	240
g519-1.pep	KRARIAESEG RKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEG RKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
	250	260	270	280	290	300
g519-1.pep	LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
m519-1	LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
	250	260	270	280	290	300
	310					
g519-1.pep	ISAGMKIIDS SKTAKX					
m519-1	ISAGMKIIDS SKTAKX					
	310					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3055>:

a519-1.seq
 1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
 51 ATCCTTTGTT GTCATCCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
 101 GGCGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
 201 ATCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
 251 GTATCATCTA TTTCCAAGTA ACCGACCCA AACTCGCCTC ATACGGTTCG
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
 351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTGAAGAA CGCGACGAAA

```

401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TCGGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTACAGCGC AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAA TATCGACAGC AGCAAAACCG CCAATAAT

```

This corresponds to the amino acid sequence <SEQ ID 3056; ORF 519-1.a>:

a519-1.pep.

```

1  MEFFIILLAA VVVFGEKSFV.VIPQEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGQAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQIQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 ORFs 519-1 and 519-1.a showed a 99.0% identity in 315 aa overlap

a519-1.pep	10	20	30	40	50	60
	MEFFIILLAAVVVFGEKSFV.VIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSI					
m519-1	MEFFIILLVAVAVFGEKSFV.VIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSI					
	10	20	30	40	50	60
a519-1.pep	70	80	90	100	110	120
	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
a519-1.pep	130	140	150	160	170	180
	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQQAQITAERE					
	130	140	150	160	170	180
a519-1.pep	190	200	210	220	230	240
	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
a519-1.pep	250	260	270	280	290	300
	LVAEANAIAIRQIAAALQIQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
m519-1	LVAEANAIAIRQIAAALQIQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
	250	260	270	280	290	300
a519-1.pep	310					
	ISAGMKIIDSSKTAKX					
m519-1	ISAGMKIIDSSKTAKX					
	310					

576 and 576-1 gnm22.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3057>:

```
m576.seq.. (partial)
1  ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
51  GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
151 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
201 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
451 GTGATTCCGG GTTGGACCGA AGCGGTACAG CTTCTGAAAG AAGGCGGCGA
501 AGCCACGTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551 GCGACAAAAT CCGTCCGAAC GCCACTTGG TATTGATGT GAAACTGGTC
601 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651 CATCAAAAAA GTAAATTAA
```

This corresponds to the amino acid sequence <SEQ ID 3058; ORF 576>:

```
m576.pep.. (partial)
1  ..MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVKLV
201 KIGAPENAPA KQPAQVDIKK VN*
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3059>:

```
g576.seq.. (partial)
1  ..atgggcgtgg acatcggacg ctccctgaaa caaatgaagg aacaggggcg
51  ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaaatgacc gaagagcagg cccaggaagt gatgatgaaa
151 ttctgcagg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccg
251 aagacggcgt gaagaccact gcttcgggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcggtt ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccgcc caccttcctt ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtgcgg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactggtca aaatcggcgc acccgaaaa
601 gcgcccgcga agcagccgga tcaagtcgac atcaaaaaag taaattaa
```

This corresponds to the amino acid sequence <SEQ ID 3060; ORF 576.ng>:

```
g576.pep.. (partial)
1  ..MGVDIGRSLK QMKEQGAIED LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51  FLQEQQAKAV EKHKADAKAN KEKGAEFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIPGWTE
151 GVRLLEKGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 ORFs 576 and 576.ng showed a 97.2% identity in 215 aa overlap

```

              10      20      30      40      50      60
m576.pep  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQAQEVMMKFLQ
              |||:|||||

```

```

g576          MGVDIGRSLKQMKEQGAIEDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLQ
                10      20      30      40      50

                70      80      90      100     110     120
m576.pep      EQQAKAVEKHKADAKANKEKGEAFLKENAAKDGVKTTASGLQYKITKQEGEGKQPTKDDIV
                |||||:|||||:|||||:|||||:|||||:|||||
g576          EQQAKAVEKHKADAKANKEKGEAFLKENAAEDGVKTTASGLQYKITKQEGEGKQPTKDDIV
                60      70      80      90      100     110

                130     140     150     160     170     180
m576.pep      TVEYEGRLIDGTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYRE
                |||||:|||||:|||||:|||||:|||||:|||||
g576          TVEYEGRLIDGTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYRE
                120     130     140     150     160     170

                190     200     210     220
m576.pep      QGAGDKIGPNATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN
                |||||:|||||:|||||:|||||
g576          QGAGEKIGPNATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN
                180     190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3061>:

```

a576.seq
1   ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTT'TCCG CCGCTT'TGGC
51  ACTTTCGCCG TGCGGCAAAA AAGAAGCCGC CCCC GCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCTTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 3062; ORF 576.a>:

```

a576.pep
1   MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAIEDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLKENAA KDGKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

m576/a576 ORFs 576 and 576.a showed a 99.5% identity in 222 aa overlap

```

                10      20      30
m576.pep      MQQASYAMGV DIGRSLKQMKEQGAIEDLKV
                |||||:|||||:|||||:|||||:|||||:|||||
a576          CGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV DIGRSLKQMKEQGAIEDLKV
                30      40      50      60      70      80

                40      50      60      70      80      90
m576.pep      FTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKHKADAKANKEKGEAFLKENAA
                |||||:|||||:|||||:|||||:|||||:|||||
a576          FTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKHKADAKANKEKGEAFLKENAA
                90      100     110     120     130     140

```


	100	110	120	130	140	150
m576.pep	KDGVKTTASGLQYKITYKQEGKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ					
a576	KDGVKTTASGLQYKITYKQEGKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ					
	150	160	170	180	190	200
	160	170	180	190	200	210
m576.pep	VIPGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA					
a576	VILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA					
	210	220	230	240	250	260
	220					
m576.pep	KQPAQVDIKKVN					
a576	KQPAQVDIKKVN					
	270					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3063>:

```
m576-1.seq
1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA
```

This corresponds to the amino acid sequence <SEQ ID 3064; ORF 576-1>:

```
m576-1.pep
1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*
```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3065>:

```
g576-1.seq
1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTGCCGCG CAGGGCGACA CCTCTCAAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
201 ACAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGATG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCCCAGGAAG TGATGATGAA ATTCCTGCAG GAGCAGCAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
401 TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
451 CTGCAATACA AAATACCAA ACAGGGTGAA GGCAAACAGC CGACAAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG CCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
```

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701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 3066; ORF 576-1.ng>:

```

g576-1.pep
  1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPDQVDIKK VN*

```

g576-1/m576-1 ORFs 576-1 and 576-1.ng showed a 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISAL	TLSAALALSA	CGKKEAAPAS	ASEPAASAA	QGDTSSIGST	MQQASYAMGV
m576-1	MNTIFKISAL	TLSAALALSA	CGKKEAAPAS	ASEPAASSA	QGDTSSIGST	MQQASYAMGV
	10	20	30	40	50	60
	70	80	90	100	110	120
g576-1.pep	DIGRSLKQMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEEQ	AQEVMKFLQ	EQQAKAVEKH
m576-1	DIGRSLKQMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEEQ	AQEVMKFLQ	EQQAKAVEKH
	70	80	90	100	110	120
	130	140	150	160	170	180
g576-1.pep	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITKQGE	GKQPTKDDIV	TVEYEGRLID
m576-1	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITKQGE	GKQPTKDDIV	TVEYEGRLID
	130	140	150	160	170	180
	190	200	210	220	230	240
g576-1.pep	GTVPDSSKAN	GGPATFPLSQ	VIPGWTEGVR	LLKEGGEATF	YIPSNLAYRE	QGAGEKIGPN
m576-1	GTVPDSSKAN	GGPATFPLSQ	VIPGWTEGVR	LLKEGGEATF	YIPSNLAYRE	QGAGEKIGPN
	190	200	210	220	230	240
	250	260	270			
g576-1.pep	ATLVFDVKLV	KIGAPENAPA	KQPDQVDIKK	VN		
m576-1	ATLVFDVKLV	KIGAPENAPA	KQPDQVDIKK	VN		
	250	260	270			

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3067>:

```

a576-1.seq
  1 ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
 51 ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCAGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAA CAGGCGCCCG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCCG
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCCG

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701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 3068; ORF 576-1.a>:

a576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLQOMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 ORFs 576-1 and 576-1.a showed a 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a576-1.pep	DIGRSLQOMKEQGAEIDLKVFTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLQOMKEQGAEIDLKVFTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
	130	140	150	160	170	180
a576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
	250	260	270			
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

919 gnm43.seq

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3069>:

m919.seq

```

1  ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TACGGCATCG CCGCCGCCAT
51  CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGCGGCGCG CGGGGCCGTC TATACCGTTG TACCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATT TCGCCAAAAGC CTGCAATCCT
251 TCCGCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGCCCCAAG CCTTCAAAC CCCCGTCCAT TCCTTTCAGG CAAAACAGTT
351 TTTTGAACGC TATTACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGACAGG

```

```

451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCCG ATTCCCATC ACCGCGCGCA CAACAGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCGATACT CGGTTACGCC
751 GAAGACCCTG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCyTA CGTTTCCATC GGACGCTATA TGGCGGATAA GGGCTACCTC
901 AAATCGGAC AAACCTCCAT GCAGGCATT AAGTCTTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCCGCTGA TGGGGGAATA TGCCGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGTGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCACGAAG CCGGCGAACT
1251 TGCCGGCAA CAGAAAACCA CGGGATATGT CTGGCAGCTC CTACCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3070; ORF 919>:

m919.pep

```

1  MKKYLFRAL YGIAAILAA CQSKIQTFF QPDSVINGP DRPVGIPDPA
51  GTTVGGGAV YTVPHLSLP HWAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIQTGKN SGTIDNTGGT
201 HTADLSRFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KSYMQRNPQR LAEVLGQNPS YIFFRELAGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTGYVWQL LPNGMKPEYR P*

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 3071>:

g919.seq

```

1  ATGAAAAAAC ACCTGCTCCG CTCGCCCTG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCC GACCGGCCG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATTT TGCCAAAAGC CTGCAATCCT
251 TCCGCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTCACGC cgtGGCaggt tgcaggcaAC GGAAGcCTTG
401 Caggtacggt TACCGGCTAT TACGAACCG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACCGCCG ACCTCTCCCG ATTCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCgcgCTT GACGGCAAag cccCCATCCT CggttacgcC
751 GAagaccCcG tcgaacttTT TTTCATGCAC AtccaaggCT CGGGCCGCCT
801 GAAAACCCcg tccggcaaat acatCCGCAt cggaTacgcc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcatc aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCCGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GGCACGAAG CCGGCGAACT
1251 TGCCGGCAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 3072; ORF 919.ng>:

g919.pep

1	<u>MKKHLLRSAL</u>	<u>YGIAAAILAA</u>	CQSRSIQTFP	QPDTSVINGP	DRPAGIPDPA
51	GTTVAGGGAV	YTVVPHLSMP	HWAAQDFAKS	LQSFRLGCAN	LKNRQGWQDV
101	CAQAFQTPVH	SFQAKRFFER	YFTPWQVAGN	GSLAGTVTGY	YEPVLKGDGR
151	RTERARFPIY	GIPDDFISVP	LPAGLRGGKN	LVRIRQTGKN	SGTIDNAGGT
201	HTADLSRFPI	TARTTAIKGR	FEGRSFLPYH	TRNQINGGAL	DGKAPILGYA
251	EDPVELFFMH	IQGSGRLKTP	SGKIYIRIGYA	DKNEHPYVSI	GRYMADKGYL
301	KLQOTSMQGI	KAYMRQNPQR	LAEVLGQNPS	YIFKRELASG	QNEGPVGALG
351	TPLMGEYAGA	IDRHYITLGA	PLFVATAHPV	TRKALNRLIM	AQDTGSAIKG
401	AVRVDYFWGY	GDEAGELAGK	QKTTGYVWQL	LPNGMKPEYR	P*

ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF 919.ng) from *N. gonorrhoeae*:

m919/g919					
	10	20	30	40	50
m919.pep	MKKYLFR	AAALYGIAAA	ILAACQSKSIQ	TFFPQPDTSV	INGPDRPVGI
	60				
	10	20	30	40	50
g919	MKKHLLRS	ALYGIAAA	ILAACQSRSIQ	TFFPQPDTSV	INGPDRPAGI
	60				
	70	80	90	100	110
m919.pep	YTVVPHLS	LPHWAAQDFA	KSLSQSFRLG	CANLKNRQGW	QDVCAQAFQT
	120				
	70	80	90	100	110
g919	YTVVPHLS	MPHWAAQDFA	KSLSQSFRLG	CANLKNRQGW	QDVCAQAFQT
	120				
	130	140	150	160	170
m919.pep	YFTPWQVAG	NGSLAGTVTG	YIEPVVLKGD	DRRTAQARFPI	YIGIPDDFIS
	180				
	130	140	150	160	170
g919	YFTPWQVAG	NGSLAGTVTG	YIEPVVLKGD	GRRTERARFPI	YIGIPDDFIS
	180				
	190	200	210	220	230
m919.pep	LVRIRQTGK	NSGTIDNTGG	THTADLSRFP	ITARTTAIKGR	FEFSRFLPYH
	240				
	190	200	210	220	230
g919	LVRIRQTGK	NSGTIDNAGG	THTADLSRFP	ITARTTAIKGR	FEFSRFLPYH
	240				
	250	260	270	280	290
m919.pep	DGKAPILGY	AEDPVELFFM	HIQSGSRLKTP	SGKYIRIGYAD	KNEHPYVSI
	300				
	250	260	270	280	290
g919	DGKAPILGY	AEDPVELFFM	HIQSGSRLKTP	SGKYIRIGYAD	KNEHPYVSI
	300				
	310	320	330	340	350
m919.pep	KLQQTSMQG	IKSYMRQNPQ	RLAEVLGQNPS	YIFFRELAGSS	NDGPVAGLGT
	360				
	310	320	330	340	350
g919	KLQQTSMQG	IKAYMRQNPQ	RLAEVLGQNPS	YIFFRELAGSG	NEGPVAGLGT
	360				
	370	380	390	400	410
m919.pep	VDRHYITLG	APLFLVATAH	PVTRKALNRL	IMAQDTGSAIK	GAVRVDYFWG
	420				
	370	380	390	400	410
g919	IDRHYITLG	APLFLVATAH	PVTRKALNRL	IMAQDTGSAIK	GAVRVDYFWG
	420				

```

              430      440
m919.pep      QKTTGYVWQLLPNGMKPEYRPX
              |||||
g919           QKTTGYVWQLLPNGMKPEYRPX
              430      440

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3073>:

```

a919.seq
1  ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TCGGGCATCG CCGCCGCCAT
51 CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCGG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGGCGGCGG CGGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTCCAT TCCGTTTCAGG CAAAACAGTT
351 TTTTGAACGC TATTTACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCCA ATTCCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCGATACT CGGTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCGCTGA TGGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCCCAAG
1301 GTATGAAGCC CGAATACCG CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3074; ORF 919.a>:

```

a919.pep
1  MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDOR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSQFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMQQNPQR LAEVLGQNPS YIFFRELTGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

m919/a919 ORFs 919 and 919.a showed a 98.6% identity in 441 aa overlap

```

              10      20      30      40      50      60
m919.pep      MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
              |||||
a919           MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
              10      20      30      40      50      60

              70      80      90      100     110     120
m919.pep      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
              |||||
a919           YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
              70      80      90      100     110     120

```

	130	140	150	160	170	180
m919.pep	YFTPWQVAGNSLAGTVTGYE	PVLKGDDRRTAQARFPIY	GIPDDFISVPLPAGLRSGKA			
a919	YFTPWQVAGNSLAGTVTGYE	PVLKGDDRRTAQARFPIY	GIPDDFISVPLPAGLRSGKA			
	130	140	150	160	170	180
	190	200	210	220	230	240
m919.pep	LVRIRQTGKNSGTIDNTGGT	HADLSRFPITARTTAIKGR	FEGSRFLPYHTRNQINGGAL			
a919	LVRIRQTGKNSGTIDNTGGT	HADLSRFPITARTTAIKGR	FEGSRFLPYHTRNQINGGAL			
	190	200	210	220	230	240
	250	260	270	280	290	300
m919.pep	DGKAPILGYAEDPVELFFMH	IQSGRLKTPSGKYIRIGYAD	KNEHPVVSIGRYMADKGYL			
a919	DGKAPILGYAEDPVELFFMH	IQSGRLKTPSGKYIRIGYAD	KNEHPVVSIGRYMADKGYL			
	250	260	270	280	290	300
	310	320	330	340	350	360
m919.pep	KLGTSMQGIKSYMRQNPQRL	AEVLGQNPSYIFFREL	AGSSNDGPVGALGTPLMGEYAGA			
a919	KLGTSMQGIKAYMQNPQRL	AEVLGQNPSYIFFREL	TGSSNDGPVGALGTPLMGEYAGA			
	310	320	330	340	350	360
	370	380	390	400	410	420
m919.pep	VDRHYITLGAPLFVATAHPV	TRKALNRLIMAQDTGSAIK	GA VRVDYFWGYGDEAGELAGK			
a919	VDRHYITLGAPLFVATAHPV	TRKALNRLIMAQDTGSAIK	GA VRVDYFWGYGDEAGELAGK			
	370	380	390	400	410	420
	430	440				
m919.pep	QKTTGYVWQLLPNGMKPEYRPX					
a919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

121 and 121-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3075>:

m121.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCAGC CTTTACCCC TACCCGCGCA GGTACGCCG CCAATTGCTG
151 GATTTCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxGAGC TTCCTTACGA CAAAACGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACGCCACCC TAAAAGCAGG GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA

```

1051 GCAACCGGCG CATCCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG
1101 A

This corresponds to the amino acid sequence <SEQ ID 3076; ORF 121>:

m121.pap

1	METQLYIGIM	SGTSM DGADA	VLIRMDGGKW	LGAEGHAFTP	YPGRLLRQLL
51	DLQDTGADEL	HRSRI LSQEL	SRLYAQTA AE	LLCSQNLA PS	DITALGCHGQ
101	TVRHAP EHG Y	SIQLADL P L L	Axxxxxxxxx	xxxxxxxxxx	xxxxxxxxxx
151	xxxxxxxxxx	xxxxxxxxxx	xxxxxxxxxx	xxxxxxxxxx	xxxxxxxxxx
201	xxQLPYDKNG	AKSAQGNILP	QLLDRLLAHP	YFAQRHPKST	GRELFAINWL
251	ETYLDGGENR	YDVLRLTSRF	TAQTVCDAVS	HAAADARQMY	ICDGGIRNPV
301	LMADLAEFCF	TRVSLHSTAD	LNLD PQWVEA	AXFAWLAACW	INRIPGSPHK
351	ATGASKPCIL	XAGYYY*			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3077>:

g121.seq

1	ATGGAACAC	AGCTTTACAT	CGGCATTATG	TCGGAACCA	GTATGGACGG
51	GGCGGATGCC	GTGCTGGTAC	GGATGGACGG	CGGCAATGG	CTGGGCGCGG
101	AAGGGCAGCG	CTTTACCCCC	TACCTTGACC	GGTTGCGCCG	CAAATTGCTG
151	GATTTCAGG	ACACAGGCAC	AGACGAATC	CACCCGACGA	GGATGTTGTC
201	GCAAGAACTC	AGCGCGCTGT	ACGCGCAAC	CGCCGCGGAA	CTGTGTGCA
251	GTCAAAACCT	CGCTCCGTGC	GACATTACCG	CCCTCGGCTG	CCACGGGCAA
301	ACCGTCCGAC	ACGCGCCGGA	ACACGGTtac	AGCATACAGC	TTGCCGATTT
351	GCGCTGCTG	GCGGAACtGa	cgcggtattt	TACCGTCggc	gacttcCGCA
401	GCCGCGACCT	TGCTGCCGGC	GGacaAGGTG	CGCCGCTCGT	CCCCGCTTTT
451	CACGAAGCCC	TGTTTCCGCA	TGACAGGGAA	ACACCGCTGA	TACTGAACAT
501	CGCGGGGATT	GCGCAACATCA	CGCTACTCCC	CCCCGCGGCA	CCCGCTTTCG
551	GCTTCGACAC	AGGGCCGGGC	AATATGCTGA	TGGAcgcgtg	gacgcaggca
601	cacTGGcagc	TGCCTTACGA	CAAAAacggt	gcAAAGgcgg	cacAAGGCAA
651	catatTGCcg	cAACTGCTCG	gcaggetGCT	CGCCaaccCG	TATTTCTCAC
701	AACCCcacc	aaAAAGCAGC	GGgcGCGaac	Tgtttgccct	AAattggctc
751	gaacctAcc	ttgacgcggc	cgaaaaccga	tacgacgtat	tgcggagcgt
801	ttcccgattc	accgcgcgaaA	cggTttggga	cgcggtctca	CACGACGCGG
851	CAGATGCCCG	TCAATGTAC	ATTTGCGCGC	GCGGCATCCG	CAATCTGTT
901	TTAATGGCGG	ATTTGGCAGA	ATGTTTCGGC	ACACGCGTTT	CCCTGCACAG
951	CACCGCCGAA	CTGAACCTCG	ATCCTCAATG	GGTGAGGCG	gcgcCATTtg
1001	cgtggttgC	GGCGTGTTGG	ATTAACCGCA	TTCCCGGTAG	TCCGCACAAA
1051	GCGACCGGCG	CATCCAAACC	GTGTATTCTG	GGCGCGGGAT	ATTATTATTG
1101	A				

This corresponds to the amino acid sequence <SEQ ID 3078; ORF 121.ng>:

g121.pep

1	METQLYIGIM	SGTSM DGADA	VLVRMDGGKW	LGAEGHAFTP	YPDLRRKKLL
51	DLQDTGTDEL	HRSRMLSQEL	SRLYAQTAAE	LLCSQNLA PC	DITALGCHGQ
101	TVRHAP EHG Y	SIQLADLPLL	AELTRIFTVG	DFRSRDLAAG	GQGAPLVP AF
151	HEALFRDDRE	TRVVLNIGGI	ANISVLPPGA	PAFGFD TGPG	NMLMDAWTQA
201	HWQLPYDKNG	AKAAQGNILP	QLLGRLLAHP	YFSQPHPKST	GREL FALNWL
251	ETYLDGGENR	YDVLRLTSRF	TAQT VWDAVS	HAAADARQMY	ICGGGIRNPV
301	LMADLAECFG	TRVLSLSTAE	LNLD PQWVEA	AAFAWLAACW	INRIPGSPHK
351	ATGASKPCIL	GAGYYY*			

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDGADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL					
g121	METQLYIGIMSGTSMGDGADAVLVRMDGGKWLGAEGHAFTPYPDRLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPHEHGYSIQLADLPLL					


```

g121      HRSRMLSQELSRLYAQTAELLCSQNLAPCDITALGCHGQTVRHAPHEHGYSIQLADLPLL
           70      80      90      100     110     120
           130     140     150     160     170     180
m121.pep  AXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
           | : :
g121      AELTRIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRVVLNIGGIANISVLPPGA
           130     140     150     160     170     180
           190     200     210     220     230     240
m121.pep  XXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST
           : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g121      PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST
           190     200     210     220     230     240
           250     260     270     280     290     300
m121.pep  GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDASHAAADARQMYICDGGIRNPV
           | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g121      GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDASHAAADARQMYICGGGIRNPV
           250     260     270     280     290     300
           310     320     330     340     350     360
m121.pep  LMADLAECFGTRVSLHSTADLNLDPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g121      LMADLAECFGTRVSLHSTAE LNLDPQWVEAAFAWLAACWINRIPGSPHKATGASKPCIL
           310     320     330     340     350     360

m121.pep  XAGYYYYX
           | | | | |
g121      GAGYYYYX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3079>:

```

a121.seq
1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTACGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGGCGCGGC GGACAAGGCG CGCCGCTCGT CCCCCTTTT
451 CACGAAGCCC TGTTCGCGCA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCACGCA CCGCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTGCGAC
701 AACCCACCC TAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATT ACCGCGCAAA CCGTTTTTCA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCC TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCC
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3080; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGLRRLKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPESY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV

```

301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK
 351 ATGASKPCIL GAGYYY*

m121/a121 ORFs 121 and 121.a showed a 74.0% identity in 366 aa overlap

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSM	GADAVLIRMDGGKWL	GAEGHAFTPYPGRL	RRQLLDLQDTGADEL		
a121	METQLYIGIMSGTSM	GADAVLIRMDGGKWL	GAEGHAFTPYPGRL	RRQLLDLQDTGADEL		
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSR	LYAQTAELLCSQNL	APSDITALGCHGQ	TVRHAPENHGY	SIQLADLPLL	
a121	HRSRILSQELSR	LYAQTAELLCSQNL	APSDITALGCHGQ	TVRHAPENHGY	SIQLADLPLL	
	70	80	90	100	110	120
	130	140	150	160	170	180
m121.pep	XXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXX
		:	:	:	:	:
a121	AERTQIFTVGDFR	SRDLAAGGQGAP	LVPFHEALFRDD	RETRAVLNIGGI	ANISVLP	PPDA
	130	140	150	160	170	180
	190	200	210	220	230	240
m121.pep	XXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXX
	:	:	:	:	:	:
a121	PAFGFDTGPGN	MLMDAWMQAHW	QLPYDKNGAKA	QAQGNILPQLLD	RLLAHFYAQR	HPKST
	190	200	210	220	230	240
	250	260	270	280	290	300
m121.pep	GRELFAINWLET	YLDGGENRYD	VLRTLSRFTAQ	TVCDVSHAAAD	ARQMYICDGG	IRNPV
a121	GRELFAINWLET	YLDGGENRYD	VLRTLSRFTAQ	TVCDVSHAAAD	ARQMYICDGG	IRNPV
	250	260	270	280	290	300
	310	320	330	340	350	360
m121.pep	LMADLAECFGTR	VSLHSTADLNL	DPQWVEAAXFA	WLAACWINRI	PGSPHKATG	ASKPCIL
a121	LMADLAECFGTR	VSLHSTADLNL	DPQWVEAAXFA	WLAACWINRI	PGSPHKATG	ASKPCIL
	310	320	330	340	350	360
m121.pep	XAGYYYYX					
a121	GAGYYYYX					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3081>:

m121-1.seq

1	ATGGAAACAC	AGCTTTACAT	CGGCATCATG	TCGGGAACCA	GCATGGACGG
51	GGCGGATGCC	GTA CTGATAC	GGATGGACGG	CGGCAAATGG	CTGGGCGCGG
101	AAGGGCACGC	CTTTACCCCC	TACCCCGGCA	GGTTACGCCG	CCAATTGCTG
151	GATTTGCAGG	ACACAGGCGC	AGACGAACTG	CACCGCAGCA	GGATTTTGTC
201	GCAAGAACTC	AGCCGCCTAT	ATGCGCAAAC	CGCCGCCGAA	CTGCTGTGCA
251	GTCAAAACCT	CGCACCGTCC	GACATTACCG	CCCTCGGCTG	CCACGGGCAA
301	ACCGTCCGAC	ACGCGCCGGA	ACACGGTTAC	AGCATACAGC	TTGCCGATTT
351	GCCGCTGCTG	GCGGAACGGA	CGCGGATTTT	TACCGTCGGC	GACTTCCGCA
401	GCCGCGACCT	TGCGGCGCGC	GGACAAGGCG	CGCCACTCGT	CCCCGCCTTT
451	CACGAAGCCC	TGTTCCGCGA	CAACAGGGAA	ACACGCGCGG	TACTGAACAT
501	CGGCGGGATT	GCCAACATCA	CGGTACTCCC	CCCCGACGCA	CCCGCCTTCG
551	GCTTCGACAC	AGGGCCGGGC	AATATGCTGA	TGGACGCGTG	GACGCAGGCA
601	CACTGGCAGC	TTCCTTACGA	CAAAAACGGT	GCAAAGGCGG	CACAAGGCAA
651	CATATTGCCG	CAACTGCTCG	ACAGGCTGCT	CGCCCACCCG	TATTTGCGAC
701	AACCCACACC	TAAAAGCACG	GGGCGCGAAC	TGTTTGCCCT	AAATTGGCTC
751	GAAACCTACC	TTGACGGCGG	CGAAAACCGA	TACGACGTAT	TGCGGACGCT
801	TTCCCGTTTT	ACGCGCGAAA	CCGTTTGCGA	CGCCGTCTCA	CACGCAGCGG

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851 CAGATGCCCC TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGNATTTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG ANCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3082; ORF 121-1>:

```

m121-1.pep
  1 METQLYIGIM SGTSMGDGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRQLL
  51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
 101 TVRHAPHEGY SIQLADLPLL AERTRIFTVG DFRSRDLAAG GQGAPLVPAPF
 151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDTPGP NMLMDAWTQA
 201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
 251 ETYLDGGENR YDVLRTLSRF TAQTVCDAYS HAAADARQMY ICGGGIRNPV
 301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
 351 ATGASKPCIL XAGYYY*

```

m121-1/g121 ORFs 121-1 and 121.ng showed a 95.6% identity in 366 aa overlap

m121-1.pep	10	20	30	40	50	60
	METQLYIGIMSGTSMGDGADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLLDLQDTGADEL					
	: : : : :					
g121	10	20	30	40	50	60
	METQLYIGIMSGTSMGDGADAVLVRMDGGKWLGAEGHAFTPYPDRLLRKLDDLQDTGTDEL					
	: : : : :					
m121-1.pep	70	80	90	100	110	120
	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPHEGYSIQLADLPLL					
	: : : : :					
g121	70	80	90	100	110	120
	HRSRMLSQELSRLYAQTAAELLCSQNLAPCDITALGCHGQTVRHAPHEGYSIQLADLPLL					
	: : : : :					
m121-1.pep	130	140	150	160	170	180
	AERTRIFTVGDFRSRDLAAGGQAPLVPAPFHEALFRDNRETRAVLNIGGIANISVLPPDA					
	: : : : :					
g121	130	140	150	160	170	180
	AELTRIFTVGDFRSRDLAAGGQAPLVPAPFHEALFRDDRETRVVLNIGGIANISVLPPGA					
	: : : : :					
m121-1.pep	190	200	210	220	230	240
	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	: : : : :					
g121	190	200	210	220	230	240
	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST					
	: : : : :					
m121-1.pep	250	260	270	280	290	300
	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDAVSHAAADARQMYICGGGIRNPV					
	: : : : :					
g121	250	260	270	280	290	300
	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDAVSHAAADARQMYICGGGIRNPV					
	: : : : :					
m121-1.pep	310	320	330	340	350	360
	LMADLAECFGTRVSLHSTADLNLDPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
	: : : : :					
g121	310	320	330	340	350	360
	LMADLAECFGTRVSLHSTAELNLDPQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	: : : : :					
m121-1.pep	XAGYYYYX					
g121	GAGYYYYX					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3083>:

```

a121-1.seq
  1 ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG

```

```

51  GCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTACGCGG CAAATTGCTG
151 GATTTGCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TGCCCGATT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGGCGCGGC GGACAAGGCG CGCCGCTCGT CCCCCTTTT
451 CACGAAGCCC TGTTCCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCCGCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACCGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCCG TATTTCGCAC
701 AACCCACACC TAAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCATTTC ACCGCGCAAA CCGTTTTCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAAGAAGC GCCGCGTTCG
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCAAACC GTGTATTCTG GGCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3084; ORF 121-1.a>:

a121-1.pep

```

1  METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPESY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPOWVEA AFAWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

m121-1/a121-1 ORFs 121-1 and 121-1.a showed a 96.4% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLLDLQDTGADEL					
a121-1	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLLDLQDTGADEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSRLYAQTAAELLCSONLAPSDITALGCHGQTVRHAPHEHGYISQLADLPLL					
a121-1	HRSRILSQELSRLYAQTAAELLCSONLAPSDITALGCHGQTVRHAPESYSVQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121-1.pep	AERTQIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDRETRAVLNIGGIANISVLPPDA					
a121-1	AERTQIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121-1.pep	PAFGFDTPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
a121-1	PAFGFDTPGNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121-1.pep	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADARQMYICGGGIRNPV					
a121-1	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFCDVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300

```

          310      320      330      340      350      360
m121-1.pep  LMADLAECFGTRVSLHSTADLNLDLPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL
          |||||:|||||:|||||:|||||:|||||
a121        LMADLAECFGTRVSLHSTAE LNLDLPQWVEAAAFAWMAACWVNRIPGSPHKATGASKPCIL
          310      320      330      340      350      360

m121-1.pep  XAGYYYYX
          |||||
a121        GAGYYYYX

```

128 and 128-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3085>:

```

m128.seq (partial)
1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AATCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCG AATCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTG
201 GGGCGTGGTG TCGCACCTCA ACTGCGTCGC CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAATGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAA AACCAACTC AACCAC
1  TACGCCAGCG AAAAAGTGGC CGAAGCCAAA TACGCGTTCA GCGAAACCGA
51  wGTCAAAAAA TAYTTCCcyG TCGGCAAwGT ATTAACCGGA CTGTTGCCCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAAC yGTCCCCGTC
151 TGGCACAAAG ACGTGCCTTA TtTGAATTG CAACAAAACG GCGAAmCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAAA CGCGGCGGCG
251 CGTGGATGAA CGACTACAAA GGCCGCCGCC GTTTTTCAGA CGGCACGCTG
301 CAAYTGCCCA CCGCCTACCT CGTCTGCAAC TTCGCCCCAC CCGTCGGCGG
351 CAGGGAAGCC CGCyTGAGCC ACGACGAAAT CCTCATCCTC TTCCACGAAA
401 CCGGACACGG GCTGCACCAC CTGCTTACCC AAGTGGACGA ACTGGGCGTA
451 TCCGGCATCA ACGGCGTAKA ATGGGACGCG GTCGAACTGC CCAGCCAGTT
501 TATGGAATAA TTCGTTTGGG AATACAATGT CTTGGCACAA mTGTAGCCC
551 ACGAAGAAAC CGGcgTTCCC yTGCCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCCGCCAAAA ACTTCCAAsG CGGCATGTTC yTsGTCCGGC AAwTGGAGTT
651 CGCCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCCGTCTGA
701 AAAACTGGCA ACAGGTTTGA GACAGCGTGC GCAAAAAAGT CGCCGTCTAT
751 CAGCCGCCCC AATACAACCG CTTCGCCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGCAGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCCGCC TTTGAAGAAA GCGACGATGT CGCCGCCACA
901 GGCAAACGCT TTTGGCAGGA AATCTTCGCC GTCGGGGnAT CGCGCAGCGG
951 nGCAGAATCC TTCAAAGCCT TCCGCGGCCG CGAACCGAGC ATAGACGCAC
1001 TCTTGCGCCA CAGCGGTTTC GACAACGCGG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 3086; ORF 128>:

```

m128.pep (partial)
1  MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWG
51  NTVEPLTGIT ERVGRWGVV SHLNCVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NH

//
1  YASEKLREAK YAFSETXVKK YFPVGXVLNG LFAQXKKLYG IGFTEKTVPV
51  WHKDVRYXEL QONGEXIGGV YMDLYAREGK RGGAWMNDYK GRRRFS DGTL
101 QLPTAYLVCN FAPPVGGREA RLSHDEILIL FHETGHGLHH LLTQVDELGV
151 SGINGVXWDA VELPSQFMEN FVWEYNVLAQ XSAHEETGVP LPKELXDKXL
201 AAKNFQXGMF XVRQXEFALF DMMIYSEDDE GRLKNWQQVL DSVRKKVAVI
251 QPPEYNRFAL SFGHIFAGGY SAAXYSYAWA EVLSADAYAA FEESDDVAAT
301 GKRFWQEILA VGXSRSGAES FKAFRGREPS IDALLRHSGF DNAV*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3087>:

```

g128.seq
1   atgattgaca acgCActgct ccacttgggc gaagaaccCC GTTTtaatca
51  aatccaaacc gaagACAtca AACCCGCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTGCA ACGCTTTCCT CCGCACAAAA AACCAAGCTC GATCACGACC
401 TGCGCGATTT CGTATTGAGC GCGCGGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAAAC CGAAGGCGCG CAACTTTCCT CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTATACC AATACGCCGG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGcctaa cTGCTCGGCT TTAAAAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACGCCC GAACAGGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCTTA CGCCGAAAAA GACCTGCGCG AAGTCAAAGC
951 CTTGCGCCGC GAACACCTCG GTCTCGCCGA CCCGACGCCG TGGGACTTGA
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTTCTGGCAG GCCTGTTTCG
1101 CCAAATCAAA AACTCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCAAAACC
1201 ATCGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACCGGCGCG
1251 CGCGTGGATG AACGACtaca AAGGCCGCCG CCGCTTTGCC GACGgcacGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACCC TCTTCCACGA
1401 AacCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGGCAT CAacggcgta GAATGGGACG CGGTGCAACT GCCGACCCAG
1501 TTTATGGAAA ACTTCGTTTG GGAATACAAT GTATTGGCAC AAATGTCCGC
1551 CCACGAAGAA AccgGCGAGC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TcgCGCCCAA AACTTCCAG CGCGGTATGT TCCTCGTCCG GCAAATGGAG
1651 TTCGCCCTCT TCGATATGAT GATTACAGT GAAAGCGACG AATGCCGTCT
1701 GAAAAACTGG CAGCAGGTTT TAGACAGCGT GCGCAAAGAA GTcGCCGTCA
1751 TCCAACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCacatctTC
1801 GCcggcGGCT ATTCCGcAGG CTATTACAGC TACGCATGGG CCGAAGTCct
1851 cAGCACCGAT GCCTACGCCG CCTTTGAAGA AAGcGACGac gtcGCCGCCA
1901 CAGGCAAACG CTTCTGGCAA GAAAtccttg ccgtcggcgg ctCCCGCAGC
1951 gcgCGGGAAT CCTCAAAAGC CTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTGCTGCGC Caaagcgggt TCGACAACGC gCcttgA

```

This corresponds to the amino acid sequence <SEQ ID 3088; ORF 128.ng>:

```

g128.pep
1   MIDNALLHLG EEPFRNQIQT EDIKPAVQTA IAEARGQIAA VKAQHTTGWA
51  NTVERLTGIT ERVGRIGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEI SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDSYAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQQNGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTLQLPTAY LVCNFAPPVG
451 GKEARLSHDE IITLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS ESDECRLKNW QQVLDSVRKE VAVIQPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYAAFEESDD VAATGKRFWQ EILAVGGSRS

```

651 AAESFKAFRG REPSIDALLR QSGFDNAA*

ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng)
from *N. gonorrhoeae*:

m128/g128

g128.pep	10	20	30	40	50	60
	MIDNALLHLGEEPRFNQIQTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT					
m128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGWANTVEPLTGIT					
	10	20	30	40	50	60
g128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
g128.pep	130	140	150	160	170	180
	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128	TLSPAQKTKLNH					
	130					
	//					
g128.pep	340	350	360			
	YAGEKLREAKYAFSETEVKKYFPVGKVLG					
m128	YASEKLREAKYAFSETXVKKYFPVGXVLNG					
	10	20	30			
g128.pep	370	380	390	400	410	420
	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQQNGKTIGGVYMDLYAREGKRGGAWMNDYK					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQQNGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
g128.pep	430	440	450	460	470	480
	GRRRFADGTLQLPTAYLVCNFAPPVVGKEARLSHDEILTLFHETGHGLHLLTQVDELGV					
m128	GRRRFSGTLQLPTAYLVCNFAPPVVGREARLSHDEILILFHETGHGLHLLTQVDELGV					
	100	110	120	130	140	150
g128.pep	490	500	510	520	530	540
	SGINGVEWDVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQRGMF					
m128	SGINGVXWDVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKMLAAKNFQXGMF					
	160	170	180	190	200	210
g128.pep	550	560	570	580	590	600
	LVRQMEFALFDMMIYSESDECRKKNWQQVLDVSRKEVAVIQPPEYNRFANSFGHIFAGGY					
m128	XVRQXEFALFDMMIYSEDEGRKKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
g128.pep	610	620	630	640	650	660
	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRGREPS					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRGREPS					
	280	290	300	310	320	330

```

          670      679
g128.pep  IDALLRQSGFDNAA
          |||||:|||||:
m128      IDALLRHSGFDNAVX
          340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3089>:

```

a128.seq
1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTCAC CGACACGCCC GAACTGCGCG
251 CCGCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACACGATC
401 TGCGCGATTT CGTCTCAGC GGCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTATCC AATACGCCGA CAACCGCAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCGCGCCGCG CCAAACCCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCGCCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTCCG
1101 CCAAATCAAA AAATCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCGC CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCTAC CTCGTCTGCA ACTTCACCCC GCGCGTCGGC
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAA ATTTCGTTTG GGAATACAAT GTCTTGCGCG AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCGCCCAA AAATCTCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAAT CTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3090; ORF 128.a>:

```

a128.pep
1  MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51  NTVEPLTGIT ERVGRIWGVV SHLNSVTDTP ELRAAYNELM PEITVFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME

```


551 FALFDMMIYS EDDEGR LKNW QQVLD SVRKE VAVVRPPEYN RFANSFGHIF
 601 AGGYSAGYYS YAWAEVLSAD AYA AFEESDD VAATGKRFWQ EILAVGGSRS
 651 AAESFKAFRG REPSIDALLR HSGFDNAA*

m128/a128 ORFs 128 and 128.a showed a 66.0% identity in 677 aa overlap

m128.pep	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGTWANTVEPLTGIT					
a128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGTWANTVEPLTGIT					
	10	20	30	40	50	60
m128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
m128.pep	130	-----				
	TLSPAQKTKLNH-----					
a128	TLSHAQKTKLNHDLRDFVLGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
m128.pep	-----					
a128	FDDAAPLAGIPEDALAMFAAAAQSEGKTYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
	190	200	210	220	230	240
m128.pep	-----					
a128	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNHLHDL					
	250	260	270	280	290	300
m128.pep	-----					140
	-----					YASEKLREAKYAFSETXVKKYFPVGX
a128	ARRAKPYAEKDLAEVKAFARESGLADLQPWDLGYAGEKLREAKYAFSETEVKKYFPVGK					150
	310	320	330	340	350	360
m128.pep	160	170	180	190	200	210
	VLNGLFAQXKKLYGIGFTEKTPVWHKDVRYXELQQNGEXIGGVYMDLYAREGKRGGAWM					
a128	VLNGLFAQIKKLYGIGFTEKTPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
m128.pep	220	230	240	250	260	270
	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD					
a128	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
	430	440	450	460	470	480
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQ					
a128	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540
m128.pep	340	350	360	370	380	390
	XGMFXVRQXEFALFDMMIYSEDDEGR LKNWQQVLD SVRKKVAVIQPPEYNRFALSFGHIF					
a128	RGMFLVRQMEFALFDMMIYSEDDEGR LKNWQQVLD SVRKEVAVVRPPEYNRFANSFGHIF					
	550	560	570	580	590	600

```

400      410      420      430      440      450
m128.pep  AGGYSAAXYSYAWAEVLSADAYAAFEESDDVAATGKRWFQEILAVGXSRSGAESFKAFRG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a128      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRWFQEILAVGGSRSAAESFKAFRG
          610      620      630      640      650      660

460      470
m128.pep  REPSIDALLRHSGFDNAVX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a128      REPSIDALLRHSGFDNAAX
          670

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3091>:

m128-1.seq							
1	ATGACTGACA	ACGCACTGCT	CCATTTGGGC	GAAGAACCCC	GTTTGTATCA		
51	AATCAAAACC	GAAGACATCA	AACCCGCCCT	GCAAACCGCC	ATCGCCGAAG		
101	CGCGCGAACA	AATCGCCGCC	ATCAAAGCCC	AAACGCACAC	CGGCTGGGCA		
151	AACACTGTGC	AACCCCTGAC	CGGCATCACC	GAACGCGTCC	GCAGGATTTG		
201	GGCGGTGGTG	TCGCACCTCA	ACTCCGTGCG	CGACACGCCG	GAACTGCGCG		
251	CCGTCTATAA	CGAACTGATG	CCCGAAATCA	CCGTCTTCTT	CACCGAAATC		
301	GGACAAGACA	TCGAGCTGTA	CAACCGCTTC	AAAACCATCA	AAAATTCCCC		
351	CGAATTGAC	ACCCTCTCCC	CCGCACAAAA	AACCAAATC	AACCACGATC		
401	TGCGCGATTT	CGTCTCTAGC	GGCGCGGAAC	TGCCGCCCGA	ACAGCAGGCA		
451	GAACTGGCAA	AACTGCAAAAC	CGAAGGCGCG	CAACTTTCGG	CCAAATTCTC		
501	CCAAAACGTC	CTAGACGCGA	CCGACGCGTT	CGGTCCGCAT	TTTGACGATG		
551	CCGACCCGCT	TGCCCGCATT	CCGAAGACG	CGCTCGCCAT	GTTTGCCGCG		
601	GCCGCGCAAA	GCGAAAGCAA	AACAGGCTAC	AAATCGGCTT	TGCAGATTCC		
651	ACACTACCTC	GCCGTCATCC	AATACGCCGA	CAACCGCGAA	CTGCGCGAAC		
701	AAATCTACCG	CGCCTACGTT	ACCCGCGCCA	GCGAACTTTC	AGACGACGGC		
751	AAATTCGACA	ACACCGCCAA	CATCGACCGC	ACGCTCGCAA	ACGCCCTGCA		
801	AACCGCCAAA	CTGCTCGGCT	TCAAAAACTA	CGCCGAATTG	TCGCTGGCAA		
851	CCAAAATGGC	GGACACGCC	GAACAAGTTT	TAAACTTCTT	GCACGACCTC		
901	GCCCGCCGCG	CCAAACCTTA	CGCGCAAAA	GACCTCGCCG	AAGTCAAAGC		
951	CTTCGCCCGC	GAAAGCCTGA	ACCTCGCCGA	TTTGCAACCG	TGGGACTTTG		
1001	GCTACGCCAG	CGAAAACTTG	CGCGAAGCCA	AATACGCGTT	CAGCGAAACC		
1051	GAAGTCAAAA	AATACTTCCC	CGTCGGCAAA	GTATTAAACG	GACTGTTTCG		
1101	CCAAATCAAA	AAACTCTACG	GCATCGGATT	TACCGAAAAA	ACCGTCCCCG		
1151	TCTGGCACAA	AGACGTGCGC	TATTTTGAAT	TGCAACAAAA	CGGCGAAACC		
1201	ATAGCGCGCG	TTTATATGGA	TTTGTACGCA	CGCGAAGGCA	AACGCGGCGG		
1251	CGCGTGGATG	AACGACTACA	AAGCGCGCGC	CCGTTTTC	GACGGCACGC		
1301	TGCAACTGCC	CACCGCCTAC	CTCGTCTGCA	ACTTCGCCCC	ACCGCTCGGC		
1351	GGCAGGGAAG	CCCGCCTGAG	CCACGACGAA	ATCCTCATCC	TCTTCCACGA		
1401	AACCGGACAC	GGGCTGCACC	ACCTGCTTAC	CCAAGTGGAC	GAAGTGGGCG		
1451	TATCCGGCAT	CAACGGCGTA	GAATGGGACG	CGGTGGAAT	GCCCAGCCAG		
1501	TTTATGAAAA	ATTTCTGTTT	GGAATACAAT	GTCTTGGCAC	AAATGTCAGC		
1551	CCACGAAGAA	ACCGCGGTTT	CCCTGCCGAA	AGAACTCTTC	GACAAAAATG		
1601	TCGCCGCCAA	AAACTTCCAA	CGCGGCATGT	TCTCTGTCG	GCAAAATGGG		
1651	TTCGCCCTCT	TTGATATGAT	GATTTACAGC	GAAGACGACG	AAGCGCGTCT		
1701	GAAAAACTGG	CAACAGGTTT	TAGACAGCGT	GCGCAAAAAA	GTCGCCGTCA		
1751	TCCAGCCGCC	CGAATACAAC	CGCTTCGCCT	TGAGCTTCGG	CCACATCTTC		
1801	GCAGGCGGCT	ATTCCGCAGG	CTATTACAGC	TACGCGTGGG	CGGAAGTATT		
1851	GAGCGCGGAG	GCATACGCCG	CCTTTGAAGA	AAGCGACGAT	GTCGCCGCCA		
1901	CAGGCAAAAC	CTTTTGCGAG	GAAATCCTCG	CCGTGCGCGG	ATCGCGCAGC		
1951	GCGGCAGAAT	CCTTCAAAGC	CTTCGCGCGC	CGCGAACC	GCATAGACGC		
2001	ACTCTTGCGC	CACAGCGGTT	TCGACAACGC	GGTCTGA			

This corresponds to the amino acid sequence <SEQ ID 3092; ORF 128-1>:

ml28-1.p.p.

1	MTDNALLHLG	EEPRFDQIKT	EDIKPALQTA	IAEAREQIAA	IKAQHTGWA
51	NTVEPLTGIT	ERVGRIWGVV	SHLNSVADTP	ELRAVYNELM	PEITVFETEI

```

101  GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151  ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201  AAQSESKTGY KIGLQIPHYL AVIQYADNRE LREQIYRAYV TRASELSDDG
251  KFDNTANIDR TLANALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301  ARRAKPYAEK DLAEVKAFAR ESLNLADLQP WDLGYASEKL REAKYAFSET
351  EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQQNGET
401  IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFAPPVG
451  GREARLSHDE ILILFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501  FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551  FALFDMMIYS EDDEGRLLKNW QQVLDVSRKK VAVIQPPEYN RFALSFGHIF
601  AGGYSAGYYS YAWAEVLSAD AYAAFESDD VAATGKRFWQ EILAVGGSRS
651  AAESFKAFRG REPSIDALLR HSGFDNAV*

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The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3093>:

g128-1.seq (partial)

```

1   ATGATTGACA ACGCACTGCT CCACTTGGGC GAAGAACCCC GTTTTAATCA
51  AATCAAAACC GAAGACATCA AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AACCGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTGCA ACGCTTTCCC CCGCACAAA AACCAGCTC GATCACGACC
401 TGC GCGATT TCGTATTGAGC GCGCGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTTCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACGCT TGCCGCGATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAA GCGAAGGCAA AACAGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCCGG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGCCAAA CTGCTCGGCT TTAATAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACGCCC GAACAGGTTT TAACTTCTCT GCACGACCTC
901 GCCGCGCGC CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCGCCCCG GAACACCTCG GTCTCGCCGA CCCGCAGCCG TGGGACTTGA
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTTCTGGCAG GCCTGTTGCG
1101 CCAAATCAAA AAACCTTACG GCATCGGATT CGCCGAAAAA ACCGTTCCTG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCAAAACC
1201 ATCGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CCGTGGATG AACGACTACA AAGGCCGCGC CCGCTTTGCC GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGCAT CAACGGCGTA AAA

```

This corresponds to the amino acid sequence <SEQ ID 3094; ORF 128-1.ng>:

g128-1.pep (partial)

```

1   MIDNALLHLG EEPRFNQIKT EDIKPAVQTA IAEARGQIAA VKAQHTGWGA
51  NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKTYG KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDSLAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQQNGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTLLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV K

```

m128-1/g128-1 ORFs 128-1 and 128-1.ng showed a 94.5% identity in 491 aa overlap

g128-1.pep	MIDNALLHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQHTGTWANTVERLTGIT
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT
	10 20 30 40 50 60
g128-1.pep	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
m128-1	ERVGRIWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
	70 80 90 100 110 120
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
g128-1.pep	FDDAAPLAGIPEDALAMFAAAAQSEGKTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAAQSESKTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV
	190 200 210 220 230 240
g128-1.pep	TRASELSNDGKFDNTANIDRTLENALKTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
	250 260 270 280 290 300
g128-1.pep	ARRAKPYAEKD LAEVKAFAREHLGLADPQPWDL SYAGEKLREAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKD LAEVKAFARESLNLADLPWDLGYASEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQQNGKTIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD
	430 440 450 460 470 480
g128-1.pep	ELGVSGINGVK
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
	490 500 510 520 530 540

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3095>:

```

a128-1.seq
1  ATGACTGACA  ACGCACTGCT  CCATTGGGC  GAAGAACCCC  GTTTTGATCA
51  AATCAAAACC  GAAGACATCA  AACCCGCCCT  GCAAACCGCC  ATTGCCGAAG
101 CGCGCGAACA  AATCGCCGCC  ATCAAAGCCC  AAACGCACAC  CGGCTGGGCA
151 AACACTGTCG  AACCCTGAC  CGGCATCACC  GAACGCGTCG  GCAGGATTTG
201 GGGCGTGGTG  TCGCACCTCA  ACTCCGTCAC  CGACACGCCC  GAACTGCGCG
251 CCGCCTACAA  TGAATTAAATG  CCCGAAATTA  CCGTCTTCTT  CACCGAAATC
301 GGACAAGACA  TCGAGCTGTA  CAACCGCTTC  AAAACCATCA  AAAACTCCCC
351 CGAGTTCGAC  ACCCTCTCCC  ACGCGCAAAA  AACCAAACTC  AACCACGATC
401 TGC GCGATT  T  CGTCCTCAGC  GCGCGGAAC  TGCCGCCCGA  ACAGCAGGCA
451 GAATTGGCAA  AACTGCAAAC  CGAAGCGCG  CAACTTCCG  CCAAATTCTC

```

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501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTATCC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCGCCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTCCG
1101 CCAATCAAAA AAATCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGCGG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTCA GACGGCAGCG
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAAGTGGCGG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAT ATTTCTTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAATTTCCAA CGCGGAATGT TCCTCGTCCG CCAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCGCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAACG CTTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAAT CTTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3096; ORF 128-1.a>:

a128-1.pep

```

1 MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51 NTVEPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRLNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRWFQ EILAVGGSRS
651 AAESFKAERG REPSIDALLR HSGFDNAA*

```

m128-1/a128-1 ORFs 128-1 and 128-1.a showed a 97.8% identity in 677 aa overlap

	10	20	30	40	50	60
a128-1.pep	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT					
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a128-1.pep	ERVGRWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
m128-1	ERVGRWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130	140	150	160	170	180

a128-1.pep	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
a128-1.pep	190 200 210 220 230 240
	FDDAAPLAGIPEDALAMFAAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAAQSESKTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV
	190 200 210 220 230 240
a128-1.pep	250 260 270 280 290 300
	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMDTPEQVLNLFHDL
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMDTPEQVLNLFHDL
	250 260 270 280 290 300
a128-1.pep	310 320 330 340 350 360
	ARRAKPYAEKDIAEVKAFARESLGLADLQPWDLGYAGEKLREAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDIAEVKAFARESLNLADLQPWDLGYASEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
a128-1.pep	370 380 390 400 410 420
	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
a128-1.pep	430 440 450 460 470 480
	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPVGGREARLSHDEILILFHETGHLHLLTQVD
	430 440 450 460 470 480
a128-1.pep	490 500 510 520 530 540
	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
	490 500 510 520 530 540
a128-1.pep	550 560 570 580 590 600
	RGMFLVRQMEFALFDMMIYSEDDEGRKNWQQVLDVSRKEVAVVRPPEYNRFANSFGHIF
m128-1	RGMFLVRQMEFALFDMMIYSEDDEGRKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIF
	550 560 570 580 590 600
a128-1.pep	610 620 630 640 650 660
	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
m128-1	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
	610 620 630 640 650 660
a128-1.pep	670 679
	REPSIDALLRHSGFDNAAX
m128-1	REPSIDALLRHSGFDNAVX
	670

```

1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GGC GGCGAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAr AACGCCCTCA ACGTCAAGCT GCCCGCGACC
301 GCCCGCGACA TGGCGGCGGC AAGCCGgAAA ATCCCCGAcA GCCGcyTCAA
351 GGCCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGTACTCAC
401 ACGTCGGACT CTACATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 3098; ORF 206>:

m206.pep..

```

1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR
101 ARDMAAASRK IPDSRXKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3099>:

g206.seq

```

1  atgttttccc ccgacaaaac ctttttcctc tgtctcggcg cactgctcct
51  cgcctcatgc ggcacgacct ccggcaaaca ccgccaaccg aaacccaaac
101 agacagtccg gcaaatccaa gccgtccgca tcagccacat cggccgcaca
151 caaggctcgc aggaactcat gctccacagc ctccggactca tcggcacgcc
201 ctacaaatgg ggcggcagca gcaccgcaac cggcttcgac tgcagcggca
251 tgattcaatt ggtttacaaa aacgccctca acgtcaagct gccgcgcacc
301 gcccgcgaca tggcggcgcc aagccgcaaa atccccgaca gccgcctcaa
351 ggccggcgac atcgtattct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcgaat tcatccatgc ccccggcagc
451 ggcaaaacca tcaaaaccga aaaactctcc acaccgtttt acgccaaaaa
501 ctaccttggg gcgcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 3100; ORF 206.ng>:

g206.pep

```

1  MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPR
101 ARDMAAASRK IPDSRLKAGD IVFFNTGGAH RYSHVGLYIG NGEFIHAPGS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

```

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	:					
g206	MFSPDKTLFLCLGALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRXKAGD					
g206	LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPR TARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS GKTIKTEKLSTPFYAKNYLGAHTFFTEX					
	:					
g206	IVFFNTGGAH RYSHVGLYIG NGEFIHAPSS GKTIKTEKLSTPFYAKNYLGAHTFFTE					

130 140 150 160 170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3101>:

```
a206.seq
1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAAGTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GCGGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCCC GCGACA TGGCGGCGGC AAGCCGCAAA ATCCCGGACA GCCGCCTTAA
351 GGCCGGCGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCAGCAGC
451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 3102; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRP
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 ORFs 206 and 206.a showed a 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	10	20	30	40	50	60
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPRPTARDMAAASRKIPDSRXKAGD					
a206	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPRPTARDMAAASRKIPDSRLKAGD					
	70	80	90	100	110	120
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	

287

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3103>:

```
m287.seq
1  ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTTC CCCTTTCAGC
51  CTGCGGGGCG GCGGTGGCG GATCGCCCGA TGTCAAGTCG GCGGACACGC
101 TGTCAAACCC TGCCGCCCTT GTTGT'TTCTG AAAAAGAGAC AGAGGCAAAG
151 GAAGATGCGC CACAGGCAGG TTCTCAAGGA CAGGGCGCGC CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CGGTTCGGA AGAAATACA GGCAATGGCG
251 GTGCGGTAAC AGCGGATAAT CCCAAAAATG AAGACGAGGT GGCACAAAT
301 GATATGCCGC AAAATGCCGC CGGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGGATCCG AATATGCTTG CCGGAAATAT GGAAATCAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCCG GCAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGGACGA TCCGTGCGCA GGCGGGCAAA ATGCGGGCAA
501 TACGGCTGCC CAAGGTGCAA ATCAAGCCGG AAACAATCAA GCCGCCGGTT
551 CTTAGATCC CATCCCGCG TCAAACCTG CACCTGCGAA TGGCGGTAGC
```



```

601 AATTTTGGAA GGGTTGATTT GGCTAATGGC GTTTTGATTG ACGGGCCGTC
651 GCAAAATATA AC GTTGACCC ACTGTAAAGG CGATTCTTGT AGTGGCAATA
701 ATTTCTTGGA TGAAGAAGTA CAGCTAAAT CAGAATTGA AAAATTAAGT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTCGGTTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTTA TAAACCTAAA CCCACTTCAT TTGCGCGATT TAGGCGTTCT
901 GCACGGTCGA GCGGTCGCT TCCGCGCGAG ATGCCGCTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTCAGC CTGACGGGGC
1001 ATTCCGGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCGG CGGATCGTAT GCCCTTCGTG TTCAAGGCGA
1101 ACCGGCAAAA GCGGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATTT CCATACGAA AACGGCCGTC CGTACCCGAC CAGGGGCAGG
1201 TTTGCCGCAA AAGTCGATTT CGGCAGCAA TCTGTGGACG GCATTATCGA
1251 CAGCGGCGAT GATTTCGATA TGGGTACGCA AAAATTCAAA GCCGCCATCG
1301 ATGGAACGCG CTTTAAGGGG ACTTGGACGG AAAATGGCAG CGGGGATGTT
1351 TCCGGAAAGT TTTACGGCCC GGCCGCGAG GAAGTGGCGG GAAAATACAG
1401 CTATCGCCCG ACAGATGCGG AAAAGGGCGG ATTCGGCGTG TTTGCCGGCA
1451 AAAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 3104; ORF 287>:

m287.pep

```

1 MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSKPAAP VVSEKETEAQ
51 EDAPQAGSQG QGAPSAQGSQ DMAAVSEENT GNNGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMANAA
151 DGMQGDPSA GGQNAGNTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NFRVVDLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRRS
301 ARSRRSLPAE MPLIPVNQAD TLIVDGEAVS LTGHSNIFA PEGNYRYLTY
351 GAEKLPGGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDFGSK SVDGIIDSGD DLHMGTKQFK AAIDNGFKG TWTENGSGDV
451 SGKFYGPAGE EVAGKYSYRP TDAEKGFGV FAGKKEQD*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3105>:

g287.seq

```

1 atgttttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51 ctgtgggggc ggcggtggcg gatcgccga tgtcaagtcg gcggacacgc
101 cgtcaaaacc ggcgcccc gttgttgctg aaaatgccg ggaaggggtg
151 ctgccgaaag aaaagaaaaga tgaggaggca gcggcggtg cgccgcaagc
201 cgatacgagc gacgcaaccg ccggagaagg cagccaagat atggcggcag
251 tttcggcaga aaatacaggc aatggcggtg cggcaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaaa atgcccgcca
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 ccccgcgctc aaacctgcc cctgcgaatg gcggtagcga ttttgaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtcgc aaaaataaac
501 gttgaccac tgtaaaaggc attcttgtaa tgggtgataat ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaagcgat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagg gtaaaaaagg atggaactaa caaatatata atcttctata
701 cggacaaacc acctactcgt tctgcacggt cgaggaggtc gcttcgggcc
751 gagattccgc tgattccgct caatcaggcc gatacgctga ttgtgtagg
801 ggaagcggtc agcctgacgg ggcattccgg caatatcttc gcgcccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcggatcg
901 tatgccctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttgttgg
951 cacggccgtg tacaacggcg aagtgtgca tttccatatg gaaaacggcc
1001 gtccgtaccc gtccggaggc aggtttgccg caaaagtcga tttcggcagc
1051 aaatctgttg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaattc aaagccgcca tcgatggaaa cggctttaag gggacttgga
1151 cggaaaatgg cggcggggat gtttcggaa ggttttacgg cccggccggc
1201 gaggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaaggg
1251 cggattcggc gtgtttgccg gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 3106; ORF 287.ng>:

g287.pep

```

1 MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTFSKPAAP VVAENAGEGV

```

51	LPKEKKDEEA	AGGAPQADTQ	DATAGEGSQD	MAAVSAENTG	NGGAATTDNP
101	KNEDAGAQN	MPQNAAESAN	QTGNNQAGS	SDSAPASNPA	PANGGSDFR
151	TNVGNSVVID	GPSQNTLTH	CKGDSNNGDN	LLDEEAPS	EFEKLSDEEK
201	IKRYKKDEQR	ENFVGLVADR	VKKDGTNKYI	IFYTDKPPTR	SARSRRSLPA
251	EIPLIPVNQA	DTLIMVGEAV	SLTGHSGNIF	APEGNYRYLT	YGAEKLPGGS
301	YALRVQGEPA	KGEMLVGTAV	YNGEYLFHFM	ENGRPYPSGG	RFAAKVDFGS
351	KSVVDGIIDSG	DDLHMGTKQF	KAAIDGNGFK	GTWTENGSGD	VSGRFYGPAG
401	EEVAGKYSYR	PTDAEKGFGF	VFAGKKDRD*		

m287/g287 ORFs 287 and 287.ng showed a 70.1% identity in 499 aa overlap

	10	20	30	40	49
m287.pep	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSE-----	KETEAA			
g287	MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPKEKKDEEA				
	10	20	30	40	50
	60	70	80	90	100
m287.pep	KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNNGAVTADNPKNEDDEVAQNDMPQNAAGT				
g287	AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNNGAATTDNPKNEDAGAQNNDMPQNAA--				
	70	80	90	100	110
	120	130	140	150	160
m287.pep	DSSTPNHTPDFNMLAGNMENQATDAGESSQPANQPDMANAADGMQGDDPSAGGQNAGNTA				
g287	-----				
	170	180	190	200	210
m287.pep	AQGANAQAGNNQAAGSSDPIASNPAPANGGSNFGVRDLANGVLIDGPSQNIITLTHCKGDS				
g287	-ESANQTGNNQFAGSSDSAPASNPAPANGGSDFGRNTVNGNSVVIDGPSQNIITLTHCKGDS				
	120	130	140	150	160
	170	180	190	200	210
m287.pep	CSGNNFLDEEVQLKSEFEKLSADADKISNYKKDKGKNDKFVGLVADSVQMKGINQYIIFYKP				
g287	CNGDNLLEEAAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVKKDGTNKYIIFYTD				
	180	190	200	210	220
	230	240	250	260	270
m287.pep	KPTSFAFRFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLT				
g287	KPPT-----RSARSRRSLPAEIPVNPQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLT				
	240	250	260	270	280
	290	300	310	320	330
m287.pep	YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGS				
g287	YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPYPSGGRFAAKVDFGS				
	300	310	320	330	340
	350	360	370	380	390
m287.pep	KSVDDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSCKFYGPAGEEVAGKYSYR				
g287	KSVDDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYR				
	360	370	380	390	400
	410	420	430	440	450
m287.pep	PTDAEKGFGVFAGKKEQDX				
g287	PTDAEKGFGVFAGKKEQDX				
	470	480	489		

g287 PTDAEKGGFGVFAGKKDRDX
420 430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3107>:

a287.seq

1	ATGTTTAAAC	GCAGTGTGAT	TGCAATGGCT	TGTATTGTTG	CCCTTTCAGC
51	CTGTGGGGGC	GGCGGTGGCG	GATCGCCCGA	TGTTAAGTCG	GCGGACACGC
101	TGTCAAACC	TGCCGCCCT	GTTGTTACTG	AAGATGTCGG	GGAGAGAGTG
151	CTGCCGAAG	AAAAGAAAG	TGAGGAGGCG	GTGAGTGGTG	CGCCGCAAGC
201	CGATACGCAG	GACGCAACCG	CCGGAAAAGG	CGGTCAAGAT	ATGGCGCGAG
251	TTTCGGCAGA	AAATACAGGC	AATGGCGGTG	CGGCAACAAC	GGATAATCCC
301	GAAATAAAG	ACGAGGGACC	GCAAAATGAT	ATGCCGCAAA	ATGCCGCCGA
351	TACAGATAGT	TCGACACCGA	ATCACACCCC	TGCACCGAAT	ATGCCAACCA
401	GAGATATGGG	AAACCAAGCA	CCGGATGCCG	GGGAATCGCG	ACAACCCGGCA
451	AACCAACCG	ATATGSCAAA	TGCGGGCGAC	GGAATGCGAG	GGGACGATCC
501	GTCGGCAGGG	GAAAATGCCG	GCAATACGGC	AGATCAAGCT	GCAAACTAAG
551	CTGAAAACAA	TCAAGTCGGC	GGCTCTCAA	ATCCTGCCTC	TTCAACCAAT
601	CCTAACGCCA	CGAATGGCGG	CAGCGATTTT	GGAAGGATAA	ATGTAGCTAA
651	TGGCATCAAG	CTTGACAGCG	GTTCGGAAAA	TGTAACGTTG	ACACATTGTA
701	AAGACAAAGT	ATGCGATAGA	GATTCTTAG	ATGAAGAAGC	ACCACCAAAA
751	TCAGAAATTT	AAAAATTAAG	TGATGAAGAA	AAATTAATA	AATATAAAAA
801	AGACGAGCAA	CGAGAGAAAT	TTGTGCGTTT	TGTGTCTGAC	AGGGTAGAAA
851	AGAATGGAAC	TAACAAATAT	GTCAATCATTT	ATAAAGACAA	GTCCGCTTCA
901	TCTTCATCTG	CGCGATTGAG	GCGTTCTGCA	CGGTGAGGCG	GGTGCCTTCC
951	GGCCGAGATG	CCGCTGATTC	CCGTAATCA	GGCGGATACG	CTGATTGTCG
1001	ATGGGGGAAG	GGTCAGCCTG	ACGGGGCATT	CCGGCAATAT	CTTCGCGCCC
1051	GAAGGGAATT	ACCGGTATCT	GACTTACGGG	GCGGAAAAAT	TGTCCGGCTTG
1101	ATCGTATGCC	CTCAGTGTGC	AAGCGCAACC	GCGCAAAAGG	GAAATGCTTG
1151	CGGGCACGGC	CGTGTACAAC	AGGCAAGTGC	TGCATTTCCA	TATGAAAAAC
1201	GGCCGTCCGT	CCCCGTCCGG	AGGCAGGTTT	GCCGCAAAAG	TCGATTTCGG
1251	CAGCAAATCT	GTGGACGGCA	TTATCGACAG	CGGCGATGAT	TTGCATATGG
1301	GTACGCAAAA	ATTCAAAGCC	GTATCGATG	GAAACGGCTT	TAAGGGGACT
1351	TGGACGGAAA	ATGGCGGCGG	GGATGTTTCC	GGAAGGTTTT	ACGGCCCGGC
1401	CGGCGAAGAA	GTGGCGGGAA	AATCAGCTA	TCGCCGCACA	GATGCGGAAA
1451	AGGGCGGATT	CGGCGTGT	CCCGGCAAAA	AAGAGCAGGA	TTGA

This corresponds to the amino acid sequence <SEQ ID 3108; ORF 287.a>:

```

a287.pep
1  MFKRSVIAMA  CIVALSACGG  GGGGSPDVKs  ADTLskPAAP  VVTEDVGEEV
51  LPKEKKDEEA  VSGAPQADTQ  DATAGKGGQD  MAAVSAENTG  NGGAATTDNP
101 ENKDEGPQND  MPQNAADTDS  STPNHTPApN  MPTRDMGNQA  PDAGESAQPA
151 NQPDMANAAD  GMQGDDPSAG  ENAGNTADQA  ANQAENNQVG  GSQNpASSTN
201 PNATNGGSDF  GRINVANGIK  LDSGSENVTL  THCKDKVCDR  DFLDEEAPPK
251 SEFEKLSDEE  KINKYKKDEQ  RENFVGLVAD  RVEKNGTNKY  VIYKDKSAS
301 SSSARFRRSA  RSRRLSPAEY  PLIPVnQADT  LIVDGEAVSL  TGHSGNIFAP
351 EGNRYRLTYG  AEKLSGGSYA  LSVQGEPAGK  EMLAGTAVSN  GEVLHFHFM
401 GRPSPSGGRF  AAKVDFGSKS  VDGIIDSGDD  LHMGTQKFKA  VIDNGnFKGT
451 WTENGgGDVS  GRFYGPAGEE  VAGKYSYRPT  DAEKGQFGVF  AGKKEOD*

```

m287/a287 ORFs 287 and 287.a showed a 77.2% identity in 501 aa overlap

[illegible]

	110	120	130	140	150	160	169
m287.pep	DSSTPNHTPDNMLAGNMENQATDAGESSQPANQPDMANAADGMQGGDDPSAGGQNAGNTA						
a287	DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADGMQGGDDPSAG-ENAGNTA						
	120	130	140	150	160	170	
	170	180	190	200	210	220	229
m287.pep	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQNITLTHCKGDS						
a287	DQAANQAENNQVGGSQNPASSTNPATNGGSDFRINVANGIKLDGSENVTLTHCKDKV						
	180	190	200	210	220	230	
	230	240	250	260	270	280	289
m287.pep	CSGNNFLDEEVQLKSEFEKLSADKISNYKKDKNDKVFVGLVADSVQMGINQYIIFYKP						
a287	CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVIIYKD						
	240	250	260	270	280	290	
	290	300	310	320	330	340	
m287.pep	KP--TSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRY						
a287	KSASSSSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRY						
	300	310	320	330	340	350	
	350	360	370	380	390	400	
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF						
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF						
	360	370	380	390	400	410	
	410	420	430	440	450	460	
m287.pep	GSKSVDGIIDSGDDLHMGTKQFKAAIDGNFGKGTWTENGSGDVSGKFYGPAGEEVAGKYS						
a287	GSKSVDGIIDSGDDLHMGTKQFKAVIDGNFGKGTWTENGSGDVSGRFGYPAGEEVAGKYS						
	420	430	440	450	460	470	
	470	480	489				
m287.pep	YRPTDAEKGFGVVFAGKKEQDX						
a287	YRPTDAEKGFGVVFAGKKEQDX						
	480	490					

406

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3109>:

m406.seq

```

1   ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAA
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAAC TGAATATTTT GCAGTAGACA

```

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701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACGGAAG GATTAATGGT CGATTTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3110; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPYRETT AETTSAGGLTG LTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSKEIK PTEGLMVDFS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGP *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3111>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTCTGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAAT
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTGCGGCG GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTCTTCTCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3112; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPYRETT AETTSAGGLTG LTSLSTLNA PALSRTQSDG SGSRSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSKEIK PTEGLMVDFS DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGP *

```

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAAVKDMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAAVKDMDLQALHGR					

	10	20	30	40	50	60
	70	80	90	100	110	120
g406.pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGGLTG					
m406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGGLTG					
	130	140	150	160	170	180
g406.pep	LTTSLSTLNAPALSRTQSDGSGSRSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
m406	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	190	200	210	220	230	240
g406.pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	250	260	270	280	290	300
g406.pep	IKPKTNAFEAAYKENYALWMGPYKVSKGIKPTEGLMVDIFSIDIQPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAYKENYALWMGPYKVSKGIKPTEGLMVDIFSIDIQPYGNHTGNSAPSVEADN					
	310	320				
g406.pep	SHEGYGYSDEAVRQHRQGQPX					
m406	SHEGYGYSDEVVRQHRQGQPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3113>:

```

a406.seq
1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAAC TGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTTAA CCGACAGAAG GATTAATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGGCAG GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3114; ORF 406.a>:

```

a406.pep
1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTPRYETT AETTSGGLTG LTTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA

```

251 AYKENYALWM GPYKVSKEGIK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN
 301 SHEGYGYSDE AVRRHRQGQP *

m406/a406 ORFs 406 and 406.a showed a 98.8% identity in 320 aa overlap

	10	20	30	40	50	60
m406.pep	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKMDLQALHGR					
a406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m406.pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGGLTG					
a406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m406.pep	LTTSLSLTLNAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTTNPRDTAFLSHLVQTVF					
a406	LTTSLSLTLNAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m406.pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
a406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSKEGIKPTGLMVDFS DIRPYGNHTGNSAPSVEADN					
a406	IKPKTNAFEAAAYKENYALWMGPYKVSKEGIKPTGLMVDFS DIQPYGNHMGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
m406.pep	SHEGYGYSDEVVRQHRQGQPX					
a406	SHEGYGYSDEAVRRHRQGQPX					
	310	320				

EXAMPLE 2

Expression of ORF 919

The primer described in Table 1 for ORF 919 was used to locate and clone ORF 919. The predicted gene 919 was cloned in pET vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 919-His fusion protein purification. Mice were immunized with the purified 919-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; PP, purified protein, TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm

that 919 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 919 are provided in Figure 10. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 3

Expression of ORF 279

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 11. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 4

Expression of ORF 576 and 576-1

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera

were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).. These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 576 are provided in Figure 12. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 5

Expression of ORF 519 and 519-1

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. The predicted gene 519 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 13. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 6

Expression of ORF 121 and 121-1

The primer described in Table 1 for ORF 121 was used to locate and clone ORF 121. The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 121 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 121 are provided in Figure 14. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 121 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 7

Expression of ORF 128 and 128-1

The primer described in Table 1 for ORF 128 was used to locate and clone ORF 128. The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 128 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 128 are provided in Figure 15. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J.*

Immunol 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 128 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 8

Expression of ORF 206

The primer described in Table 1 for ORF 206 was used to locate and clone ORF 206. The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worthnoting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a recative band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 206 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 16. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 206 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 9

Expression of ORF 287

The primer described in Table 1 for ORF 287 was used to locate and clone ORF 287. The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A). These experiments confirm that 287 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 287 are provided in Figure 17. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 287 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 10

Expression of ORF 406

The primer described in Table 1 for ORF 406 was used to locate and clone ORF 406. The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 406 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 406 are provided in Figure 18. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 406 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 11

Table 2 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 225 among different strains.

Table 2

225 gene variability: List of used *Neisseria* strains

Identification Strains number	Source / reference
Group B	
zo01_225 NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo02_225 BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zo03_225 NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo04_225 297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zo05_225 1000	R. Moxon / Seiler <i>et al.</i> , 1996
zo06_225 BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zo07_225 BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zo08_225 528	R. Moxon / Seiler <i>et al.</i> , 1996
zo09_225 NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zo10_225 BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zo11_225 NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zo12_225 NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zo13_225 NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zo14_225 NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zo15_225 SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zo16_225 NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zo17_225 NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zo18_225 BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zo19_225 BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zo20_225 44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zo21_225 MC58	R. Moxon
zo96_225 2996	Our collection
Group A	
zo22_225 205900	R. Moxon
zo23_225 F6124	R. Moxon
z2491 Z2491	R. Moxon / Maiden <i>et al.</i> , 1998
Group C	
zo24_225 90/18311	R. Moxon
zo25_225 93/4286	R. Moxon

Others

zo26_225 A22 (group W) R. Moxon / Maiden *et al.*, 1998
 zo27_225 E26 (group X) R. Moxon / Maiden *et al.*, 1998
 zo28_225 860800 (group Y) R. Moxon / Maiden *et al.*, 1998
 zo29_225 E32 (group Z) R. Moxon / Maiden *et al.*, 1998

Gonococcus

zo32_225 Ng F62 R. Moxon / Maiden *et al.*, 1998
 zo33_225 Ng SN4 R. Moxon

 fa1090 FA1090 R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

>FA1090 <SEQ ID 3115>
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
 NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
 GFMQHIFKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
 RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKNDPSRFLN*

Z2491 <SEQ ID 3116>
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRVPARRAGNA
 DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF
 MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKNDPSRFLN*

Z001_225 <SEQ ID 3117>
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
 VKNDPSRFLN*

Z002_225 <SEQ ID 3118>
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
 VKNDPSRFLN*

Z003_225 <SEQ ID 3119>
 MDSFFKPAVWAVLWLMFAVRLALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
 VKNDPSRFLN*

Z004_225 <SEQ ID 3120>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z005_225 <SEQ ID 3121>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z006_225 <SEQ ID 3122>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z007_225 <SEQ ID 3123>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z008_225 <SEQ ID 3124>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z009_225 <SEQ ID 3125>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z010_225 <SEQ ID 3126>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z011_225 <SEQ ID 3127>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRFI
HAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN*

Z012_225 <SEQ ID 3128>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z013_225 <SEQ ID 3129>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFIQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSRFLN*

Z014_225 <SEQ ID 3130>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSRFLN*

Z015_225 <SEQ ID 3131>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCS
GFMQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Z016_225 <SEQ ID 3132>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
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DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSRFLN*

Z017_225 <SEQ ID 3133>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
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DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
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VKKNDPSRFLN*

Z018_225 <SEQ ID 3134>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
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DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSRFLN*

Z019_225 <SEQ ID 3135>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
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DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
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VKKNDPSRFLN*

Z020_225 <SEQ ID 3136>

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DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNR
FIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Z021_225 <SEQ ID 3137>

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DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDPSRFLN*

Z022_225 <SEQ ID 3138>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
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DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR

SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNFPSRFLN*

Z023_225 <SEQ ID 3139>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNFPSRFLN*

Z024_225 <SEQ ID 3140>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
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DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNFPSRFLN*

Z025_225 <SEQ ID 3141>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNFPSRFLN*

Z026_225 <SEQ ID 3142>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNFPSRFLN*

Z027_225 <SEQ ID 3143>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
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DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNFPSRFLN*

Z028_225 <SEQ ID 3144>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNFPSRFLN*

Z029_225 <SEQ ID 3145>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNFPSRFLN*

Z032_225 <SEQ ID 3146>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
GFMQHIFKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKNFPSRFLN*

Z033_225 <SEQ ID 3147>

MDSFFKPAVWAVLWLMFAVRSALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
GFMQHIFKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKNFPSRFLN*

Z096_225 <SEQ ID 3148>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
 NADELIGSAMGLNEQPVLVPVNRVPARRAGNADELIGNAMGLNEQPVLVPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDEPSRFLN*

Figure 19 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 225, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 12

Table 3 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 235 among different strains.

Table 3

235 gene variability: List of used *Neisseria* strains

Identification Strains number	Reference
Group B	
gnmzq01 NG6/88	Seiler <i>et al.</i> , 1996
gnmzq02 BZ198	Seiler <i>et al.</i> , 1996
gnmzq03 NG3/88	Seiler <i>et al.</i> , 1996
gnmzq04 1000	Seiler <i>et al.</i> , 1996
gnmzq05 1000	Seiler <i>et al.</i> , 1996
gnmzq07 BZ169	Seiler <i>et al.</i> , 1996
gnmzq08 528	Seiler <i>et al.</i> , 1996
gnmzq09 NGP165	Seiler <i>et al.</i> , 1996
gnmzq10 BZ133	Seiler <i>et al.</i> , 1996
gnmzq11 NGE31	Seiler <i>et al.</i> , 1996
gnmzq13 NGE28	Seiler <i>et al.</i> , 1996
gnmzq14 NGH38	Seiler <i>et al.</i> , 1996
gnmzq15 SWZ107	Seiler <i>et al.</i> , 1996
gnmzq16 NGH15	Seiler <i>et al.</i> , 1996
gnmzq17 NGH36	Seiler <i>et al.</i> , 1996
gnmzq18 BZ232	Seiler <i>et al.</i> , 1996
gnmzq19 BZ83	Seiler <i>et al.</i> , 1996
gnmzq21 MC58	Virji <i>et al.</i> , 1992
Group A	
gnmzq22 205900	Our collection

gnmzq23 F6124 Our collection
 z2491 Z2491 Maiden *et al.*, 1998

Group C

gnmzq24 90/18311 Our collection
 gnmzq25 93/4286 Our collection

Others

gnmzq26 A22 (group W) Maiden *et al.*, 1998
 gnmzq27 E26 (group X) Maiden *et al.*, 1998
 gnmzq28 860800 (group Y) Maiden *et al.*, 1998
 gnmzq29 E32 (group Z) Maiden *et al.*, 1998
 gnmzq31 *N. lactamica* Our collection

Gonococcus

gnmzq32 Ng F62 Maiden *et al.*, 1998
 gnmzq33 Ng SN4 Our collection

fa1090 FA1090 Dempsey *et al.* 1991

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.
 Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279
 Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3149>
 MKPLILGLAAVLALSACQVRKAPDLDTYSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

GNMZQ01 <SEQ ID 3150>
 MKPLILGLAAVLALSACQVQKAPDFDYSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVSAVVNQIANNLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ02 <SEQ ID 3151>
 MKPLILGLAAVLALSACQVQKAPDFDYSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ03 <SEQ ID 3152>
 MKPLILGLAAVLALSACQVQKAPDFDYSFKESKPASILVVPPLNESPDVNGTWGVLAST

AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ04 <SEQ ID 3153>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ05 <SEQ ID 3154>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ07 <SEQ ID 3155>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ08 <SEQ ID 3156>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ09 <SEQ ID 3157>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
AEPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITITEYGT
YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ10 <SEQ ID 3158>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ11 <SEQ ID 3159>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ13 <SEQ ID 3160>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ14 <SEQ ID 3161>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ15 <SEQ ID 3162>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGT
YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ16 <SEQ ID 3163>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ17 <SEQ ID 3164>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ18 <SEQ ID 3165>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ19 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ21 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ22 <SEQ ID 3167>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ23 <SEQ ID 3168>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ24 <SEQ ID 3169>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ25 <SEQ ID 3170>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ26 <SEQ ID 3171>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ27 <SEQ ID 3172>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ28 <SEQ ID 3173>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGT
 YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ29 <SEQ ID 3174>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGT
 YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ31 <SEQ ID 3175>
 MKPLILGLAAVLALSACQVQKAPDFDYTAFKESKPASILVVPPLNESPDVNGTWGMLAST
 AEPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITITEYGT
 YQILDSVTTVSARARLVDSRNGKVLWGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
 DRGYQVSKAAAYDLLSPYSHNGILKGPRFVEEQPK*

GNMZQ32 <SEQ ID 3176>
 MKPLILGLAAVLALSACQVRKAPDLDTYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPLSEAGYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGT
 YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

GNMZQ33 <SEQ ID 3177>
 MKPLILGLAAVLALSACQVRKAPDLDTYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPLSEAGYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGT
 YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

Z2491 <SEQ ID 3178>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGT
 YQILDSVTTVSAKARLVDSRNGKELWGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

Figure 20 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 235, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 13

Table 4 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 287 among different strains.

Table 4

287 gene variability: List of used *Neisseria* strains

Identification Strains number	Reference
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Group B

287_2	BZ198	Seiler <i>et al.</i> , 1996
287_9	NGP165	Seiler <i>et al.</i> , 1996
287_14	NGH38	Seiler <i>et al.</i> , 1996
287_21	MC58	Virji <i>et al.</i> , 1992

Group A

z2491	Z2491	Maiden <i>et al.</i> , 1998
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Gonococcus

fa1090	FA1090	Dempsey <i>et al.</i> 1991
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References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.
 Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279
 Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

287_14 <SEQ ID 3179>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
 QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNMPQNAADTDSLTPNHTPAS
 NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNQ
 TAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGPSQNTLTHCKGDCSGNNFLDEEV
 QLKSEFEKLSADAKISNYKKDGKNDGKNDKFVGLVADSVQMKGINQYIIFYKPKPTSFA
 RRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLP
 GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSRGRFAAKVDFGSKSVDGII
 DSGDGLHMGTKQFKAAIDGNGFKGTWTENGGDVSCKFYGPAGEEVAGKYSYRPTDAEKG
 GFGVFAGKKEQD*

287_2 <SEQ ID 3180>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
 QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNMPQNAADTDSLTPNHTPAS
 NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNQ
 TAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGPSQNTLTHCKGDCSGNNFLDEEV
 QLKSEFEKLSADAKISNYKKDGKNDGKNDKFVGLVADSVQMKGINQYIIFYKPKPTSFA
 RRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLP
 GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSRGRFAAKVDFGSKSVDGII
 DSGDGLHMGTKQFKAAIDGNGFKGTWTENGGDVSCKFYGPAGEEVAGKYSYRPTDAEKG
 GFGVFAGKKEQD*

287_21. <SEQ ID 3181>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
 QGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGTDSSTPNHTPDP
 NMLAGNMENQATDAGESSQPANQPDMAANTADGMQGGDDPSAGGQAGNTAAQGANQAGNNQ
 AAGSSDPIPASNPANGGNSNFRVLDLANGVLIDGPSQNTLTHCKGDCSGNNFLDEEV
 QLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKPKPTSFAFRRS

ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGSY
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVVDGIIDSGD
DLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGGFGV
FAGKKEQD*

287_9 <SEQ ID 3182>

MFKRSVIAMACIVALSACGGGGGGSPDVKSADTLSPKPAAPVVTEDEVGEEVLPKEKKDEEA
VSGAPQADTQDATAGKGGQDMAAVSAENTGNGGAATTDNPNKDEGPQNDMPQNAADTDS
STPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMAAADGMQGGDDPSAGENAGNTADQA
ANQAEENNQVGGSQNPASSTNPNATNGGSDFGRLNVANGIKLDSGSENVTLTHCKDKVCDR
DFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVIIYKDKSAS
SSSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYG
AEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHFMENGRPSPSGGRFAAKVDFGSKS
VDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPT
DAEKGGFGVFAGKKEQD*

FA1090 <SEQ ID 3183>

MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPEKKKDEEA
AGGAPQADTQDATAGEGSQDMAAVSAENTGNGGAATTDNPKNEDEGAQNDMPQNAAESAN
QTGNNQFAGSSDSAPASNPAANGGSDFGRTNVGNSVVIDGPSQNTLTHCKGDSNGDN
LLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVKKDGTNKYIIIFYTDKPPT
SARSRRSLPAEIPVQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGG
YALRVQGEPAKGEMLVGTAVYNGEVLHFHFMENGRPYPSGGRFAAKVDFGSKSVVDGIIDSG
DDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPTDAEKGGFG
VFAGKKDRD*

Z2491 <SEQ ID 3184>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
QGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNDMPQNAAGTDSSTPNHTPDP
NMLAGNMENQATDAGESSQPANQPDMAAADGMQGGDDPSAGGQAGNTAAQGANQAGNNQ
AAGSSDPIPASNPAPANGGNSFGRVDLANGVLIDGPSQNTLTHCKGDSGSGNNFLDEEV
QLKSEFEKLSADAKISNYKKDKNDKFVGLVADSVQMKGINQYIIIFYKPKPTSFARFRRS
ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGSY
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVVDGIIDSGD
DLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGGFGV
FAGKKEQD*

Figure 21 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 287, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 14

Table 5 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 519 among different strains.

Table 5

519 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
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number**Group B**

zv01_519	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv02_519	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zv03_519ass	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv04_519	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zv05_519	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zv06_519ass	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zv07_519	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zv11_519	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zv12_519	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zv18_519	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zv19_519	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zv20_519ass	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zv21_519ass	MC58	R. Moxon
zv96_519	2996	Our collection

Group A

zv22_519ass	205900	R. Moxon
z2491_519	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

Others

zv26_519	A22	(group W) R. Moxon / Maiden <i>et al.</i> , 1998
zv27_519	E26	(group X) R. Moxon / Maiden <i>et al.</i> , 1998
zv28_519	860800	(group Y) R. Moxon / Maiden <i>et al.</i> , 1998
zv29_519ass	E32	(group Z) R. Moxon / Maiden <i>et al.</i> , 1998

Gonococcus

zv32_519	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
fa1090_519	FA1090	R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090_519 <SEQ ID 3185>
MEFFIIILLAAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKE SNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

Z2491_519 <SEQ ID 3186>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV01_519 <SEQ ID 3187>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV02_519 <SEQ ID 3188>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV03_519 <SEQ ID 3189>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV04_519 <SEQ ID 3190>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV05_519 <SEQ ID 3191>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV06_519ASS <SEQ ID 3192>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERK
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV07_519 <SEQ ID 3193>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV11_519 <SEQ ID 3194>

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV12_519 <SEQ ID 3195>

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV18_519 <SEQ ID 3196>

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV19_519 <SEQ ID 3197>

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV20_519ASS <SEQ ID 3198>

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSM
ISAGMKIIDSSKTAK*

ZV21_519ASS <SEQ ID 3199>

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV22_519ASS <SEQ ID 3200>

MEFFIILLAAVVVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV26_519 <SEQ ID 3201>

MEFFIILLAAVVVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV27_519 <SEQ ID 3202>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV28_519 <SEQ ID 3203>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV29_519ASS <SEQ ID 3204>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSIVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSNKTAK*

ZV32_519 <SEQ ID 3205>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV96_519 <SEQ ID 3206>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

Figure 22 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 519, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 15

Table 6 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 919 among different strains.

Table 6

919 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
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number**Group B**

zm01	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm02	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zm03	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm04	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zm05	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zm06	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zm07	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zm08n	528	R. Moxon / Seiler <i>et al.</i> , 1996
zm09	NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zm10	BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zm11asbc	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zm12	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zm13	NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zm14	NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zm15	SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zm16	NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zm17	NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zm18	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zm19	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zm20	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zm21	MC58	R. Moxon
zm96	2996	Our collection

Group A

zm22	205900	R. Moxon
zm23asbc	F6124	R. Moxon
z2491	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

Group C

zm24	90/18311	R. Moxon
zm25	93/4286	R. Moxon

Others

zm26	A22 (group W)	R. Moxon / Maiden <i>et al.</i> , 1998
zm27bc	E26 (group X)	R. Moxon / Maiden <i>et al.</i> , 1998
zm28	860800 (group Y)	R. Moxon / Maiden <i>et al.</i> , 1998
zm29asbc	E32 (group Z)	R. Moxon / Maiden <i>et al.</i> , 1998
zm31asbc	<i>N. lactamica</i>	R. Moxon

Gonococcus

zm32asbc	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
zm33asbc	Ng SN4	R. Moxon
fa1090	FA1090	R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3207>

MKKHLLRSALYGIAAAILAACQSRSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRTERARFPIYGI PDDFISVPLPAGLRGGKN
LVRIRQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSGNEGPVGALGTPLMGEYAGA
IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

Z2491 <SEQ ID 3208>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMQNPQRLAEVLGQNPSYIFFRELGTSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM01 <SEQ ID 3209>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM02 <SEQ ID 3210>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM03 <SEQ ID 3211>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM04 <SEQ ID 3212>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
 YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
 LVRIRQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMQONPQRLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM05 <SEQ ID 3213>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
 YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
 LVRIRQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM06 <SEQ ID 3214>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
 YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
 LVRIRQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM07 <SEQ ID 3215>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
 YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
 LVRIRQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM08N <SEQ ID 3216>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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 YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
 LVRIRQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM09 <SEQ ID 3217>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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 YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
 LVRIRQTGKNSGTIDNTGGHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM10 <SEQ ID 3218>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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 YFTPWQVAGNGSLAGTVTGYEPEVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
 LVRIRQTGKNSGTIDNTGGHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL

KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM11ASBC <SEQ ID 3219>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM12 <SEQ ID 3220>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVPVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM13 <SEQ ID 3221>

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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQOTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM14 <SEQ ID 3222>

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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSRNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM15 <SEQ ID 3223>

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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM16 <SEQ ID 3224>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPGRPVGIPDPAGTTVGGGGAV
YTVPVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM17 <SEQ ID 3225>

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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRI RQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFREL TGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM18 <SEQ ID 3226>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRI RQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFREL TGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM19 <SEQ ID 3227>

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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRI RQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFREL TGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM20 <SEQ ID 3228>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRI RQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
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KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFREL TGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM21 <SEQ ID 3229>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRI RQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFREL TGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM22 <SEQ ID 3230>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRI RQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMQNPQRLAEVLGQNPSYIFFREL TGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM23ASBC <SEQ ID 3231>

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YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRI RQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL

KLQGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGETAGK
MKEPGYVWQLLPNGMKPEYRP*

ZM24 <SEQ ID 3232>

MKKYLFRAALCGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
YTVPVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTFPQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFREL TSGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM25 <SEQ ID 3233>

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YFTFPQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFREL TSGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
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ZM26 <SEQ ID 3234>

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YFTFPQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQGTSMQGIKAYMQNPQRLAEVLGQNPSYIFFREL TSGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM27BC <SEQ ID 3235>

MKKYLFRAALYGISAAAILAACQSKSIQTFFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
YTVPVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTFPQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFREL TSGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGETAGK
MKEPGYVWQLLPNGMKPEYRP*

ZM28 <SEQ ID 3236>

MKKYLFRAALCGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVPVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTFPQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQGTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM29ASBC <SEQ ID 3237>

MKKYLFRAALCGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTFPQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFREL TSGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLFVATHPITR KALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM31ASBC <SEQ ID 3238>

MKKHLFRAALYGIAAAILAACQSKSIQTFPQPDTSIIKGPDRPAGIPDPAGTTVGGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQAARFPIYGI PDDFISVPLPAGLRSGKA
 LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYVFFRELAGSGNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM32ASBC <SEQ ID 3239>

MKKHLLRSALYGIAAAILAACQSRSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
 YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTARFPIYGI PDDFISVPLPAGLRGGKA
 LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSGDGPVGALGTPLMGGYAGA
 IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM33ASBC <SEQ ID 3240>

MKKHLLRSALYGIAAAILAACQSRSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
 YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTARFPIYGI PDDFISVPLPAGLRGGKN
 LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSGNEGPVGALGTPLMGEYAGA
 IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM96 <SEQ ID 3241>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQAARFPIYGI PDDFISVPLPAGLRSGKA
 LVRIRQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

Figure 23 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 919, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 16

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

Table 7: Oligonucleotides used for PCR to amplify complete or partial ORFs

ORF primer Sequence		Restriction sites
001	Forward CGCGGATCCCATATG-TGGATGGTGCTGGTCAT	BamHI- NdeI
	Reverse CCCGCTCGAG-TGCCGTCTTGTCCAC	XhoI
003	Forward CGCGGATCCCATATG-GTCGTATTCGTGGC	BamHI- NdeI
	Reverse CCCGCTCGAG-AAAATCATGAACACGCGC	XhoI
005	Forward CGCGGATCCCATATG-GACAATATTGACATGT	BamHI- NdeI
	Reverse CCCGCTCGAG-CATCACATCCGCCCCG	XhoI
006	Forward CGCGGATCCCATATG-CTGCTGGTGCTGG	BamHI- NdeI
	Reverse CCCGCTCGAG-AGTTCCGGCTTTGATGT	XhoI
007	Forward CGCGGATCCCATATG-GCCGACAACAGCATCAT	BamHI- NdeI
	Reverse CCCGCTCGAG-AAGGCGTTCATGATATAAG	XhoI
008	Forward CGCGGATCCCATATG-AACAACAGACATTTTG	BamHI- NdeI
	Reverse CCCGCTCGAG-CCTGTCCGGTAAAAGAC	XhoI
009	Forward CGCGGATCCCATATG-CCCCGCGCTGCT	BamHI- NdeI
	Reverse CCCGCTCGAG-TGGCTTTTGCCACGTTTT	XhoI
011	Forward CGCGGATCCCATATG-AAGACACACCGCAAG	BamHI- NdeI
	Reverse CCCGCTCGAG-GGCGGTCAGTACGGT	XhoI
012	Forward CGCGGATCCCATATG-CTCGCCCGTTGCC	BamHI- NdeI
	Reverse CCCGCTCGAG-AGCGGGGAAGAGGCAC	XhoI
013	Forward CGCGGATCCCATATG-CCTTTGACCATGCT	BamHI- NdeI
	Reverse CCCGCTCGAG-CTGATTCGGCAAAAAAATCT	XhoI
018	Forward CGCGGATCCCATATG-CAGCAGAGGCAGTT	BamHI- NdeI
	Reverse CCCGCTCGAG-GACGAGGCGAACGCC	XhoI
019	Forward AAAGAATTC-CTGCCAGCCGGCAAGACCCCGGC	Eco RI
	Reverse AAAGTGCAG-TCAGCGGGCGGGGACAATGCCCAT	Pst I
023	Forward AAAGAATTC-AAAGAATATTCGGCATGGCAGGC	Eco RI
	Reverse AAAGTGCAG-TTACCCCCAAATCACTTTAACTGA	Pst I
025	Forward AAAGAATTC-TGCGCCACCCAACAGCCTGCTCC	Eco RI
	Reverse AAAGTGCAG-TCAGAACGCGATATAGCTGTTCGG	Pst I
031	Forward CGCGGATCCCATATG-GTCTCCCTTCGCTT	BamHI- NdeI
	Reverse CCCGCTCGAG-ATGTAAGACGGGGACAAC	XhoI
032	Forward CGCGGATCCCATATG-CGGCGAAACGTGC	BamHI-

	Reverse	CCCGCTCGAG-CTGGTTTTTTGATATTTGTG	NdeI
033	Forward	CGCGGATCCCATATG-GCGGCGGCAGACA	XhoI
	Reverse	CCCGCTCGAG-ATTTGCCGCATCCCGAT	BamHI-
034	Forward	CGCGGATCCCATATG-GCCGAAAACAGCTACGG	NdeI
	Reverse	CCCGCTCGAG-TTTGACGATTTGGTTCAATT	XhoI
036	Forward	CGCGGATCCCATATG-CTGAAGCCGTGCG	BamHI-
	Reverse	CCCGCTCGAG-CCGGACTGCGTATCGG	NdeI
038	Forward	CGCGGATCCCATATG-ACCGATTTCGCCA	XhoI
	Reverse	CCCGCTCGAG-TTCTACGCCGTAAGTCC	BamHI-
039	Forward	CGCGGATCCCATATG-CCGTCCGAACCGC	NdeI
	Reverse	CCCGCTCGAG-TAGGATGACGAGGTAGG	XhoI
041	Forward	CGCGGATCCCATATG-TTCGTGCGCAACCGC	BamHI-
	Reverse	CCCGCTCGAG-GCCCAAAAACCTCTTTCAA	NdeI
042	Forward	CGCGGATCCCATATG-ACGATGATTTGCTTGC	XhoI
	Reverse	CCCGCTCGAG-TTTGCAGCCTGCATTTGAC	BamHI-
043	Forward	AAAAAAGGTACC-ATGGTTGTTTCAAATCAAATATC	NdeI
	Reverse	AAACTGCAG-TTATTGCGCTTCACCTTCCGCCG	XhoI
043a	Forward	AAAAAAGGTACC-GCAAAAGTGCATGGCGGCTTGGACGGTGC	Kpn I
	Reverse	AAAAAACTGCAG-TTAATCCTGCAACACGAATTCGCCCCGTCCG	Pst I
044	Forward	CGCGGATCCCATATG-CCGTCCGACTAGAG	Kpn I
	Reverse	CCCGCTCGAG-ATGCGCTACGGTAGCCA	Pst I
046	Forward	AAAGAATTC-ATGTCGGCAATGCTCCCGACAAG	BamHI-
	Reverse	AAACTGCAG-TCACTCGGCGACCCACACCGTGAA	NdeI
047	Forward	CGCGGATCCCATATG-GTCATCATACAGGCG	XhoI
	Reverse	CCCGCTCGAG-TCCGAAAAAGCCCATTTTG	Eco RI
048	Forward	AAAGAATTC-ATGCTCAACAAAGGCGAAGAATTGCC	Pst I
	Reverse	AAACTGCAG-TCAAGATTGACGGGGATGATGCC	Eco RI
049	Forward	AAAGAATTC-ATGCGGGCGCAGGCGTTTGATCAGCC	Pst I
	Reverse	AAACTGCAG-AAGGCGTATCTGAAAAAATGGCAG	BamHI-
050	Forward	CGCGGATCCCATATG-GGCGCGGGCTGG	NdeI
	Reverse	CCCGCTCGAG-AATCGGGCCATCTTCGA	XhoI
052	Forward	AAAAAAGAATTC-ATGGCTTTGGTGGCGGAGGAAAC	Eco RI
	Reverse	AAAAAAGTCGAC-TCAGGCGGCGTTTTTTACCTTCCT	Sal I
052a	Forward	AAAAAAGAATTC-GTGGCGGAGGAAACGGAAATATCCGC	Eco RI

	Reverse	AAAAAACTGCAG-TTAGCTGTTTTTGGAAACGCCGTCCAACCC	Pst I
073	Forward	CGCGGATCCCATATG-TGTATGCCATATAAGAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACCGGATTGTCCGAC	XhoI
075	Forward	CGCGGATCCCATATG-CCGTCTTACTTCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCACCAATGCCGATTATTT	XhoI
077a	Forward	AAAAAAGAATTC-GGCGGCATTTTCATCGACACCTTCCT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGAACATCTGCACAAACGCAAT	Pst I
080	Forward	AAAGAATTC-GCGTCCGGGCTGGTTTGGTTTTACAATTC	Eco RI
	Reverse	AAACTGCAG-CTATTCTTCGGATTCTTTTTTCGGG	Pst I
081	Forward	AAAGAATTC-ATGAAACCACTGGACCTAAATTTTCATCTG	Eco RI
	Reverse	AAACTGCAG-TCACTTATCCTCCAATGCCTC	Pst I
082	Forward	AAAGAATTC-ATGTGGTTGTTGAAGTTGCCTGC	Eco RI
	Reverse	AAACTGCAG-TTACGCGGATTTCGGCAGTTGG	Pst I
084	Forward	AAAGAATTC-TATCACCAGAATATGAATACGGCTACCG	Eco RI
	Reverse	AAACTGCAG-TTATACTTGGGCGCAACATGA	Pst I
085	Forward	CGCGGATCCCATATG-GGTAAAGGGCAGGACT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAAGCCTTAAACGCTTCG	XhoI
086	Forward	AAAAAAGGTACC-TATTTGGCATCAAAAGAAGGCGG	Kpn I
	Reverse	AAACTGCAG-TTACTCCACCCGATAACCGCG	Pst I
087	Forward	AAAGAATTC-ATGGGCGGTAAAACCTTTATGC	Eco RI
	Reverse	AAACTGCAG-TTACGCCGCACACGCAATCGC	Pst I
087a	Forward	AAAAAAGAATTC-AAGCTATTAGGCGTGCCGATTGTGATTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCTGCAAGATGCCAGCTTGCC	Pst I
088	Forward	AAAAAAGAATTC-ATGTTTTTATGGCTCGCACATTTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAGCGGATTTTGAGGGTACTCAAACC	Pst I
089	Forward	CGCGGATCCCATATG-CCGCCAAAATCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCGCATACCAAAGCCA	XhoI
090	Forward	CGCGGATCCCATATG-CGCATAGTCGAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAAAACGGCGGTACG	XhoI
091	Forward	AAAGAATTC-ATGGAAATACCCGTACCGCCGAGTCC	Eco RI
	Reverse	AAACTGCAG-TCAGCGCAGGGGGTAGCCCAAGCC	Pst I
092	Forward	AAAGAATTC-ATGTTTTTTTATTTCAATCCG	Eco RI
	Reverse	AAACTGCAG-TCAAATCTGTTTCGACAATGC	Pst I
093	Forward	AAAGAATTC-ATGCAGAATTTTGGCAAAGTGGC	Eco RI
	Reverse	AAACTGCAG-CTATGGCTCGTCATACCGGGC	Pst I
094	Forward	AAAGAATTC-ATGCCGTCACGGAAGCGCATCAACTC	Eco RI
	Reverse	AAACTGCAG-TTATCCCGGCCATACCGCCGAACA	Pst I
095	Forward	AAAGAATTC-ATGTCCTTTTCATTTGAACATGGACGG	Eco RI
	Reverse	AAACTGCAG-TCAACGCCGCAGGCACTAACGCC	Pst I
096	Forward	AAAGAATTC-ATGGCTCGTCATACCGGGCAGGG	Eco RI

	Reverse	AAACTGCAG-TCAAAGGAAAAGGCCGTCTGAAAAGCG	Pst I
097	Forward	AAAGAATTC-ATGGACACTTCAAAACAAACACTGTTG	Eco RI
	Reverse	AAACTGCAG-TCAGCCCAAATACCAGAATTTTCAG	Pst I
098	Forward	AAAGAATTC-GATGAACGCAGCCCAGCATGGATACG	Eco RI
	Reverse	AAACTGCAG-TTACGACATTCTGATTTGGCA	Pst I
102	Forward	AAAAAAGAATTC-GGCCTGATGATTTTGGAAGTCAACAC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
105	Forward	CGCGGATCCCATATG-TCCGCAAACGAATACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGTTCTGCCAGTTTCAG	XhoI
107	Forward	AAAAAAGAATTC- CTGATGATTTTGGAAGTCAACACCCATTATCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
107b	Forward	AAAAAAGAATTC- GATACCCAAGCCCCCGCCGGCACAACACTACTG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGCGTCGCCTTTAAAGTATTTGAGCAGGCTGGAGAC	Pst I
108	Forward	AAAGAATTC-ATGTTGCCGGGCTTCAACCG	Eco RI
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Pst I
108a	Forward	AAAAAAGAATTC-GGTAACACATTCCGGCAGCTTAGACGGTGG	Eco RI
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Pst I
109	Forward	AAAGAATTC-ATGTATTATCGCCGGGTATGGG	Eco RI
	Reverse	AAACTGCAG-CTAGCCCAAAGATTTGAAGTGTC	Pst I
111	Forward	CGCGGATCCCATATG-TGTTTCGGAACAAACCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGAGCAGTTTTTCAA	XhoI
114	Forward	CGCGGATCCCATATG-GCTTCCATCACTTCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATCCGCGAAATCGTC	XhoI
117	Forward	AAAAAAGGTACC-ATGGTCGAAGAAGTGAAGTGGCTG	Kpn I
	Reverse	AAACTGCAG-TTAAAGCCGGGTAACGCTCAATAC	Pst I
118	Forward	AAAGTCGACATGTGTGAGTTCAAGGATATTATAAG	Sal I
	Reverse	AAAGCATGC-CTATTTTTTGTGTAATAATCAAATC	Sph I
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATAATAATATCCCGCGCCC	XhoI
122	Forward	CGCGGATCCCATATG-GTCATGATTAAATCCGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AATCTTGGTAGATTGGATT	XhoI
125	Forward	AAAGAATTC-ATGTCGGGCAATGCCTCCTCTCC	Eco RI
	Reverse	AAACTGCAG-TCACGCCGTTTCAAGACG	Pst I
125a	Forward	AAAAAAGAATTC-ACGGCAGGCAGACCGCCGCACAGGTTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTATTTTGCCACGTCGGTTTCTCCGGTGAACAACGC	Pst I
126	Forward	CGCGGATCCCATATG-CCGTCTGAAACCC	BamHI-

	Reverse	CCCGCTCGAG-ATATTCCGCCGAATGCC	NdeI
127	Forward	AAAGAATTC-ATGGAAATATGGAATATGTTGGACACTTG	XhoI
	Reverse	AAACTGCAG-TTAAAGTGTTCGGAGCCGGC	Eco RI
127a	Forward	AAAAAAGAATTC-AAGGAACTGATTATGTGTCTGTCGGG	Pst I
	Reverse	AAACTGCAG-TTAAAGTGTTCGGAGCCGGC	Eco RI
128	Forward	CGCGGATCCCATATG-ACTGACAACGCACT	Pst I
	Reverse	CCCGCTCGAG-GACCGCGTTGTGCGAAA	BamHI-
130	Forward	CGCGGATCCCATATG-AAACAACCTCCGCGA	NdeI
	Reverse	CCCGCTCGAG-GAATTTTGCACCGGATTG	XhoI
132	Forward	AAAGAATTC-ATGGAACCCTTCAAACCTTAATTTG	BamHI-
	Reverse	AAAAAACTGCAG-TCACCATGTCTGGCATTGAAAAAC	NdeI
134	Forward	CGCGGATCCCATATG-TCCCAAGAAATCCTC	XhoI
	Reverse	CCCGCTCGAG-CAGTTTGACCGAATGTTC	Eco RI
135	Forward	CGCGGATCCCATATG-AAATACAAAAGAATCGTATT	Pst I
	Reverse	CCCGCTCGAG-AAATTCGGTCAGAAGCAGG	BamHI-
137	Forward	AAAAAAGGTACC-ATGATTACCCATCCCCAATTCGATCC	NdeI
	Reverse	AAAAAACTGCAG-TCAGTGCTGTTTTTTCATGCCGAA	XhoI
137a	Forward	AAAAAAGAATTC-GGCCGCAAACACGGCATCGGCTTCCT	Kpn I
	Reverse	AAAAAACTGCAG-TTAAGCGGGATGACGCGGCAGCATACC	Pst I
138	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTGGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Pst I
141	Forward	AAAGAATTC-ATGAGCTTCAAACCGATGCCGAAATCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAACAAGCCGTGAATCACGCC	Xba I
142	Forward	CGCGGATCCCATATG-CGTGCCGATTTCATG	Eco RI
	Reverse	CCCGCTCGAG-AAACTGCTGCACATGGG	Pst I
143	Forward	AAAAAAGAATTC- ATGCTCAGTTTCGGCTTCTCGGCGTTCAGAC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAACCCCGCCGTGTGTTTCTTTAAT	Pst I
144	Forward	AAAAAAGAATTC-GGTCTGATCGACGGGCGTGCCGTAAC	Eco RI
	Reverse	AAAAAATCTAGA-TCGGCATCGGCCGGCATATGTCCG	Xba I
146	Forward	AAAAAAGAATTC- CGCCAAGTCGTCATTGACCACGACAAAGTC	Eco RI
	Reverse	AAAAAACTGCAG-TTAGGCATCGGCAAATAGGAACTGGG	Pst I
147	Forward	AAAAAAGAATTC-ACTGAGCAATCGGTGGATTGGAAC	Eco RI
	Reverse	AAAAAATCTAGA-TTAGGTAAAGCTGCGGCCCATTTGCGG	Xba I
148	Forward	AAAAAAGAATTC- ATGGCGTTAAAAACATCAAACCTGGAACACGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGCCCTTCATACAGCCTTCGTTTTG	Xba I
149	Forward	CGCGGATCCCATATG-CTGCTTGACAACAAAGT	BamHI-

	Reverse	CCCGCTCGAG-AAACTTCACGTTACGCC	NdeI
150	Forward	CGCGGATCCCATATG-CAGAACACAAATCCG	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATAAACATCACGCTGATAGC	NdeI
151	Forward	AAAAAAGAATTC- ATGAAACAAATCCGCAACATCGCCATCATCGC	XhoI
			Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCAGCTTTTAAAGTGGCGGCG	Pst I
152	Forward	AAAAAAGAATTC- ATGAAAAACAAAACCAAAGTCTGGGACCTCCC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGGACAGGAGCAGGATGGCGGC	Pst I
153	Forward	AAAAAAGAATTC-ATGGCGTTTGCTTACGGTATGAC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTCATGTTTTCCGTTTCATT	Pst I
153a	Forward	AAAAAAGAATTC-CGGACTTCGGTATCGGTTCCCAGCATTG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGCCGACGAAATACTCAGACTTTTCGG	Pst I
154	Forward	CGCGGATCCCATATG-ACTGACAACAGCCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCGGCTTCCTTTCGGG	XhoI
155	Forward	AAAAAAGAATTC-ATGAAAATCGGTATCCACGCGAGTC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCCTTTCTTAAACATATTCAGCAT	Pst I
156	Forward	AAAAAAGAATTC-GCACAGCAAAACGGTTTTGAAGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGCAGCCGCGACAAACAGCCC	Pst I
157	Forward	CGCGGATCCCATATG-AGGAACGAGGAAAAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAAACACAATATCCCCGC	XhoI
158	Forward	AAAAAAGAATTC-GCGGAGCAGTTGGCGATGGCAAATTCTGC	Eco RI
	Reverse	AAAAAATCTAGA-TTATCCACAGAGATTGTTTCCAGTTC	Xba I
160	Forward	CGCGGATCCCATATG-GACATTCTGGACAAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTTTGCCCCGCCTTCTTT	XhoI
163	Forward	AAAAAAGGTACC-ACCGTGCCGGATCAGGTGCAGATGTG	Kpn I
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCCACCTGCTCGTG	Xba I
163a	Forward	AAAAAAGAATTC-CGGCTGGTGCAGATAATGAGCCAGAC	Eco RI
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCCACCTGCTCGTG	Xba I
164	Forward	CGCGGATCCCATATG-AACCGGACTTATGCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTGTTTCCGTCAAACCTGC	XhoI
165	Forward	CGCGGATCCGCTAGC-GCTGAAGCGACAGACG	BamHI-
			NheI
	Reverse	CCCGCTCGAG-AATATCCAATACTTTCGCG	XhoI
206	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTCTGTAAAAAAAGTATGTGC	XhoI
209	Forward	CGCGGATCCCATATG-CTGCGGCATTTAGGA	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-TACCCCTGAAGGCAAC	XhoI
211	Forward	AAAAAAGAATTC-ATGTTGCGGGTTGCTGCTGC	Eco RI
	Reverse	AAAAAACTGCAG-CTATCCTGCGGATTGGCATTGAAA	Pst I
212	Forward	CGCGGATCCCATATG-GACAATCTCGTATGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGGGTTAGATCCTTCC	XhoI
215	Forward	CGCGGATCCCATATG-GCATGGTTGGGTCGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATATCTTTTGTATCATAAATC	XhoI
216	Forward	CGCGGATCCCATATG-GCAATGGCAGAAAACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TACAATCCGTGCCGCC	XhoI
217	Forward	CGCGGATCCCATATG-GCGGATGACGGTGTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACCCCGAATATCGAATCC	XhoI
218	Forward	CGCGGATCCCATATG-GTCGCGGTCGATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TAACTCATAGAATCCTGC	XhoI
219	Forward	CGCGGATCCGCTAGC-ACGGCAAGGTTAAG	BamHI- NheI
	Reverse	CCCGCTCGAG-TTTAAACCATCTCCTCAAAAC	XhoI
223	Forward	CGCGGATCCCATATG-GAATTCAGGCACCAAGTA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCTTCCCGCGTGTC	XhoI
225	Forward	CGCGGATCCCATATG-GACGAGTTGACCAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTTCAGAAAGCGGGAC	XhoI
226	Forward	AAAGAATTC-CTTGCGATTATCGTGCGCACGCG	Eco RI
	Reverse	AAACTGCAG-TCAAAATCCCAAACGGGGAT	Pst I
228	Forward	CGCGGATCCCATATG-TCGCAAGAAGCCAAACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI
229	Forward	CGCGGATCCCATATG-CAAGAGGTTTGGCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACACAATATAGCGGATGAAC	XhoI
230	Forward	CGCGGATCCCATATG-CATCCGGGTGCCGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAGTTTGGCGGCTTCGG	XhoI
232	Forward	AAAAAAGAATTC-ATGTACGCTAAAAAAGGCGGTTTGGG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGGTTTTTTCCTGATTGCCGCCGC	Pst I
232a	Forward	AAAAAAGAATTC-GCCAAGGCTGCCGATACACAAATTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACATTGTCGTTGCCGCCAGATG	Pst I
233	Forward	CGCGGATCCCATATG-GCGGACAAACCCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGCATTGAGCAG	XhoI
234	Forward	CGCGGATCCCATATG-GCCGTTTCACTGACCG	BamHI-

	Reverse	GCCCAAGCTT-ACGGTTGGATTGCCATG	NdeI
235	Forward	CGCGGATCCCATATG-GCCTGCCAAGTTCAAA	Hind III
			BamHI-
	Reverse	CCCGCTCGAG-TTTGGGCTGCTCTTC	NdeI
236	Forward	CGCGGATCCCATATG-GCGCGTTTCGCCTT	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATGGGTCGCGCGCCGT	NdeI
238	Forward	CGCGGATCCGCTAGC-AACGGTTTGGATGCCCCG	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTTGTCTAAGTTCCTGATATG	NheI
239	Forward	CCGGAATTCTACATATG-CTCCACCATAAAGGTATTG	XhoI
			EcoRI-
	Reverse	CCCGCTCGAG-TGGTGAAGAGCGGTTTAG	NdeI
240	Forward	CGCGGATCCCATATG-GACGTTGGACGATTTT	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-AAACGCCATTACCCGATG	NdeI
241	Forward	CCGGAATTCTACATATG-CCAACACGTCCAAC	XhoI
			EcoRI-
	Reverse	CCCGCTCGAG-GAATGCGCCTGTAATTAATC	NdeI
242	Forward	CGCGGATCCCATATG-ATCGGCAAACCTTGTTG	XhoI
			BamHI-
	Reverse	GCCCAAGCTT-ACCGATACGGTCGCAG	NdeI
243	Forward	CGCGGATCCCATATG-ACGATTTTTTCGATGCTGC	HindIII
			BamHI-
	Reverse	CCCGCTCGAG-CGACTTGGTTACCGCG	NdeI
244	Forward	CGCGGATCCCATATG-CCGTCTGAAGCCC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTTTTTCGGTAGGGGATTT	NdeI
246	Forward	CGCGGATCCCATATG-GACATCGGCAGTGC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-CCCGCGCTGCTGGAG	NdeI
247	Forward	CGCGGATCCCATATG-GTCGGATCGAGTTAC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-AAGTGTTCTGTTTGCGCA	NdeI
248	Forward	CGCGGATCCCATATG-CGCAAACAGAACACT	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-CTCATCATTATTGCTAACA	NdeI
249	Forward	CGCGGATCCCATATG-AAGAATAATGATTGCTTC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTCCCGACCTCCGAC	NdeI
251	Forward	CGCGGATCCCATATG-CGTGCTGCGGTAGT	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TACGAAAGCCGGTCGTG	NdeI
253	Forward	AAAAAAGAATTC-ATGATTGACAGGAACCGTATGCTGCG	XhoI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Eco RI
			Pst I

253a	Forward	AAAAAAGAATTC-AAAATCCTTTTGAAAACAAGCGAAAACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Pst I
254	Forward	AAAAAAGAATTC-ATGTATACAGGCGAACGCTTCAATAC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATTACGTAACCGTACACGCTGAC	Xba I
255	Forward	CGCGGATCCCATATG-GCCGCGTTGCGTTAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-ATCCGCAATACCGACCAG	XhoI
256	Forward	CGCGGATCCGCTAGC-TTTTAACACCGCCGGAC	BamHI-
			NheI
	Reverse	CCCGCTCGAG-ACGCCTGTTTGTGCGG	XhoI
257	Forward	CGCGGATCCCATATG-GCGGTTTCTTTCCTG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GCGCGTGAATATCGCG	XhoI
258	Forward	AAAAAAGAATTC-GATTATTTCTGGTGGATTGTTGCGTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
258a	Forward	AAAAAAGAATTC-GCGAAGGCGGTGGCGCAAGGCGA	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
259	Forward	CGCGGATCCCATATG-GAAGAGCTGCCTCCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GGCTTTTCCGGCGTTT	XhoI
260	Forward	CGCGGATCCCATATG-GGTGCGGGTATGGT	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AACAGGGGCGACACCCT	XhoI
261	Forward	AAAAAAGAATTC-CAAGATACAGCTCGGGCATTTCG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAACCAACAAGCCTTGGTCACT	Pst I
263	Forward	CGCGGATCCCATATG-GCACGTTTAACCGTA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GGCGTAAGCCTGCAATT	XhoI
264	Forward	AAAAAAGGTACC-GCCGACGCAGTGGTCAAGGCAGAA	Kpn I
	Reverse	AAACTGCAG-TCAGCCGGCGGTCAATACCGCCCG	Pst I
265	Forward	AAAAAAGAATTC-GCGGAGGTCAAGAGAAGGTGTTTG	Eco RI
	Reverse	AAAAAACTGCAG-TTACGAATACGTCGTCAAATGGG	Pst I
266	Forward	AAAGAATTC-CTCATCTTTGCCAACGCCCCCTTC	Eco RI
	Reverse	AAACTGCAG-CTATTCCCTGTTGCGCGTGTGCCA	Pst I
267	Forward	AAAGAATTC-TTCTTCCGATTCGATGTTAATCG	Eco RI
	Reverse	AAACTGCAG-TTAGTAAAAACCTTTCTGCTTGGC	Pst I
269	Forward	AAAGAATTC-TGCAAACCTTGCGCCACGTGCCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
269a	Forward	AAAAAAGAATTC-GACTTTATCCAAAACACGGCTTCGCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
270	Forward	AAAGAATTC-GCCGTCAAGCTCGTTTTGTGCAATG	Eco RI
	Reverse	AAACTGCAG-TTATTCGGCGGTAAATGCCGTCTG	Pst I
271	Forward	CGCGGATCCCATATG-CCTGTGTGCAGCTCGAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCCCAGCCCCGTGGAG	XhoI

272	Forward	AAAGAATTC-ATGACCGCAAAGGAAGAACTGTTCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAGCAGTTCCAAATCGGGGCT	Pst I
273	Forward	AAAGAATTC-ATGAGTCTTCAGGCGGTATTTATATACCC	Eco RI
	Reverse	AAACTGCAG-TTACGCGTAAGAAAAAACTGC	Pst I
274	Forward	CGCGGATCCCATATG-ACAGATTGTTACGGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGCTTTCAGTATTATTGAA	XhoI
276	Forward	AAAAAAGAATTC- ATGATTTTGCCGTCGTCCATCACGATGATGCG	Eco RI
	Reverse	AAAAAACTGCAG-CTACACCACCATCGGCGAATTTATGGC	Pst I
277	Forward	AAAAAAGAATTC-ATGCCCCGCTTTGAGGACAAGCTCGTAGG	Eco RI
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Pst I
277a	Forward	AAAAAAGAATTC-GGGGCGGCGGCTGGGTTGGACGTAGG	Eco RI
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Pst I
278	Forward	AAAAAAGGTACC-GTCAAAGTTGTATTAATCGGGCCTTTGCC	Kpn I
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Pst I
278a	Forward	AAAAAAGAATTC-AAAACTCTCCTAATTCGTCATAGTCG	Eco RI
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Pst I
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCACGATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTAGAAGCGGGCGGCAA	XhoI
280	Forward	AAAAAAGGTACC-GCCCCCCTGCCGGTTGTAACCAG	Kpn I
	Reverse	AAAAAACTGCAG-TTATTGCTTCATCGCGTTGGTCAAGGC	Pst I
281	Forward	AAAAAAGAATTC-GCACCCGTCGGCGTATTCCTCGTCATGCG	Eco RI
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Xba I
281a	Forward	AAAAAAGAATTC-TCCTACCACATCGAAATTCCTTCCGG	Eco RI
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Xba I
282	Forward	AAAAAAGAATTC-CTTTACCTTGACCTGACCAACGGGCACAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACCTGCCAGTTGCGGGAATATCGT	Pst I
283	Forward	CGCGGATCCCATATG-GCCGTCTTTACTTGGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGGCAGTATTTGTTTACG	XhoI
284	Forward	CGCGGATCCCATATG-TTGCCTGCAAAAGAATCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCGACTTTGCAAAAAGT	XhoI
286	Forward	CGCGGATCCCATATG-GCCGACCTTCCGAAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAAGCGCGTTCCCAAG	XhoI
287	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG	EcoRI- NheI
	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTTGCC	XhoI
288	Forward	CGCGGATCCCATATG-CACACCGGACAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGTATCAAAGACTTGCGT	XhoI
290	Forward	CGCGGATCCCATATG-GCGGTTTGGGGCGGA	BamHI-

	Reverse	CCCGCTCGAG-TCGGCGCGGCGGGC	NdeI
292	Forward	CGCGGATCCCATATG-TGCGGGCAAACGCCC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTGATTTTTGCGGATGATT	NdeI
294	Forward	AAAAAAGAATTC-GTCTGGTCGATTCGGGTTGTCAGAAC	XhoI
	Reverse	AAAAAACTGCAG-TTACCAGCTGATATAAAACATCGCTTT	Eco RI
295	Forward	CGCGGATCCCATATG-AACCGGCCGGCCTCC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CGATATTTGATTCCGTTGC	NdeI
297	Forward	AAAAAAGAATTC-GCATACATTGCTTCGACAGAGAG	XhoI
	Reverse	AAAAAACTGCAG-TCAATCCGATTGCGACACGGT	Eco RI
298	Forward	AAAAAAGAATTC-CTGATTGCCGTGTGGTTCAGCCAAAACCC	Pst I
	Reverse	AAAAAACTGCAG-TCATGGCTGTGTACTTGATGGTTGCGT	Eco RI
299	Forward	CGCGGATCCGCTAGC-CTACCTGTCGCCTCCG	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-TTGCCTGATTGCAGCGG	NheI
302	Forward	AAAAAAGAATTC-ATGAGTCAAACCGATACGCAACG	XhoI
	Reverse	AAAAAACTGCAG-TTAAGGTGCGGGATAGAATGTGGGCGC	Eco RI
305	Forward	AAAAAAGGTACC-GAATTTTTACCGATTTCAGCACCGGA	Pst I
	Reverse	AAAAAACTGCAG-TCATTCCCAACTTATCCAGCCTGACAG	Kpn I
305a	Forward	AAAAAAGGTACC-TCCCGTTCGGGCAGTACGATTATGGG	Pst I
	Reverse	AAAAAACTGCAG-TTACAAACCGACATCATGCAGGGTGAA	Kpn I
306	Forward	CGCGGATCCCATATG-TTTATGAACAAATTTTCCC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CCGCATCGGCAGAC	NdeI
308	Forward	CGCGGATCCCATATG-TTAAATCGGGTATTTTATC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATCCGCCATTCCCTGC	NdeI
311	Forward	AAAAAAGGTACC-ATGTTTCAGTTTTGGCTGGGTGTTT	XhoI
	Reverse	AAACTGCAG-ATGTTTCATATTCCCTGCCTTCGGC	Kpn I
312	Forward	AAAAAAGGTACC-ATGAGTATCCCATCCGGCGAAATT	Pst I
	Reverse	AAACTGCAG-TCAGTTTTTCATCGATTGAACCGG	Kpn I
313	Forward	AAAAAAGAATTC-ATGGACGACCCGCGCACCTACGGATC	Pst I
	Reverse	AAAAAACTGCAG-TCAGCGGCTGCCGCCGATTTTGCT	Eco RI
401	Forward	CGCGGATCCCATATG-AAGGCGGCAACACAGC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CCTTACGTTTTTCAAAGCC	NdeI
402	Forward	AAAAAAGAATTC-GTGCCTCAGGCATTTTCATTTACCCTTGC	XhoI
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Eco RI
402a	Forward	AAAAAAGAATTC-AGGCTGATTGAAAACAAACACGG	Xba I
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Eco RI
406	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG	Xba I
			BamHI-
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG	NdeI
			XhoI

501	Forward	CGCGGATCCCATATG-GCAGGCGGAGATGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGTGTGATGTTACCC	XhoI
502	Forward	CGCGGATCCCATATG-GTAGACGCGCTTAAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCTGCATGGCGGCG	XhoI
503	Forward	CGCGGATCCCATATG-TGTTCGGGGAAAGGCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCGCGCATTCTCGCA	XhoI
504	Forward	CGCGGATCCCATATG-AGCGATATTGAAGTGACG	BamHI- NdeI
	Reverse	GCCCAAGCTT-TGATTCAAGTCCTTGCCG	HindIII
505	Forward	CGCGGATCCCATATG-TTTCGTTTACAATTCAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGTTTTATAGCGG	XhoI
510	Forward	CGCGGATCCCATATG-CCTTCGCGGACAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCACTGGCAGCG	XhoI
512	Forward	CGCGGATCCCATATG-GGACATGAAGTAACGGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGAATAGCCTTTGACG	XhoI
515	Forward	CGCGGATCCCATATG-GAGGAAATAGCCTTCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAATGCCGCAAAGCATC	XhoI
516	Forward	CGCGGATCCCATATG-TGTACGTTGATGTTGTGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGCGGGCGGCATC	XhoI
517	Forward	CGCGGATCCCATATG-GGTAAAGGTGTGGAAATA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGCGCCAGCCGT	XhoI
518	Forward	AAAGAATTC-GCTTTTTTACTGCTCCGACCGGAAGG	Eco RI
	Reverse	AAACTGCAG-TCAAATTTAGACTCTGCCAC	Pst I
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC	XhoI
520	Forward	CGCGGATCCCATATG-CCTGCGCTTCTTTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATATTTACATTTAGTCGGC	XhoI
521	Forward	CGCGGATCCCATATG-GCCAAAATCTATACCTGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATACGCCCCAGTTCC	XhoI
522	Forward	CGCGGATCCCATATG-ACTGAGCCGAAACAC	BamHI- NdeI
	Reverse	GCCCAAGCTT-TTCTGATTTCAAATCGGCA	HindIII
523	Forward	CGCGGATCCCATATG-GCTCTGCTTTCCGCG	BamHI- NdeI

525	Reverse	CCCGCTCGAG-AGGGTGTGTGATAATAAGAAG	XhoI
	Forward	CGCGGATCCCATATG-GCCGAAATGGTTCAAATC	BamHI- NdeI
527	Reverse	CCCGCTCGAG-GCCCGTGCATATCATAAA	XhoI
	Forward	AAAGAATTC-TTCCCTCAATGTTGCCGTTTTCG	Eco RI
529	Reverse	AAACTGCAG-TTATGCTAAACTCGAAACAAATTC	Pst I
	Forward	CGCGGATCCGCTAGC-TGCTCCGGCAGCAAAAC	BamHI- NheI
530	Reverse	GCCCAAGCTT-ACGCAGTTCGGAATGGAG	HindIII
	Forward	CGCGGATCCCATATG-AGTGCGAGCGCGG	BamHI- NdeI
531	Reverse	CCCGCTCGAG-ACGACCGACTGATTCCG	XhoI
	Forward	AAAAAAGAATTC-TATGCCGCCGCTACCAAATCTACGG	Eco RI
532	Reverse	AAAAAACTGCAG-TTAAACAGCGCCGTGCCGACGACAAG	Pst I
	Forward	AAAAAAGAATTC-ATGAGCGGTCAGTTGGGCAAAGGTGC	Eco RI
532a	Reverse	AAAAAACTGCAG-TCAGTGTTCCAAGTGGTCGGTATCAAA	Pst I
	Forward	AAAAAAGAATTC-TTGGGTGTGCGGTTTGAGCCGGAAGT	Eco RI
535	Reverse	AAAAAACTGCAG-TCAGTGTTCCAAGTGGTCGGTATCAAA	Pst I
	Forward	AAAGAATTC-ATGCCCTTTCCCGTTTTTCAGAC	Eco RI
537	Reverse	AAACTGCAG-TCAGACGACCCCGCCTTCCCC	Pst I
	Forward	CGCGGATCCCATATG-CATACCCAAAACCAATCC	BamHI- NdeI
538	Reverse	CCCGCTCGAG-ATCCTGCAAATAAAGGGTT	XhoI
	Forward	CGCGGATCCCATATG-GTCGAGCTGGTCAAAGC	BamHI- NdeI
539	Reverse	CCCGCTCGAG-TGGCATTTCGGTTTCGTC	XhoI
	Forward	CGCGGATCCGCTAGC-GAGGATTTGCAGGAAA	BamHI- NheI
542	Reverse	CCCGCTCGAG-TACCAATGTCGGCAAATC	XhoI
	Forward	AAAGAATTC-ATGCCGTCTGAAACCGTGTC	Eco RI
543	Reverse	AAACTGCAG-TTACCGCGAACCGGTCAGGAT	Pst I
	Forward	AAAAAAGAATTC-GCCTTCGATGGCGACGTTGTAGGTAC	Eco RI
543a	Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
	Forward	AAAAAAGAATTC-GGCAAAACTCGTCATGAATTTGC	Eco RI
544	Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
	Forward	AAAGAATTC-GCGCCCGCCTTCTCCCTGCCCGACCTGCACGG	Eco RI
544a	Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
	Forward	AAAAAAGAATTC- GCAAATGACTATAAAAAACAAAACTTCCAAGTACTTGC	Eco RI
547	Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
	Forward	AAAGAATTC-ATGTTCTGTAGATAACGGATTTAATAAAAC	Eco RI
548	Reverse	AAACTGCAG-TTAACAACAAAAACAAACCGCTT	Pst I
	Forward	AAAGAATTC-GCCTGCAAACCTCAAGACAACAGTGCGGC	Eco RI

	Reverse	AAACTGCAG-TCAGAGCAGGGTCCTTACATCGGC	Pst I
550	Forward	AAAAAAGTCGAC- ATGATAACGGACAGGTTTCATCTCTTTTCATTTTCC	Sal I
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAAATCCCC	Pst I
550a	Forward	AAAAAAGAATTC-GTAAATCACGCCTTTGGAGTCGCAAACGG	Eco RI
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAAATCCCC	Pst I
552	Forward	AAAAAAGAATTC-TTGGCGCGTTGGCTGGATAC	Eco RI
	Reverse	AAACTGCAG-TTATTTCTGATGCCTTTTCCCAAC	Pst I
554	Forward	CGCGGATCCCATATG-TCGCCC GCGCCCAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCCCTGTCAGACAC	XhoI
556	Forward	AAAGAATTC-GCGGGCGGTTTTGTTTGGACATCCCG	Eco RI
	Reverse	AAACTGCAG-TTAACGGTGCGGACGTTTCTGACC	Pst I
557	Forward	CGCGGATCCCATATG-TGCGGTTTCCACCTGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCCGCCTTCAGAAAGG	XhoI
558	Forward	AAAGAATTC-GAGCTTTATATGTTTCAACAGGGGACGGC	Eco RI
	Reverse	AAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
558a	Forward	AAAAAAGAATTC-ATTAGATTCTATCGCCATAAACAGACGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
560	Forward	AAAAAAGAATTC- TCGCCTTTCCGGGACGGGGCGCACAAGATGGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATGCGGTTTCAGACGGCATTTTGGC	Pst I
561	Forward	CCGGAATTCTACATATG-ATACTGCCAGCCCGT	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCAAGCTTTCTTCAGATG	XhoI
562	Forward	CGCGGATCCCATATG-GCAAGCCCGTCGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGACCAACTCCAACCTCGT	XhoI
565	Forward	CGCGGATCCCATATG-AAGTCGAGCGCGAAATAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCATTGATCGGCGGC	XhoI
566	Forward	CGCGGATCCCATATG-GTCGGTGGCGAAGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCATGGGCGAAGTCA	XhoI
567	Forward	CCGGAATTCTACATATG-AGTGCGAACATCCTTG	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCCCCGACACCCTCG	XhoI
568	Forward	CGCGGATCCCATATG-CTCAGGGTCAGACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGCGGCGTTTCAG	XhoI
569	Forward	AAAAAAGAATTC-CTGATTGCCTTGTGGGAATATGCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TTATGCATAGACGCTGATAACGGCAAT	Pst I
570	Forward	CGCGGATCCCATATG-GACACCTTCCAAAAAATCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGGCGTTTCATTTCTTT	XhoI

571	Forward	AAAAAAGAATTC- ATGGGTATTGCCGGCGCCGTAAATGTTTTGAACCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATGGCCGACGCGCGGCTACCTGACG	Pst I
572	Forward	CGCGGATCCCATATG-GCGCAAAAAGGCAAAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCAGTGTGCCGATA	XhoI
573	Forward	CGCGGATCCCATATG-CCCTGTTTGTGCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGTGTCAATTCGCC	XhoI
574	Forward	CGCGGATCCCATATG-TGGTTTGCCGCCCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACTTCGATTTTATTCGGG	XhoI
575	Forward	CGCGGATCCCATATG-GTTTCGGGCGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGAATCTGAACAG	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTTGATGTCGAC	XhoI
577	Forward	CGCGGATCCCATATG-GAAAGGAACGGTGTATTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGCTGTTTGGTAGATTCG	XhoI
578	Forward	CGCGGATCCCATATG-AGAAGGTTTCGTACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCAACGCCTCCACG	XhoI
579	Forward	CGCGGATCCCATATG-AGATTGGGCGTTTCCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGAATTGATGATGTGTATGT	XhoI
580	Forward	CGCGGATCCCATATG-AGGCAGACTTCGCCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACTTCCCCCGAAGTG	XhoI
581	Forward	CGCGGATCCCATATG-CACTTCGCCCAGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCCGTTTGGCTTTGG	XhoI
582	Forward	AAAAAAGAATTC-TTTGGAGAGACCGCGCTGCAATGCGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATGCCGTCCCAGTCGTTGAA	Xba I
583	Forward	AAAAAAGAATTC-ACTGCCGGCAATCGACTGCATAATCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGGAGGTCAATATGATGAAATTG	Pst I
584	Forward	AAAAAAGAATTC- GCGGCTGAAGCATTGAATTACAATATTGTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGAACTGAACCGTCCCATTGACGCT	Pst I
585	Forward	AAAAAAGGTACC-TCTTTCTGGCTGGTGCAGAACACCCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTTCGCACTTTTTTCTGTTTTGGA	Pst I
586	Forward	CGCGGATCCCATATG-GCAGCCCATCTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTCAGCGAATCAAGTTTC	XhoI
587	Forward	CGCGGATCCCATATG-GACCTGCCCTTGACGA	BamHI-

	Reverse	CCCGCTCGAG-AAATGTATGCTGTACGCC	NdeI
			XhoI
588	Forward	AAAAAAGAATTC-GCCGTCCTGACTTCCTATCAAGAACCAGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTGTTTTTGGGCAGTTTCACTTC	Pst I
589	Forward	AAAAAAGAATTC- ATGCAACAAAAAATCCGTTTCCAAATCGAAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAATCGATTTTTACCCGTTTCAGGCG	Pst I
590	Forward	AAAAAAGAATTC-ATGAAAAAACCTTTGATTTCAGTTGCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTGCTGCGGCTCTGAAACCAT	Pst I
591	Forward	AAAAAAGAATTC-CACTACATCGTTGCCAGATTGTGCGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAACCGAGCAGCCGGGTAAACGTCGTT	Pst I
592a	Forward	AAAAAAGAATTC-CGCGATTACACCGCCAAGCTGAAAATGGG	Eco RI
	Reverse	AAAAAACTGCAG-TTACCAAACGTCGGATTTGATACG	Pst I
593	Forward	CGCGGATCCGCTAGC-CTTGAACCTGAACGGACTC	BamHI- NheI
	Reverse	CCCGCTCGAG-GCGGAAGCGGACGATT	XhoI
594a	Forward	AAAAAAGAATTC-GGTAAGTTCGCCGTTTCAGGCCTTTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCGCCGTTTCCTGACACTCGCG	Pst I
595	Forward	AAAAAAGAATTC-TGCCAGCCGCCGGAGGCGGAGAAAGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCAAGCCGAGTATGCCGCG	Pst I
596	Forward	CGCGGATCCCATATG-TCCCAACAATACGTC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCGTTACCGGTTTGT	XhoI
597	Forward	CGCGGATCCCATATG-CTGCTTCATGTCAGC	BamHI- NdeI
	Reverse	GCCCAAGCTT-ACGTATCCAGCTCGAAG	HindIII
601	Forward	CGCGGATCCCATATG-ATATGTTCCCAACCGGCAAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAACAATCCTCAGGCAC	XhoI
602	Forward	CGCGGATCCGCTAGC-TTGCTCCATCAATGC	BamHI- NheI
	Reverse	CCCGCTCGAG-ATGCAGCTGCTAAAAGCG	XhoI
603	Forward	AAAAAAGAATTC-CTGTCCTCGCGTAGGCGGGGACGGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAGATGCCGGCAAGTTCGGC	Pst I
604	Forward	CGCGGATCCGCTAGC-CCCGAAGCGCACTT	BamHI- NheI
	Reverse	CCCGCTCGAG-GACGGCATCTGCACGG	XhoI
606a	Forward	AAAAAAGAATTC-CGCGAATACCGCGCCGATGCGGGCGC	Eco RI
	Reverse	AAAAAACTGCAG-TTAAAGCGATTTGAGGCGGGCGATACG	Pst I
607	Forward	AAAAAAGAATTC-ATGCTGCTCGACCTCAACCGCTTTTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGGCCTTATGCGATCTGAC	Pst I
608	Forward	AAAAAAGAATTC-ATGTCCGCCCTCCTCCCCATCATCAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGTCTATCCAAATGTCGCGTTC	Pst I
609	Forward	CGCGGATCCCATATG-GTTGTGGATAGACTCG	BamHI- NdeI

	Reverse CCCGCTCGAG-CTGGATTATGATGTCTGTC	XhoI
610	Forward CGCGGATCCCATATG-ATTGGAGGGCTTATGCA	BamHI- NdeI
	Reverse CCCGCTCGAG-ACGCTTCAACATCTTTGCC	XhoI
611	Forward CGCGGATCCCATATG-CCGTCTCAAAACGGG	BamHI- NdeI
	Reverse CCCGCTCGAG-AACGACTTTGAACGCGCAA	XhoI
613	Forward CGCGGATCCCATATG-TCGCGTTCGAGCCG3	BamHI- NdeI
	Reverse CCCGCTCGAG-AGCCTGTAAAATAAGCGGC	XhoI
614	Forward CGCGGATCCCATATG-TCCGTCGTGAGCGGC	BamHI- NdeI
	Reverse CCCGCTCGAG-CCATACTGCGGCGTTC	XhoI
616	Forward AAAAAAGAATTC-ATGTCAAACACAATCAAAATGGTTGTCGG	Eco RI
	Reverse AAAAAATCTAGA-TTAGTCCGGGCGGCAGGCAGCTCG	Xba I
619a	Forward AAAAAAGAATTC-GGGCTTCTCGCCGCTCGCTTGC	Eco RI
	Reverse AAAAAACTGCAG-TCATTTTTTGTGTTTTAAAACGAGATA	Pst I
622	Forward CGCGGATCCCATATG-GCCGCCCTGCCTAAAG	BamHI- NdeI
	Reverse CCCGCTCGAG-TTTGTCCAAATGATAAATCTG	XhoI
624	Forward CGCGGATCCCATATG-TCCCCGCGCTTTTACCG	BamHI- NdeI
	Reverse CCCGCTCGAG-AGATTCGGGCCTGCGC	XhoI
625	Forward CGCGGATCCCATATG-TTTGCAACCAGGAAAATG	BamHI- NdeI
	Reverse CCCGCTCGAG-CGGCAAAATTACCGCCTT	XhoI
627a	Forward AAAAAAGAATTC-AAAGCAGGCGAGGCAGGCGCGCTGGG	Eco RI
	Reverse AAAAAACTGCAG- TTACGAATGAAACAGGGTACCCGTCATCAAGGC	Pst I
628	Forward AAAAAAGGTACC-GCCTTACAAACATGGATTTTGC GTTC	Kpn I
	Reverse AAAAAACTGCAG-CTACGCACCTGAAGCGCTGGCAA	Pst I
629a	Forward AAAAAAGAATTC-GCCACCTTTATCGCGTATGAAAACGA	Eco RI
	Reverse AAAAAACTGCAG-TTACAACACCGCCGTCCGGTTCAAACC	Pst I
630a	Forward AAAAAAGAATTC-GCGGCTTTGGGTATTTCTTTCGG	Eco RI
	Reverse AAAAAACTGCAG-TTAGGAGACTTCGCCAATGGAGCCGGG	Pst I
635	Forward AAAAAAGAATTC- ATGACCCAGCGACGGGTCGGCAAGCAAAACCG	Eco RI
	Reverse AAAAAACTGCAG-TTAATCCACTATAATCCTGTTGCT	Pst I
638	Forward AAAAAAGAATTC-ATGATTGGCGAAAAGTTTATCGTAGTTGG	Eco RI
	Reverse AAAAAACTGCAG-TCACGAACCGATTATGCTGATCGG	Pst I
639	Forward CGCGGATCCCATATG-ATGCTTTATTTTGTTTCG	BamHI- NdeI
	Reverse CCCGCTCGAG-ATCGCGGCTGCCGAC	XhoI
642	Forward CGCGGATCCCATATG-CGGTATCCGCCGCAAT	BamHI- NdeI
	Reverse CCCGCTCGAG-AGGATTGCGGGGCATTA	XhoI

643	Forward	CGCGGATCCCATATG-GCTTCGCCGTCGGCAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACCGAAAAACAGACCGC	XhoI
644	Forward	AAAAAAGAATTC- ATGCCGTCTGAAAGGTCGGCGGATTGTTGCC	Eco RI
	Reverse	AAAAAATCTAGA-CTACCCGCAATATCGGCAGTCCAATAT	Pst I
645	Forward	AAAAAAGAATTC-GTGGAACAGAGCAACACGTAAATCG	Eco RI
	Reverse	AAAAAACTGCAG-CTACGAGGAAACCGAAGACCAGGCCGC	Pst I
647	Forward	AAAAAAGAATTC-ATGCAAAGGCTCGCCGCAGACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGATTATCAGGGATATCCGGTAGAA	Pst I
648	Forward	AAAAAAGAATTC- ATGAACAGGCGCGACGCGCGGATCGAACG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGCTGTGTGCTGATTGAATGCGAC	Pst I
649	Forward	AAAAAAGAATTC-GGTACGTCAGAACCCGCCACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGGCGGAAACTGCCGCCGTC	Pst I
650	Forward	AAAAAAGAATTC-ATGTCCAAACTCAAACCATCGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGGCATGGCGGTCTGTTTT	Pst I
652	Forward	AAAAAAGGTACC- GCTGCCGAAGACTCAGGCCTGCCGCTTTACCG	Kpn I
	Reverse	AAAAAACTGCAG-TTATTTGCCAGTTGGTAGAATGCGGC	Pst I
653	Forward	AAAAAAGAATTC-GCGGCTTTGCCGGTAATTTTCATCGG	Eco RI
	Reverse	AAAAAACTGCAG-CTATGCCGGTCTGGTTGCCGGCGGCGA	Pst I
656a	Forward	AAAAAAGAATTC-CGGCCGACGTCGTTGCGTCCTAAGTC	Eco RI
	Reverse	AAAAAACTGCAG-CTACGATTTCCGCGATTTCACATCGT	Pst I
657	Forward	AAAAAAGAATTC-GCAGAATTTGCCGACCGCCATTTGTGCGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATAGGGACTGATGCAGTTTTTTTGC	Pst I
658	Forward	CGCGGATCCCATATG-GTGTCCGGAATTGTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCAGAATGTTTACCGTT	XhoI
661	Forward	AAAAAAGAATTC- ATGCACATCGGCGGCTATTTTATCGACAACCC	Eco RI
	Reverse	AAAAAACTGCAG-TCACGACGTGTCTGTTCGCCGTCGGGC	Pst I
663	Forward	CGCGGATCCCATATG-TGTATCGAGATGAAATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTAAAAATCGGGGCTGC	XhoI
664	Forward	CGCGGATCCCATATG-GCGGCTGGCGCGGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAATCGAGTTTTACACCAC	XhoI
665	Forward	AAAAAAGAATTC-ATGAAATGGGACGAAACGCGCTTCGG	Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCAAAATTTGCCGACGATTTC	Pst I
666	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTGGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Xba I
667	Forward	AAAAAAGAATTC- CCGCATCCGTTTGATTTCATTTCGTATTCGTCCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAATGACACAATAGGCGCAAGTC	Pst I

669	Forward	AAAAAAGAATTC-ATGCGCCGCATCATTA AAAAACACCAGCC	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTATCCGTTTGATGTCGGC	Pst I
670a	Forward	AAAAAAGAATTC-AAAAACGCTTCGGGCGTTTCGTCTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTAGGAGCTTTTGGAACGCGTCGGACTGGC	Pst I
671	Forward	CGCGGATCCCATATG-ACCAGCAGGGTAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAACTATAAAAAACGCAAG	XhoI
672	Forward	CGCGGATCCCATATG-AGGAAAATCCGCACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGGGATAGGCGGTTG	XhoI
673	Forward	AAAAAAGAATTC-ATGGATATTGAAACCTTCCTTGCAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAACCCAGCTCGCGCAGGAA	Pst I
674	Forward	AAAAAAGAATTC-ATGAAAACAGCCCGCCGCGTTCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACGGCGTTTGGGCTCGTCGGG	Pst I
675	Forward	CGCGGATCCCATATG-AACACCATCGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCTTCGTCTTCAAACCTGT	XhoI
677a	Forward	AAAAAAGAATTC-AGACGGCATTCCCGATCAGTCGATTTTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGTATGCGCGAAATCGACCGCCGC	Pst I
680	Forward	CGCGGATCCGCTAGC-ACGAAGGGCAGTTCGG	BamHI- NheI
	Reverse	CCCGCTCGAG-CATCAAAAACCTGCCGC	XhoI
681	Forward	AAAAAAGAATTC-ATGACGACGCCGATGGCAATCAGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCGTCTTCCGCAAAAAACAGC	Pst I
683	Forward	CGCGGATCCCATATG-TGCAGCACACCGGACAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAGTTTTTTTCCGCATACG	XhoI
684	Forward	CGCGGATCCCATATG-TGCGGTACTGTGCAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTCGACCATCTGTTGCG	XhoI
685	Forward	CGCGGATCCCATATG-TGTTTGCTTAATAAATAACATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTTTTCCCCGCCGCA	XhoI
686	Forward	CGCGGATCCCATATG-TGCGGCGGTTCGGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGATTCTGATGAAG	XhoI
687	Forward	CGCGGATCCCATATG-TGCGACAGCAAAGTCCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCGCGGCTTTTTGTT	XhoI
690	Forward	CGCGGATCCCATATG-TGTTCTCCGAGCAAAGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TATTCGCCCCGTGTTTGG	XhoI
691	Forward	CGCGGATCCCATATG-GCCACGGCTTATATCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAGGCAGGAAGAAAG	XhoI

694	Forward	CGCGGATCCCATATG-TTGGTTTCCGCATCCGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCTGCGTCGGTGCGGT	XhoI
695	Forward	CGCGGATCCCATATG-TTGCCTCAAACCTCGTCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	XhoI
696	Forward	CGCGGATCCCATATG-TTGGGTTGCCGGCAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGATTGCCGCAATGATG	XhoI
700a	Forward	AAAAAAGAATTC- <u>GCATCGACAGACGGTGTGTCGTGGAC</u>	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCTACCGGCACGACTTCCAAACC	Pst I
701	Forward	CGCGGATCCCATATG-AAGACTTGTGTTGGATACTTC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCCGACAACAGCCTC	XhoI
702	Forward	AAAAAAGAATTC-ATGCCGTGTTCCAAAGCCAGTTGGATTTC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACCCCATTCACCCGGAGAACCGA	Pst I
703	Forward	CGCGGATCCGCTAGC-CAAACGCTGGCAACCG	BamHI- NheI
	Reverse	CCCGCTCGAG-TTTTGCAGGTTTGATGTTTG	XhoI
704a	Forward	AAAAAAGAATTC-GCTTCTACCGGTACGCTGGCGCG	Eco RI
	Reverse	AAAAAACTGCAG- TTAGTTTTGCCGGATAATATGGCGGGTGCG	Pst I
707	Forward	CGCGGATCCGCTAGC-GAAATTATTAACGATGCAGA	BamHI- NheI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGA	XhoI
708	Forward	CGCGGATCCGCTAGC-CCTTTTAAGCCATCCAAAA	BamHI- NheI
	Reverse	CCCGCTCGAG-TTGACCGGTGAGGACG	XhoI
710	Forward	CGCGGATCCCATATG-GAAACCCACGAAAAAATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACGGTTTCGGTCAG	XhoI
714	Forward	CGCGGATCCCATATG-AGCTATCAAGACATCTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGTAGGTAAATCGGAT	XhoI
716	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTAGAACCGCATTTGCC	XhoI
718	Forward	CGCGGATCCCATATG-GAGCCGATAATGGCAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCGCGGGCATGGTCTTGTC	XhoI
720	Forward	CGCGGATCCCATATG-AGCGGATGGCATAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTTGCATAGCTGTTGACCA	XhoI
723	Forward	CGCGGATCCCATATG-CGACCCAAGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AATGCGAATCCGCCGCC	XhoI

725	Forward	CGCGGATCCCATATG-GTGCGCACGGTTAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGCTTATCCTTAAGGGTTA	XhoI
726	Forward	CGCGGATCCCATATG-ACCATCTATTTCAAAAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCGATGTTTAGCGTCC	XhoI
728	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	XhoI
729	Forward	CGCGGATCCCATATG-TGCACCATGATTCCCCA	BamHI- NdeI
	Reverse	GCCCAAGCTT-TTTGTCGGTTTGGGTATC	HindIII
731	Forward	CGCGGATCCGCTAGC-GCCGTGCCGGAGG	BamHI- NheI
	Reverse	CCCGCTCGAG-ACGGGCGCGGCAG	XhoI
732	Forward	CCGGAATTCTACATATG-TCGAAACCTGTTTTTAAGAA	EcoRI- NdeI
	Reverse	CCCGCTCGAG-CTTCTTATCTTTTTTATCTTTC	XhoI
733	Forward	CGCGGATCCCATATG-GCCTGCGGCGGCAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGCTTGCCTCCTTTAC	XhoI
734	Forward	CGCGGATCCCATATG-GCCGATACTTACGGCTAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAGATTTTGAATCAAAGAG	XhoI
735	Forward	CGCGGATCCCATATG-AAGCAGCAGGCGGTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATTTCCGTAGCCGAGGG	XhoI
737	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	XhoI
739	Forward	CGCGGATCCCATATG-GCAAAAAAACCGAACA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAAGAGTTTGTGCGAGAATT	XhoI
740	Forward	CGCGGATCCCATATG-GCCAATCCGCCCGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAACGCGCCAAAATAGTG	XhoI
741	Forward	CGCGGATCCCATATG-TGCAGCAGCGGAGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGCTTGGCGGCAAGGC	XhoI
743	Forward	CGCGGATCCCATATG-GACGGTGTTGTGCCTGTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTACGGATCAAATTGACG	XhoI
745	Forward	CGCGGATCCCATATG-TTTTGGCAACTGACCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAATCAGATGCCTTTAGG	XhoI
746	Forward	CGCGGATCCCATATG-TCCGAAAACAAACAAAAC	BamHI-

	Reverse	CCCGCTCGAG-TTCATTCGTTACCTGACC	NdeI
747	Forward	CCGGAATTCTAGCTAGC-CTGACCCCTTGGG	XhoI
			EcoRI-
			NheI
	Reverse	GCCCAAGCTT-TTTTGATTTTAATTGACTATAGAAC	HindIII
749	Forward	CGCGGATCCCATATG-TGCCAGCCGCCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTCAAGCCGAGTATGC	XhoI
750	Forward	CGCGGATCCCATATG-TGTTCGCCC GAACCTG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CTTTTCCCCGCCGCAA	XhoI
758	Forward	CGCGGATCCCATATG-AACAATCTGACCGTGTT	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TGGCTCAATCCTTTCTGC	XhoI
759	Forward	CGCGGATCCGCTAGC-CGCTTCACACACACCAC	BamHI-
			NheI
	Reverse	CCCGCTCGAG-CCAGTTGTAGCCTATTTTG	XhoI
763	Forward	CGCGGATCCCATATG-CTGCCTGAAGCATGGCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTCCGCAAATACCGTTTCC	XhoI
764	Forward	CGCGGATCCCATATG-TTTTCTCCGCCCTGA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCGCTCCCTAAAGCTTTC	XhoI
765	Forward	CGCGGATCCCATATG-TTAAGATGCCGTCCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-ACGCCGACGTTTTTTATTAA	XhoI
767	Forward	CGCGGATCCCATATG-CTGACGGAAGGGGAAG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTCTGTACAGCAGGGG	XhoI
768	Forward	CGCGGATCCCATATG-GCCCCGCAAAAACCCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTCATCCCTTTTTTGAGC	XhoI
770	Forward	CGCGGATCCCATATG-TGCGGCAGCGGCGAA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GCGTTTGTCGAGATTTTC	XhoI
771	Forward	CGCGGATCCCATATG-TCCGTATATCGCACCTTC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CGGTTCTTTAGGTTTGAG	XhoI
772	Forward	CGCGGATCCCATATG-TTTCGGCGTTGGTGG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CAATGCCGACATCAAACG	XhoI
774	Forward	CGCGGATCCCATATG-TCCGTTTCACCCGTTCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	XhoI
790	Forward	CGCGGATCCCATATG-GCAAGAAGGTCAAAAAC	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-GGCGTTGTTCGGATTTCG	XhoI
900	Forward	CGCGGATCCCATATG-CCGTCTGAAATGCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATATGGAAAAGTCTGTTGTC	XhoI
901	Forward	CGCGGATCCCATATG-CCCGATTTTTCGATG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAATGGAACAATACCAGG	XhoI
902	Forward	CCGGAATTCTACATATG-TTGCACCTTCAAAGGATAATC	EcoRI- NdeI
	Reverse	CCCGCTCGAG-AAAAATGTACAATGGCGTAC	XhoI
903	Forward	CCGGAATTCTAGCTAGC-CAGCGTCAGCAGCACAT	EcoRI- NheI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGAA	XhoI
904	Forward	AAAAAAGGTACC-ATGATGCAGCACAATCGTTTC	Kpn I
	Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
904a	Forward	AAAAAAGAATTC-CGGCTCGGCATTGTGCAGATGTTGCA	Eco RI
	Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
905	Forward	CGCGGATCCCATATG-AACAAAATATACCGCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCACTGATAACCGACAGAT	XhoI
907	Forward	CGCGGATCCCATATG-GGCGCGCAACGTGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCCACTGCCAGCG	XhoI
908	Forward	AAAGAATTC-GCAGAGTTAGTAGGCGTTAATAAAAATAC	Eco RI
	Reverse	AAACTGCAG-TTAATATGGTTTTGTCTGTTTCG	Pst I
909	Forward	CGCGGATCCCATATG-TGCGCGTGGGAAACTTAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGGTTTTGAACTTTGGTTTT	XhoI
910	Forward	AAAGAATTC-GCATTTGCCGGCGACTCTGCCGAGCG	Eco RI
	Reverse	AAACTGCAG-TCAGCGATCGAGCTGCTCTTT	Pst I
911	Forward	AAAGAATTC-GCTTTCCGCGTGGCCGGCGGTGC	Eco RI
	Reverse	AAAAAACTGCAG-GTCGACTTATTCGGCGGCTTTTCCGC	Pst I
912	Forward	AAAAAAGAATTC- CAATCCGTCAAAACGCCACTCAAGTATTGAG	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTCCGTCCACGCCTTTCGC	Pst I
913	Forward	CGCGGATCCCATATG-GAAACCCGCCCCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGTTGTGTTCCAGGTTG	XhoI
915	Forward	CGCGGATCCCATATG-TGCCGGCAGGCGGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAAAATATAGGTATCAGG	XhoI
914	Forward	AAAGAATTC-GACAGAATCGGCGATTGGAAGCACG	Eco RI
	Reverse	AAACTGCAG-CTATATGCGCGGCAGGACGCTCAACGG	Pst I
916	Forward	CGCGGATCCCATATG-GCAATGATGGCGGCTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI

917	Forward	AAAAAAGAATTC-CCTGCCGAAAAACCGGCACCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCCCCGCCTTCACATCCTG	Pst I
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC	BamHI-
	Reverse	CCCGCTCGAG-CGGGCGGTATTCGGG	NdeI
920	Forward	CGCGGATCCCATATG-CACCGCGTCTGGGTC	XhoI
	Reverse	CCCGCTCGAG-ATGGTGCGAATGACCGA	BamHI-
921	Forward	AAAAAAGAATTC-TTGACGGAAATCCCCGTGAATCC	NdeI
	Reverse	AAAAAACTGCAG-TCATTTCAAGGGCTGCATCTTCAT	XhoI
922	Forward	CGCGGATCCGCTAGC-TGTACGGCGATGGAGGC	Eco RI
	Reverse	CCCGCTCGAG-CAATCCCGGGCCGCC	Pst I
923	Forward	CGCGGATCCCATATG-TGTTACGCAATATTGTCCC	BamHI-
	Reverse	CCCGCTCGAG-GGACAAGGCGACGAAG	NheI
925	Forward	CGCGGATCCCATATG-AAACAAATGCTTTTAGCCG	XhoI
	Reverse	CCCGCTCGAG-GCCGTTGCATTTGATTTC	BamHI-
926	Forward	CGCGGATCCCATATG-TGCGCGCAATTACCTC	NdeI
	Reverse	CCCGCTCGAG-TCTCGTGCGCGCCG	XhoI
927	Forward	CGCGGATCCCATATG-TGCAGCCCCGCAGC	BamHI-
	Reverse	CCCGCTCGAG-GTTTTTTGCTGACGTAGT	NdeI
929a	Forward	AAAAAAGAATTC-CGCGGTTTGCTCAAAACAGGGCTGGG	XhoI
	Reverse	AAAAAATCTAGA-TTAAGAAAGACGGAACTACTGCC	Eco RI
931	Forward	AAAAAAGAATTC-GCAACCCATGTTTTGATGGAAAC	Xba I
	Reverse	AAAAAACTGCAG-TTACTGCCCGACAACAACGCGACG	Eco RI
935	Forward	AAAAAAGAATTC-GCGGATGCGCCCGCGATTTTGGATGACAAGGC	Pst I
	Reverse	AAAAAACTGCAG-TCAAAACCGCCAATCCGCCGACAC	Eco RI
936	Forward	CGCGGATCCCATATG-GCCGCCGTGCGCGC	Pst I
	Reverse	CCCGCTCGAG-GCGTTGGACGTAGTTTTG	BamHI-
937	Forward	AAAAAAGAATTC-CCGTTTACATTCAAACCGGCGCAAC	NdeI
	Reverse	AAAAAACTGCAG-TTAAAATGTATGCTGTACGCCAAA	XhoI
939a	Forward	AAAAAAGAATTC-GGTTCCGGCAGCTGTGATGAAACC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGCAAACCTTGGATAAAGTTGGC	Pst I
950	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI-
	Reverse	CCCGCTCGAG-TTTAGAACCGCATTGTC	NdeI
953	Forward	CGCGGATCCCATATG-GCCACCTACAAAGTGGAC	XhoI
	Reverse	CCCGCTCGAG-TTGTTTGGCTGCCTCGAT	BamHI-
957	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	NdeI
			XhoI
			BamHI-

	Reverse CCCGCTCGAG-GTGAGAAAGGTCGCGC	NdeI
958	Forward CGCGGATCCCATATG-GCCGATGCCGTTGCG	XhoI
		BamHI-
	Reverse GCCCAAGCTT-GGGTCGTTTGTTCGCTC	NdeI
959	Forward CGCGGATCCCATATG-CACCACGACGGACACG	HindIII
		BamHI-
	Reverse CCCGCTCGAG-GTCGTCGCGGCGGGA	NdeI
961	Forward CGCGGATCCCATATG-GCCACAAGCGACGACG	XhoI
		BamHI-
	Reverse CCCGCTCGAG-CCACTCGTAATTGACGC	NdeI
972	Forward AAAAAAGAATTC-	XhoI
	TTGACTAACAGGGGGGAGCGAAATTAAAAAC	Eco RI
	Reverse AAAAAATCTAGA-TTAAAAATAATCATAATCTACATTTTG	Xba I
973	Forward AAAAAAGAATTC-ATGGACGGCGCACAACCGAAAAC	Eco RI
	Reverse AAAAAACTGCAG-TTACTTCACGCGGGTCGCCATCAGCGT	Pst I
982	Forward CGCGGATCCCATATG-GCAGCAAAGACGTAC	BamHI-
		NdeI
	Reverse CCCGCTCGAG-CATCATGCCGCCCATCC	XhoI
983	Forward CGCGGATCCCATATG-TTAGCTGTTGCAACAACAC	BamHI-
		NdeI
	Reverse CCCGCTCGAG-GAACCGGTAGCCTACG	XhoI
987	Forward CGCGGATCCCATATG-CCCCACTGGAAGAAC	BamHI-
		NdeI
	Reverse CCCGCTCGAG-TAATAAACCTTCTATGGGC	XhoI
988	Forward CGCGGATCCCATATG-TCTTTAAATTTACGGGAAAAAG	BamHI-
		NdeI
	Reverse GCCCAAGCTT-TGATTTGCCTTTCCGTTTT	HindIII
989	Forward CCGGAATTCTACATATG-GTCCACGCATCCGGCTA	EcoRI-
		NdeI
	Reverse CCCGCTCGAG-TTTGAATTTGTAGGTGTATTGC	XhoI
990	Forward CGCGGATCCGCTAGC-TTCAGAGCTCAGCTT	BamHI-
	2	NheI
	Reverse CCCGCTCGAG-AAACAGCCATTTGAGCGA	XhoI
992	Forward CGCGGATCCCATATG-GACGCGCCCGCCCG	BamHI-
		NdeI
	Reverse CCCGCTCGAG-CCAAATGCCCAACCATTC	XhoI
993	Forward CGCGGATCCCATATG-GCAATGCTGATTGAAATCA	BamHI-
		NdeI
	Reverse CCCGCTCGAG-GAACACATCGCGCCCG	XhoI
996	Forward CGCGGATCCCATATG-TGCGGCAGAAAATCCGC	BamHI-
		NdeI
	Reverse CCCGCTCGAG-TCTAAACCCCTGTTTTCTC	XhoI
997	Forward CCGGAATTCTAGCTAGC-CGGCACGCCGACGTT	EcoRI-
		NheI
	Reverse CCCGCTCGAG-GACGGCATCGCTCAGG	XhoI

Underlined sequences indicate restriction recognition sites.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1>:

```
g001.seq
  1  ATGCTGCCGC AGGGGAAGGC GCGCGGAGG GTGTCGGCGA ACGAGGTGTC
 51  CGGCAGGGCT TGC GCCGGA TGGTGTGGT CATCTGCCAG ACGCTGCCGA
101  AACGCGATAC TTAAACGGC TCGGGTACGC ATACTTTACC GGT TTGGGCG
151  ATTTTGCCGA GGTCTGTGCG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201  GCGGTTTTTC GGGTCGGTTT GTAAC TCGGC GCGCGGCGT TCGTCTTGTC
251  CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTTCGGT GCTGATGGTG
301  CCGTCTGAAG CGATGTTGAG GAAGAGTTCG GCGGAGAAAC ACAGCGTCCA
351  CGCGGATTGC CCGGCTTCAT CGGGCAGGTG GGACAATACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 2; ORF 001.ng>:

```
g001.pep
  1  MLPQKAARR VSANEVSGRA CARMVLVICQ TLPKRDTLNG SGTHTLPVWA
 51  ILPRSLRSKS TIITFSARFF GSVCSAARR SSCPSPKIGA VPFIGSVLMV
101  PSEAMLRKSS GEKHSVHAD C PASSGRWDNT A*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3>:

```
m001.seq
  1  ATGCTGCCGC AGGGGAAGGC GCGCGGAGG ATGTCGGCGA ACGAGGTGTC
 51  CGGcAssCTT ss.GCTTGA yGGTGTGGT CATCTGCCAA ACGCTGCCGA
101  AACGCGATAC TTAAACGGT TCGGGTACGC ATACTGTGCC GGT TTGGGCG
151  ATTTTGCCGA GATCGTTACG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201  GCGGTTTTTC GGGTCTGCTT GCAACTCGGC GCGCGGCGT TCGTCTTGTC
251  CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTTCGGT GCTGATGGTG
301  CCGTCCGAAC CGATTTTGAG GAAGAGTTCG GCGGAGAAAC ACAGCGTCCA
351  CGCGGATTGC CCCTCCGCAT CGGGCAGGTG GGACAAGACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 4; ORF 001>:

```
m001.pep
  1  MLPQKAARR MSANEVCGXL XAWXVLVICQ TLPKRDTLNG SGTHTVPVWA
 51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101  PSEPILRKSS GEKHSVHAD C PSASGRWDKT A*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 5>:

```
a001.seq
  1  ATGCTGCCGC AGGGGAAGGC GCGCGGAGG ATGTCGGCGA ACGAGGTGTC
 51  CGGCAAGGCT TGGGCTTGA TGGTGTGGT CATCTGCCAA ACGCTGCCGA
101  AACGCGATAC TTAAACGGT TCGGGTACGC ATACTGTGCC GGT TTGGGCG
151  ATTTTGCCGA GGTCTGTACG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201  GCGGTTTTTC GGGTCTGCTT GCAACTCGGC GCGCGGCGT TCGTCTTGTC
251  CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTTCGGT GCTGATGGTG
301  CCGTCCGAAC CGATTTTGAG GAAGAGTTCG GCGGAGAAAC ACAGCGTCCA
351  CGCGGATTGC CCTTGTGCAT CGGGCAGGTG GGACAAAACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 6; ORF 001.a>:

```
a001.pep
  1  MLPQKAARR MSANEVCGKA WAWMVLVICQ TLPKRDTLNG SGTHTVPVWA
 51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101  PSEPILRKSS GEKHSVHAD C PCASGRWDKT A*
```

m001/a001 96.2% identity over a 131 aa overlap

	10	20	30	40	50	60
m001.pep	MLPQKAARRMSANEVCGXLXAWXVLVICQTLPKRDTLNGSGTHTVPVWAILPRSLRSKS					
a001.pep	MLPQKAARRMSANEVCGKAWAWMVLVICQTLPKRDTLNGSGTHTVPVWAILPRSLRSKS					

	10	20	30	40	50	60
	70	80	90	100	110	120
m001.pep	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
a001.pep	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
	70	80	90	100	110	120
	130					
m001.pep	PSASGRWDKTAX					
a001.pep	PCASGRWDKTAX					
	130					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 001 shows 89.3% identity over a 131 aa overlap with a predicted ORF (ORF 001.ng) from *N. gonorrhoeae*:

m001/g001

	10	20	30	40	50	60
m001.pep	MLPQGKAARRMSANEVCGXLXAWXVLVICQTLPKRDTLNGSGTHTVPVWAILPRSLRSKS					
g001	MLPQGKAARRVSA NEVSGRACARMVLVICQTLPKRDTLNGSGTHTLPVWAILPRSLRSKS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m001.pep	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
g001	TIITFSARFFGSVCNSAARRSSCPSPKIGAVPFIGSVLMVPSEAMLRKSSGEKHSVHADC					
	70	80	90	100	110	120
	130					
m001.pep	PSASGRWDKTAX					
g001	PASSGRWDNTAX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 7>:

g003.seq

```

1  ATGGTCGTAT TCGTGGCTGA AGGCGTATTC GGTGCGCTG TTTGGGTCA
51  CTTGGTATTG CTCTTCGGTC AGGGTGC GTT TGAGTTCGGC GTCAC TCGGT
101 TTTTATACG TTGCCGCGTC GAAGCCTTTG CCTTGCGGTG CGGCTTTGGT
151 TTTGCCCGGC AGCGGTTTCGT CGGCTTTGCG GATGTCGATG TGGCAGTAGC
201 CGTTGGGGTT TTAATCAGG TAGTCCTGAT GGTATTCCTC GGCGTCGTAG
251 AAGTTTTTCA GCGGTTTCGT TTCAACAACG AGGGGCAGTT GGTATTTTTG
301 CTGCTCGCGT TTGAGGGCGG CGGCGATGAC GGCTTTTTCG GCGGGGTCGG
351 TGTAGTACAC GCCGCTGCGG TATTGCGTGC CGGTGTCGTT ACCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAA TAATATTGCA GGATGTCGTC
451 CAGgCTGagt TTGTCGGCAT CGTaggtcac tTTGACGGTC TCGGCATGAC
501 CCGTATGGCG GTaggacact tctTCgtanc TcGGGtTTTC CGTGttGCCG
551 TTGGCgttac cGGATACCGC gtcaACCACG CCGTcgatgc gttggaAATa
601 ggCTTCAAag ccccaaaagc agccgccggc gaagtaa atg gtgcccgtgt
651 tcatgattGC TGa

```

This corresponds to the amino acid sequence <SEQ ID 8; ORF 003.ng>:

g003.pep

```

1  MVVFVAEGVF GRAVLGHLVL LFGQGA FEFG VTRFFIRCRV EAFALRCGFG
51  FARQRFVGFA DVDVAVAVGV FNQVVL MVFL GVVEVFQRFV FNNEGQLVFL
101 LLAFEGGGDD GFFGGVGVVH AAVL RAGVV TLFVEAGRIN DAEIILQDVV

```


151 QAEFVGIVGH FDGLGMTRMA VGHFFVRVFR VAVGVTGYRV NHAVDAL EIG
 201 FQAPKAAAGE VNGARVHDC

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 9>:

m003.seq
 1 ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTCGCGCTG TTTTGGGTAA
 51 CTTGgTATTG CTCTTCGGTC AGGGTGCGTT TGAGTTCCGC GTCAC TCGGT
 101 TTTTATACG TTGCCCGCTC GAAGCCTTTG CCTTGCGGGG CCGTCTTGGT
 151 TTTGCCCGGC AGCGGTTCGT CAGCKTTGCG GATGTCGATG TGGCAGTAGC
 201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG
 251 AAGTTTTtCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTGT
 301 CTGCTCGCGT TTGAGGGCGk CGGCGATGAC GGCTTTTTTCG kCGGGGTCGG
 351 TG TAGTACAC GCCGCTGCGG TATTGCGTAC CCGTGTGCTT GCCCTGTTTG
 401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC
 451 TAGGCTGAGT TTGTCGGCAT CGTAGGTCAC TTTGACGGTT TCGGCGTGGC
 501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTTT CGTGTTGCCG
 551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGAAATA
 601 GGCTTCCAAG CCCCAGAAGC AGCg.CCGGC GAGGTAAATG GTGCGCGTGT
 651 TCATGATTTT TGA

This corresponds to the amino acid sequence <SEQ ID 10; ORF 003>:

m003.pep Length: 221
 1 MVVFVAEGIF GRAVLGNLXL LFGQGAFFFG VTRFFIRCRV EAFALRGGLG
 51 FARQRFVSXA DVDVAVAVGV FNQVLMVFL GIVEVFQRLV FNNEGQLVFL
 101 LLAFEGXGDD GFFXGVGVVH AAVLRTGVV ALFVEAGRIN DAEEILQDVV
 151 *AEFVGIVGH FDGFGVARMA VGHVFIARIF R VAVGVAGYR VNHAVDAL E I
 201 GFQAPEAAXG EVNGARVHDF *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 11>:

a003.seq
 1 ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTCGCGCTG TTTTGGGTAA
 51 CTTGGTATTG CTCTTCGGTC AGGGTGCGTT TGAGTTCCGC GTCAC TCGGT
 101 TTTTATACG TTGCCCGCTC GAAGCCTTTG CCTTGCGGTG CCGTCTTGGT
 151 TTTGCCCGGC AGCGGTTCGT CGGCTTTGCG GATATCGATG TGGCAGTAGC
 201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG
 251 AAGTTTTTCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTGT
 301 CTGCTCGCGT TTGAGGGCGG CGGCGATGAC GGCTTTTTTCG GCGGGGTCGG
 351 TG TAGTACAC GCCGCTGCGG TATTGCGTAC CCGTGTGCTT GCCCTGTTTG
 401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC
 451 TAGGCTGAGT TTGTCGGCAT CGTAGGTCAC TTTGACGGTT TCGGCGTGGC
 501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTTT CGTGTTGCCG
 551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGAAATA
 601 GGCTTCCAAG CCCCAGAAGC AGCCGCCGGC GAGGTAGATG GTGCGCGTGT
 651 TCATGATTTT TGA

This corresponds to the amino acid sequence <SEQ ID 12; ORF 003.a>:

a003.pep
 1 MVVFVAEGIF GRAVLGNLVL LFGQGAFFFG VTRFFIRCRV EAFALRCGLG
 51 FARQRFVGFA DIDVAVAVGV FNQVLMVFL GIVEVFQRLV FNNEGQLVFL
 101 LLAFEGGGDD GFFGGGVVH AAVLRTGVV ALFVEAGRIN DAEEILQDVV
 151 *AEFVGIVGH FDGFGVARMA VGHVFIARIF R VAVGVAGYR VNHAVDAL E I
 201 GFQAPEAAAG EVDGARVHDF *

m003/a003 95.9% identity over a 220 aa overlap

	10	20	30	40	50	60
m003.pep	MVVFVAEGIFGRAVLGNLXL LFGQGAFFFGVTRFFIRCRVEAFALRGGLGFARQRFVSXA					
a003	MVVFVAEGIFGRAVLGNLVL LFGQGAFFFGVTRFFIRCRVEAFALRCGLGFARQRFVGFA					
	10	20	30	40	50	60

	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVL	MVFLGIVEVFQRLVFN	NEGQLVFLLLAFEGXG	DDGFFXG	VG	VVH
a003						
	70	80	90	100	110	120
	DIDVAVAVGVFNQVVL	MVFLGIVEVFQRLVFN	NEGQLVFLLLAFEGG	DDGFFG	VG	VVH
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGR	INDAEEILQDVVXAEFV	GIVGHFDGFGVARM	AVGHVFI	ARIF	
a003						
	130	140	150	160	170	180
	AAAVLRTGVVALFVEAGR	INDAEEILQDVVXAEFV	GIVGHFDGFGVARM	AVGHVFI	ARIF	
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHA	VDAL	EIGFQAPEAA	XGEVNGARVH	DFX	
a003						
	190	200	210	220		
	RVAVGVAGYRVNHA	VDAL	EIGFQAPEAA	AGEVDGARVH	DFX	
	190	200	210	220		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 003 shows 88.6% identity over a 219 aa overlap with a predicted ORF (ORF 003.ng) from *N. gonorrhoeae*:

m003/g003

	10	20	30	40	50	60
m003.pep	MVVFVAEGIFGRAVLGNL	XLFLFGQGA	FEFGVTRFF	FIRCRVEA	FALRGGLGF	ARQRFVSXA
g003						
	10	20	30	40	50	60
	MVVFVAEGVFGRAVLGHL	VLLFLFGQGA	FEFGVTRFF	FIRCRVEA	FALRCGFGF	ARQRFVGFA
	10	20	30	40	50	60
	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVL	MVFLGIVEVFQRLVFN	NEGQLVFLLLAFEGXG	DDGFFXG	VG	VVH
g003						
	70	80	90	100	110	120
	DVDVAVAVGVFNQVVL	MVFLGVVEVFQRFVFN	NEGQLVFLLLAFEGG	DDGFFG	VG	VVH
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGR	INDAEEILQDVVXAEFV	GIVGHFDGFGVARM	AVGHVFI	ARIF	
g003						
	130	140	150	160	170	180
	AAAVLRAGVVTLFVEAGR	INDAEIILQDVVQAEFV	GIVGHFDGLG	MTRMAVGHFFV	-RVF	
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHA	VDAL	EIGFQAPEAA	XGEVNGARVH	DFX	
g003						
	190	200	210			
	RVAVGVAGYRVNHA	VDAL	EIGFQA	PKAAAGEVNGARVH	DC	
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 13>:

g004.seq

```

1  ATGgtagAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTTGAT
51  GCGCCCATGC CAACAagtga gccAAatgtT CGGCGGCAGG GCCTacgatT
101 TCCGCGCCGA TAAagcggcc gGTGgctTTT tCGGCataca ggcgcaTatg
151 gCCTTTGTTT ACCAgcatca cgcggctgcg accttgatTT TTGAACGATA
201 CTTCGCCgaT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTCAAAC CGACAAAGCC GATTTCGgga ctggttaaACA CCACGCCAAT
301 GGTgctgcg cGCAAACCGC TGCCGATATt cgGtagcgg ccccgcggtta
351 ttgcccgcga atcttacctt ggtcggcggc ttcatGCAGC AGGGGCagtt
401 ggttgacgc gtcgcccgcga ataAAGATAT GCGGAATgct ggtCTGCATg
451 gtCAGCGGAT CGGCAACGGG tacgccgcgc gcgtctttgT CGATATTGAT
501 GTTTTCCAAA CCGATATtgT CAACGTTCCG ACGGCgACCT ACGGCTGCCA

```

```

551 ACATATATTC GGCAACAAAT ACGCCTTTTT CGCCATCCTG CTCCCAATGG
601 ACTtctACAT TGCCGTCTGC GTCGAGTTTG ACCTCGGTTT TAGCATCCAG
651 ATGCAGTTTC AATtctTCTC CGAACACGGC TTTGCGCTCG TCTGAAACAA
701 CGGGGTCGGA AATGCCGCCG ATGATTCCGC CCAAACCGAA AATTTCAACT
751 TTCACACCCA AACGGTGCAA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 14; ORF 004.ng>:

g004 . pep

```

1 MVERHIQHLR NGHLLHMRPC QQVSQMFGR AYDFRADKAA GGFFGIQAHM
51 AFVYQHHAHA TLIFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHHAN
101 GAAQAATAADI RVAAPRYCPA ILPWSAASCS RGSWLDASPA IKICGMLVCM
151 VSGSATGTTPR ASLSILMFSK PILSTFGRRP TAANIYSATN TPFSPSCSQW
201 TSTLPSASSL TSVLASRCSF NSSPNTAFAS SETTGSEMP MIPPKPKIST
251 FPKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 15>:

m004 . seq

```

1 ATGGTAGAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTTGAT
51 GTGCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCAGG GCCTACGATT
101 TCCGCGCCGA TAAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTT ACCAGCATCA CGCGGCTGCG GCCTTGTTT TTGAACGATA
201 CTTGCGCGAT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTAGAC CGACAAAGCC GATTTGCGGA CTGGTAAACA CCACGCCGAT
301 GGTGCTGCGC CGCAAACCGC CGCCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGGCAATC TTGCCTTGGT CGGCAGCTTC ATGCAGCAGA GGCAGTTGGT
401 TGGACGCATC GCCTGCGATG AAGATATGCG GAATACTGGT CTGCATGGTC
451 AGCGGGTCGG CAACAGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATATT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCCACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCATC GAGTTTGACC TCGGTTTTAG CATCCAGATG
651 CAGTTTCAAT TCTTCGCCGA ACACGGCGTT CGCCTCGTCT GAAACGACGG
701 GGTCGGAAAT GCCGCCGATG ATTCCGCCCA AACCAGAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 16; ORF 004>:

m004 . pep

```

1 MVERHIQHLR NGHLLHMRPC QQVRQMFGR AYDFRADKAA GGFFGIQAHM
51 AFVYQHHAHA ALVFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHHAN
101 GAAPQTAADI RVAAALSPAI LPWSAASCSR GSWLDASPA KICGILVCMV
151 SGSATGTTPRA SFSILIFSKP ILSTFGRRPT AASIYSATNT PFSPSCSQWT
201 STLPSASSLT SVLASRCSFN SSPNTAFAS ETTGSEMP MIPPKPKISTF
251 TPKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 17>:

a004 . seq

```

1 ATGGTAGAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTTGAT
51 GTGCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCCGG ACCTACGATT
101 TCTGCGCCGA TGAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTT ACCAGCATCA CGCGGCTGCG GCCTTGTTT TTGAACGATA
201 CTTGCGCGAT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTCAAAC CGACAAAGCC GATTTGCGGA CTGGTGAACA CTACGCCGAT
301 GGTGCTGCGC CGCAAACCGC CGCCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGGCAATC TTGCCTTGGT CGGCGGCTTC ATGCAGCAGG GGCAGTTGGT
401 TGGACGCGTC GCCCGCAATA AAGATATGCG GAATACTGGT CTGCATAGTC
451 AGCGGATCGG CAACGGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATGTT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCCTACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCGTC GAGTTTGACC TCGGTTTTAG CATCCAAATG
651 CAGTTTCAAT TCTTACCGA ACACGGCTTT CGCCTCGTCT GAAACGACGG
701 GGTCGGAAAT GCCGCCGATG ATGCCACCA AACCAGAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 18; ORF 004.a>:

```
a004.pep
  1 MVERHIQHLR NGHLLHLMCPSS QQVRQMFQGR TYDFCADEAA GGFFGIQAHM
 51 AFVYQHHAHA ALVFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGEHYAD
101 GAAAQTAADI RVAAALSPAI LPWSAASCSR GSWLDASPAI KICGILVCIV
151 SGSATGTPRA SFSILMFSKP ILSTFGRRPT AASIYSATNT PFSPSCSQWT
201 STLPSASSLA SVLASKCSFN SSPNTAFASS ETTGSEMPPM MPPKPKISTF
251 TPKRCNA*
```

m004/a004 94.9% identity over a 257 aa overlap

```

      10      20      30      40      50      60
m004.pep MVERHIQHLRNGHLLHLMCPSSQQVRQMFQGRAYDFRADKAAGGFFGIQAHMAFVHQHHAAA
          |||||:|||||:|||||:|||||:|||||:|||||
a004      MVERHIQHLRNGHLLHLMCPSSQQVRQMFQGRTYDFCADEAAAGGFFGIQAHMAFVYQHHAHA
          10      20      30      40      50      60

      70      80      90     100     110     120
m004.pep ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHADGAAPQTAADIRVAAALSPAI
          |||||:|||||:|||||:|||||:|||||:|||||
a004      ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGEHYADGAAAQTAADIRVAAALSPAI
          70      80      90     100     110     120

      130     140     150     160     170     180
m004.pep LPWSAASCSRGSWLDASPAKICGILVCMVSGSATGTPRASFSILIFSILSKPILSTFGRRPT
          |||||:|||||:|||||:|||||:|||||:|||||
a004      LPWSAASCSRGSWLDASPAIKICGILVCIVSGSATGTPRASFSILMFSKIPILSTFGRRPT
          130     140     150     160     170     180

      190     200     210     220     230     240
m004.pep AASIYSATNTPFSPSCSQWTSTLPSASSLTSVLASRCSFNSSPNTAFASSETTGSEMPPM
          |||||:|||||:|||||:|||||:|||||:|||||
a004      AASIYSATNTPFSPSCSQWTSTLPSASSLASVLASKCSFNSSPNTAFASSETTGSEMPPM
          190     200     210     220     230     240

      250
m004.pep IPPKPKISTFTPKRCNAX
          :|||||:|||||:|||||:|||||:|||||:|||||
a004      MPPKPKISTFTPKRCNAX
          250

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 004 shows 93.4% identity over a 258 aa overlap with a predicted ORF (ORF 004.ng) from *N. gonorrhoeae*:

m004/g004

```

      10      20      30      40      50      60
m004.pep MVERHIQHLRNGHLLHLMCPSSQQVRQMFQGRAYDFRADKAAGGFFGIQAHMAFVHQHHAAA
          |||||:|||||:|||||:|||||:|||||:|||||
g004      MVERHIQHLRNGHLLHLMRQCQQVSQMFQGRAYDFRADKAAGGFFGIQAHMAFVYQHHAHA
          10      20      30      40      50      60

      70      80      90     100     110     119
m004.pep ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHADGAAPQTAADIRVAAA-LSPA
          :||:|||||:|||||:|||||:|||||:|||||:|||||
g004      TLIFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHANGAAAQTAADIRVAAPRYCPA
          70      80      90     100     110     120

      120     130     140     150     160     170     179
m004.pep ILPWSAASCSRGSWLDASPAKICGILVCMVSGSATGTPRASFSILIFSILSKPILSTFGRRPT

```

```

g004      |||||:||||:|||||:||||:|||||
          130      140      150      160      170      180
ILPWSAASCSRGSWLDASPAIKICGMLVCMVSGSATGTPRASLSILMFSKPILSTFGRRP

m004.pép  180      190      200      210      220      230      239
TAASIYSATNTPFSPSCSQWTSTLPSASSLTSVLASRCSFNSSPNTAFASSETTGSEMP
g004      |||||:||||:|||||:||||:|||||
          190      200      210      220      230      240
TAANIYSATNTPFSPSCSQWTSTLPSASSLTSVLASRCSFNSSPNTAFASSETTGSEMP

m004.pép  240      250
MIPPKPKISTFTP KRCNAX
g004      |||||
          250
MIPPKPKISTFTP KRCNA

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 19>:

g005.seq

```

1  ATGGGGATGG ACAATATTGA TATGTTTCATG CCTGAACAAG AGGAAATCCA
51  ATCAATGTGG AAAGAAATTT TACTGAATTA CGGTATTTTC CTGCTCGAAC
101 TGCTTACCGT GTTCGCGCA ATTGCGCTGA TTGTGTTGGC TATCGTACAG
151 AGTAAGAAAC AGTCGGAAG CGGCAGTGTC GTACTGACAG ATTTTTCGGA
201 AAATTATAAA AACAGCGGC AATCGTTTGA AACATTCTTT TTAAGCGAGG
251 AAGAGACAAA ACATCAGGAA AAAAAAGAAA AGAAAAGGA AAAGCGGAA
301 GCCAAAGCAG AGAAAAAGCG TTGAAGGAG GCGGGGAGA AATCTGCCGA
351 AACGCAAAAA TCCCGCCTTT TTGTGTTGGA TTTTGACGGC GATTGTATG
401 CACACGCCGT AGAATCCTTG CGTCATGAGA TTACGGCGGT GCTTTTGATT
451 GCCAAGCCTG AAGATGAGGT TCTGCTCAGA TTGGAAAGTC CGGGCGCGT
501 GGTTCACGGT TACGGTTTGG CGGCTTCGCA GCTTAGGCGT TTGCGCGAAC
551 GCAATATTCC GCTGAccgtc gccgTCGATA AGGTCGCGGC AAGCGgcggc
601 tatatgatgg cgtgtgtgGC GGATAAAATT GTTTCGCTc cgtttgcggt
651 catcggttcg gtgggtgtgg tgGcggaagt gcCGAATATC CAccgCctGT
701 TGAAAAACA TGATATTGAT GTGGATGTGA TGACGGCGGG CGAATTTAAG
751 CGCACGGTTA CTTTATGGG TGAAATACG GAAAAGGGCA AACAGAAATT
801 CCGGCAGGAA CTGGAGGAAA CGCATCAGTT GTTCAAGCAG TTTGTCAGTG
851 AAAACCGCCC CGGGTTGGAT ATTGAAAAA TAGCGACGGG CGAGCATTGG
901 TTCGGCCGGC AGGCGTTGGC GTTGAAGTTG ATTGACGAGA TTTTCGACCAG
951 TGATGATTG TTGTTGAAAG CGTTTGAAAA CAAACAGGtt aTCGAAGTGA
1001 AATATCAGGA GAAGCGAAGC CTGATCCAGC GCATTGGTTT GCAGGCGGAA
1051 GCTTCCGTTG AAAAGTTGTT TGCCAACTT GTCAACCGGC GAGCGGATGT
1101 GATGTAG

```

This corresponds to the amino acid sequence <SEQ ID 20; ORF 005.ng>:

g005.pep

```

1  MGMDNIDMFV PEQEEIQSMW KEILLNYGIF LLELLTVFGA IALIVLAIQV
51  SKKQSESGSV VLTDfsENYK KQRQSFETFF LSEEETKHQE KKEKKKEKAE
101 AKAEEKRLKE GGEKSAETQK SRLFLDfDfG DLYAHAVESL RHEITAVLLI
151 AKPEDEVLLR LESPggVVHG YGLAASQLRR LRERNIPLTV AVDKVAASGG
201 YMMACVADKI VSAPFAVIGS VGVVAEPVNI HRLKKHDID VDVMTAGFEK
251 RTVTFMGENT EKGKQKFRQE LEETHQLFKQ FVSENRPGLD IEKIATGEHW
301 FGRQALALNL IDEISTDDL LLKAFENKQV IEVKYQEKRS LIQRIGLQAE
351 ASVEKLFACL VNRRADVM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 21>:

m005.seq

```

1  ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51  GTGAAAGAAA ATTTTACTGA ATTACGGTAT TTCCTGCTC GAACTGCTTA
101 CCGTGTTCCG CGCAATTGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151 AAACAGTCGG AwAGCGGCAG TGTCGTACTG ACGGATTTTT CGGAAATTA
201 TAAAAAACAG CGGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251 CACAACATCA GGAAAAAGAG GAAAAGAAA AGGAAAAGGC GGAAGCCAAA

```

```

301 GCAGAGAAAA A.CGTTTGAA GGAGGGTGGG GAGAAATCTG CCGAAACGCA
351 nAAATCACGC CTTTTTGTGT TGGANNNNNN NNNNNNNNNN NNNNNNNNNN
401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNGCGAGCGG CGGTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGCTTCC GCTCCGTTTG CGATTGTCGG
651 TTCGGTGGGT GTGGTGGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGGCGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGGAAGAG GGCAAACAGA AATTCCGACA
801 GGAACGGAG GAAACGCATC AGTTGTTCAA GCAGTTTGTC AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGGCGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCGA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTTG AAAACAAACA GGTATTCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTGCAGGC GGAAGCTTCT
1051 GTTGAAAAGT TGTTTGCCAA ACTTGTCAAC CGGCGGGCGG ATGTGATGT A
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 22; ORF 005>:

m005.pep

```

1 MDNIDMFMP E QEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQSXSGSVVL TDFSENYKKQ RQSFEAFFLS GEEAQHQEKE EKKKEKAEAK
101 AEKXRLKEGG EKS AETXKSR LFVLXXXXXX XXXXXXXXXXX XXXXXXXXXXX
151 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXASGGYM
201 MACVADKIAS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG
301 RQALALNLID EISTSDDLLL KAFENKQVIE VKYQEKQSLI QRIGLQAEAS
351 VEKLF AKLVN RADVM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 23>:

a005.seq

```

1 ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51 GTGGAAAGAA ATTTTACTGA ATTACGGTAT TTTCTGCTC GAACTGCTTA
101 CCGTGTTCCG CGCAATTGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151 AAACAGTCGG AAAGCGGCAG TGTCGTACTG ACGGATTTT CCGAAAATTA
201 TAAAAAACAG CGGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251 CAAAACATCA GAAAAAGAG GAAAAGAAAA AGGAAAAGGC GGAAGCCAAA
301 GCAGAGAAAA AGCGTTTGAA GGAGGGTGGG GAGAAATCTT CCGAAACGCA
351 AAAATCCCGC CTTTTTGTGT TGGATTTTGA CGGCGATTG TATGCACACG
401 CCGTAGAATC CTTGCGTCAT GAGATTACGG CGGTGCTTTT GATTGCCAAG
451 CCTGAAGATG AGGTTCTGCT TAGATTGGAA AGTCCGGGCG GCGTGTTTCA
501 CGGTTACGGT TTGGCGGCTT CGCAGCTTAG GCGTTTGCGC GAACGCAATA
551 TTCCGCTGAC CGTCGCCGTC GATAAGGTGG CGGCGAGCGG TGGTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGTTTCC GCTCCGTTTG CGATTGTCGG
651 TTCGGTGGGT GTTGTAGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGGCGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGGAAGAG GGCAAACAGA AATTCCGACA
801 GGAACGGAG GAAACGCATC AGTTGTTCAA GCAGTTTGTC AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGGCGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCGA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTTG AAAACAAACA GGTATTCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTGCAGGC GGAAGCTTCT
1051 GTTGAAAAGT TGTTTGCCAA ACTTGTCAAC CGGCGGGCGG ATGTGATGTA
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 24; ORF 005.a>:

a005.pep

```

1 MDNIDMFMP E QEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQSESGSVVL TDFSENYKKQ RQSFEAFFLS GEEAKHQEKE EKKKEKAEAK
101 AEKKRLKEGG EKSSETQKSR LFVLDFDGL YAHAVESLRH EITAVLLIAK
151 PEDEVLLRLE SPGGVVHGYG LAASQLRRLR ERNIPLTVAV DKVAASGGYM
201 MACVADKIVS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG

```

301 RQALALNLID EISTSDDLLL KAFENKQVIE VKYQEKQSLI QRIQLQAEAS
 351 VEKLFKLVN RRADVM*

m005/a005 79.2% identity over a 366 aa overlap

m005.pep	MDNIDMFMPQE ¹⁰ EEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQ ²⁰ SXSGSVVL
a005	MDNIDMFMPQE ¹⁰ EEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQ ²⁰ SESGSVVL
m005.pep	TDFSEN ⁷⁰ YKKQRSFEAFFLSGEEAQHQEKEEKKKEKAEAKAEKXRLKEGGEKSAETXKSR
a005	TDFSEN ⁷⁰ YKKQRSFEAFFLSGEEAKHQEKEEKKKEKAEAKAEKXRLKEGGEKSS ⁸⁰ ETQKSR
m005.pep	LFVLXX
a005	LFVLDFDGDLYAHAVESLRHEITAVLLIAKPEDEVLLRLESPGGVVHGYGLAASQLRRLR
m005.pep	XXXXXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSVGVVAEVPNIHRLKKHDIDVD
a005	ERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAIVGSVGVVAEVPNIHRLKKHDIDVD
m005.pep	VMTAGEFKRTVTFMGENT ²⁵⁰ EKGKQKFRQELEETHQLFKQFVSENRPQLDIEEVATGEHWFG
a005	VMTAGEFKRTVTFMGENT ²⁵⁰ EKGKQKFRQELEETHQLFKQFVSENRPQLDIEEVATGEHWFG
m005.pep	RQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEKQSLIQRIQLQAEASVEKLFKLVN
a005	RQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEKQSLIQRIQLQAEASVEKLFKLVN
m005.pep	RRADVMX
a005	RRADVMX

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 005 shows 77.0% identity over a 366 aa overlap with a predicted ORF (ORF 005.ng) from *N. gonorrhoeae*:

m005/g005

m005.pep	MDNIDMFMPQE ¹⁰ EEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQ ²⁰ SXSGSV
g005	MGMDNIDMFMPQE ¹⁰ EEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQ ²⁰ SESGSV
m005.pep	VLTD ⁶⁰ SEN ⁷⁰ YKKQRSFEAFFLSGEEAQHQEKEEKKKEKAEAKAEKXRLKEGGEKSAETXK
g005	VLTD ⁶⁰ SEN ⁷⁰ YKKQRSFETFFLSEETKHQEKKEKKKEKAEAKAEKXRLKEGGEKSAETQK

	120	130	140	150	160	170
m005.pep	SRLFVLXXX					
		:				
g005	SRLFVLDFDGDLYAHAVESLRHEITAVLLIAKPEDEVLLRLESPPGGVVHGYGLAASQLRR					
	130	140	150	160	170	180
	180	190	200	210	220	230
m005.pep	XXXXXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSVGVVAEVPNIHRLKKHDID					
	:					
g005	LRERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAVIGSVGVVAEVPNIHRLKKHDID					
	190	200	210	220	230	240
	240	250	260	270	280	290
m005.pep	VDVMTAGEFKRTVTFMGENTTEKGKQKFRQLEETHQLFKQFVSENRPQLDIEEVATGEHW					
g005	VDVMTAGEFKRTVTFMGENTTEKGKQKFRQLEETHQLFKQFVSENRPGLDIEKIATGEHW					
	250	260	270	280	290	300
	300	310	320	330	340	350
m005.pep	FGRQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLF					
g005	FGRQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEKRSIQRIGLQAEASVEKLF					
	310	320	330	340	350	360
	360					
m005.pep	VNRADVMX					
g005	VNRADVMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 25>:

g006.seq

```

1  ATGCTGCTGG TGCTggaatt ttggttCGGc gtGtCGGCGG TGGGCatact
51  tgCGTTGTTT TTATGGCttt TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTC CG CCTGAACAAC AGCTTGAAC gcgACAACCA CTTTATCCGA
151 AAAGGCGACG AGCGGCAGCT GTACCGCCAT TACGGACTGG TTTCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGTCGGCG
251 CGGCGATGGG TATTTGTTC GGCTTGCTT TTGTGATGAT GACGCTCAA
301 GGCTACGCA GCGCGGGCA TATTTATTCG GTCGGCACTT ATCTGTGGAT
351 GTTTGCCATG AGTTGGACG ATGTGCCGCG ATTGGTCGAA CAATATCCA
401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTCGGAACG GAACATCAA
451 GCCGGAACCTT GA

```

This corresponds to the amino acid sequence <SEQ ID 26; ORF 006.ng>:

g006.pep

```

1  MLLVLEFWFG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
51  KGDERQLYRH YGLVSRLRLV ISNREAFGYL CVGAAMGILF GFAFVMTLK
101 GYGSAGHIYS VGTYLWMFAM SLDDVPRLVE QYSNLKDIGQ RIEWSERNIK
151 AGT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 27>:

m006.seq

```

1  ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT
51  TGCGTTGTTT TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTC CG CCTGAACAAC AGCTTGAAC GCGACAACCA CTTTATCCGA
151 AAAGGCGACC GCGGCAGCT GTACCGCCAT TACGGACTGC TTGCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGTCGGCA
251 CGGCGATGGG TATTTGTTC GGCTTGCTT TTGTGATGAT GACGCTCAA
301 GGCTACAGCA GCGCGGGCA TGTCTATTCG GTCGGCACTT ATCTGTGGAT

```



```

351  GTTTGCCATG AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA
401  ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAAA
451  GCCGGAACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 28; ORF 006>:

m006.pep

```

1  MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
51  KGDRRQLYRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMMTLK
101 GYSSAGHVYS VGTYLWMFAM SLDDVPRLVE QYSNLKDIGQ RIEWSERNIK
151 AGT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 29>:

a006.seq

```

1  ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT
51  TGCCTTGTTT TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCCTG CCTGAAGAAC AGCTTGGAAC GCGACAACCA CTTTATCCGA
151 AAAGGCGACG AGCGGCAGCT GGACCGCCAT TACGGACTGC TTGCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TGCCTCGGCA
251 CGGCGATGGG TATTTTGTTT GGCTTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACAGCA GCGCGGGGCA TGTCTATTCG GTCGGCACTT ATCTGTGGAT
351 GTTTGCCATA AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA
401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAAA
451 GCCGGAACCT GA

```

This corresponds to the amino acid sequence <SEQ ID 30; ORF 006.a>:

a006.pep

```

1  MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLKN SLERDNHFIR
51  KGDERQLDRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMMTLK
101 GYSSAGHVYS VGTYLWMFAI SLDDVPRLVE QYSNLKDIGQ RIEWSKRNIK
151 AGT*

```

m006/a006 96.7% identity over a 153 aa overlap

	10	20	30	40	50	60
m006.pep	MLLVLEFWVGVS					
a006	MLLVLEFWVGVS					
	10	20	30	40	50	60
	SAVGILALFLWLLPRFAAISENLYFRLNNSLERDNHFIRKGD					
	RRQLYRH					
	70	80	90	100	110	120
m006.pep	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSAGHVYSVGTYLWMFAM					
a006	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSAGHVYSVGTYLWMFAI					
	70	80	90	100	110	120
	SLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					
	SLDDVPRLVEQYSNLKDIGQRIEWSKRNIKAGTX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 006 shows 95.4% identity over a 153 aa overlap with a predicted ORF (ORF 006.ng) from *N. gonorrhoeae*:

m006/g006

	10	20	30	40	50	60
m006.pep	MLLVLEFWVGVS					
	SAVGILALFLWLLPRFAAISENLYFRLNNSLERDNHFIRKGD					
	RRQLYRH					

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```

|||||
g006  MLLVLEFWFGVSAVGILALFLWLLPRFAAISENLYFRLNNSLERDNHFIRKGDERQLYRH
      10      20      30      40      50      60

      70      80      90      100     110     120
m006.pep YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSAGHVYSVGTYLWMFAM
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g006  YGLVSRLRVLISNREAFGYLCVGAAMGILFGFAFVMMTLKGYGSAGHIYSVGTYLWMFAM
      70      80      90      100     110     120

      130     140     150
m006.pep SLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX
      |||||
g118  SLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGT
      130     140     150

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 31>:

```

g006-1.seq
1  ATGTGGAAAA TGTTGAAACA CATAGCCAAA ACCCACCACA AGCGATTGAT
51  TGGCACATTT TCCCCGGTCG GACTGGAAAA CCTTTTGATG CTGGGGTATC
101 CGGTGTTTGG CGGCTGGGCG ATTAATGCCG TGATTGCGGG GAGGGTGTGG
151 CAGGCGTTGC TGTACGCTTT GGTGTGATTT TTGATGTGGC TGGTCGGTGC
201 GGCACGGCGG ATTGCCGATA CGCGCACGTT TACGCGGATT TATACCGAAA
251 TCGCCGTGCC GGTGTGTGTTG GAACAACGGC AGCGGCAAGT CCCGCATCA
301 GCGGTAAGTG CACGGGTTGC CCTGTGCGGT GAATTTGTCA GCTTTTTTGA
351 AGAACACCTG CCGATTGCCG CGACATCCGT CGTATCCATA TTCGGCGCGT
401 GCATCATGCT GCTGGTGCTG GAATTTTGGG TCGGCGTGTC GGCGGTGGGC
451 ATACTTGCGT TGTTTTTATG GCTTTTGCCA CGTTTTGCCG CCATCAGCGA
501 AAACCTGTAT TTCCGCCTGA ACAACAGCTT GGAACGCGAC AACCACTTTA
551 TCCGAAAAGG CGACGAGCGG CAGCTGTACC GCCATTACGG ACTGGTTTCG
601 CGCCTGCGTG TGCTGATTTT CAACCGCGAA GCCTTCGGCT ATCTCTGCGT
651 CGGCGCGGCG ATGGGTATTT TGTTTCGGCT TGCTTTTGTG ATGATGACGC
701 TCAAAGGCTA CGGCAGCGCG GGCATATTT ATTCGGTCGG CACTTATCTG
751 TGGATGTTTG CCATGAGTTT GGACGATGTG CCGCGATTGG TCGAACAATA
801 TTCCAATTTG AAAGACATCG GACAACGGAT AGAGTGGTCG GAACGGAACA
851 TCAAAGCCGG AACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 32; ORF 006-1.ng>:

```

g006-1.pep
1  MWKMLKHIAK THRKRIGTF SPVGLNLLM LGYPVFGGWA INAVIAGRNV
51  QALLYALVVE LMWLVGAARR IADTRTFTRI YTEIAPVVL EQQRQVPHS
101 AVTARVALSR EFVSFFEEHL PIAATSVVSI FGACIMLLVL EFWVGVSAVG
151 ILALFLWLLP RFAAISENLY FRLNNSLERD NHFIRKGDER QLYRHYGLVS
201 RLRVLISNRE AFGYLCVGAA MGILFGFAFV MMTLKGYGSA GHIYSVGTYL
251 WMFAMSLDDV PRLVEQYSNL KDIGQRIEWS ERNIKAGT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 33>:

```

m006-1.seq
1  ATGTGGAAAA TGTTGAAACA CATAGCCCAA ACCCACCACA AGCGATTGAT
51  TGGCACATTT TCCCTGGTCG GACTGGAAAA CCTTTTGATG CTGGGTGTATC
101 CGGTGTTTGG CGGCCGGGCG ATCAATGCCG TGATTGCGGG GGAGGTGTGG
151 CAGGCGTTGC TGTACGCTTT GGTGTGCTT TTGATGTGGC TGGTCGGTGC
201 GGTGCGGCGG ATTGCCGATA CGCGCACGTT TACGCGGATT TATACCGAAA
251 TCGCCGTGCC GGTGCTGTTG GAACAGCGC AGCGACAAGT CCCGCATTTC
301 GCGGTAAGTG CGCGGTTGC CCTGTGCGGT GAGTTTGTCA GCTTTTTTGA
351 AGAACACCTG CCGATTGCCG CGACATCCGT CGTATCCATA TTCGGCGCGT
401 GCATCATGCT GCTGGTGCTG GAATTTTGGG TCGGCGTGTC GGCGGTGGGC
451 ATACTTGCGT TGTTTTTATG GCTTTTGCCA CGTTTTGCCG CCATCAGCGA
501 AAACCTGTAT TTCCGCCTGA ACAACAGCTT GGAACGCGAC AACCACTTTA
551 TCCGAAAAGG CGACCGGCGG CAGCTGTACC GCCATTACGG ACTGCTTGCG
601 CGCCTGCGTG TGCTGATTTT CAACCGCGAA GCCTTCGGCT ATCTCTGCGT

```

```

651 CGGCACGGCG ATGGGTATTT TGTTCCGGCTT TGCTTTTGTG ATGATGACGC
701 TCAAAGGCTA CAGCAGCGCG GGCATGTCT ATTCGGTCGG CACTTATCTG
751 TGGATGTTG CCATGAGTTT GGACGACGTG CCGCGATTGG TCGAACAATA
801 TTCCAATTG AAAGACATCG GACAACGGAT AGAGTGGTCG GAACGGAACA
851 TCAAAGCCGG AACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 34; ORF 006-1>:

m006-1.pep

```

1 MWKMLKHIAQ THRRLIGTF SLVGLENLLM LVYPVFGGRA INAVIAGEVW
51 QALLYALVVL LMWLVGAVRR IADTRTFTRI YTEIAPVVVL EQRQRQVPHS
101 AVTARVALSR EFVSFFEEHL PIAATSVVSI FGACIMLLVL EFWVGSAVG
151 ILALFLWLLP RFAAISENLY FRLNNSLERD NHFIRKGD RR QLYRHYGLLA
201 RLRVLISNRE AFGYLCVGTA MGILFGFAFV MMTLKGYSSA GHVYSVGTYL
251 WMFAMSLDDV PRLVEQYSNL KDIGQRIEWS ERNIKAGT*

```

m006-1/g006-1 95.5% identity in 288 aa overlap

	10	20	30	40	50	60
m006-1.pep	MWKMLKHIAQ	THRRLIGTF	SLVGLENLLM	LVYPVFGGRA	INAVIAGEVW	QALLYALVVL
g006-1	MWKMLKHIAK	THRRLIGTF	SPVGLNLLM	LGYPVFGG	WAINAVIAGR	VWQALLYALVVF
	10	20	30	40	50	60
	70	80	90	100	110	120
m006-1.pep	LMWLVGAVRR	IADTRTFTRI	YTEIAPVVLE	QQRQVPHSA	VTARVALSR	EFVSFFEEHL
g006-1	LMWLVGAARR	IADTRTFTRI	YTEIAPVVLE	QQRQVPHSA	VTARVALSR	EFVSFFEEHL
	70	80	90	100	110	120
	130	140	150	160	170	180
m006-1.pep	PIAATSVVSI	FGACIMLLVL	EFWVGSAVG	ILALFLWLL	PRFAAISEN	LYFRLNNSLERD
g006-1	PIAATSVVSI	FGACIMLLVL	EFWVGSAVG	ILALFLWLL	PRFAAISEN	LYFRLNNSLERD
	130	140	150	160	170	180
	190	200	210	220	230	240
m006-1.pep	NHFIRKGD RR	QLYRHYGLLA	RLRVLISNRE	AFGYLCVGT	AMGILFGFA	FVMMTLKGYSSA
g006-1	NHFIRKGD ER	QLYRHYGLV	SRLRVLISNRE	AFGYLCVGA	AMGILFGFA	FVMMTLKGYGSA
	190	200	210	220	230	240
	250	260	270	280	289	
m006-1.pep	GHVYSVGTYL	WMFAMSLDDV	PRLVEQYSNL	KDIGQRIEWS	ERNIKAGTX	
g006-1	GHIYSVGTYL	WMFAMSLDDV	PRLVEQYSNL	KDIGQRIEWS	ERNIKAGTX	
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 35>:

a006-1.seq (partial)

```

1 ..AGCCAAAACC ACCGCAAGCG ATTGATTGGC ACATTTTTC TGGTCGGACT
51 GGAAACCTT TTGATGCTGG TGTATCCGGT GTTTGGCGGC TGGGCGATTA
101 ATGCCGTGAT TGCGGGCGAG GCGTGGCAGG CGTTGCTGTA CGCTTTGGTT
151 GTGCTTTTGA TGTGGCTGGT CCGTGC GGCG CGGCGGATTG CCGATACGCG
201 CACGTTTACG CGGATTTATA CCGAAATCGC CGTGCCGGTT GTGTTGGAAC
251 AGCGGCAGCG GCAAGTCCCG CATTGCGCGG TAACTGCGCG GGTGCGCCTG
301 TCGCGTGAGT TTGTCAGCTT TTTGAAGAA CACCTGCCGA TTGCCGCGAC
351 ATCCGTCGTA TCCATATTCG GCGCGTGCAT CATGCTGCTG GTGCTGGAAT
401 TTTGGGTCGG CGTGTGCGCG GTGGGCATAC TTGCGTTGTT TTTATGGCTT
451 TTGCCACGTT TTGCCGCCAT CAGCGAAAAC CTGTATTTCC GCCTGAAGAA
501 CAGCTTGGA ACGCGACAACC ACTTTATCCG AAAAGGCGAC GAGCGGCAGC
551 TGGACCGCCA TTACGGACTG CTGCGCGGCC TCGGTGTGCT GATTTCCAAC
601 CGCGAAGCCT TCGGCTATCT CTGCGTCGGC ACGGCGATGG GTATTTTGTT
651 CGGCTTTGCT TTTGTGATGA TGACGCTCAA AGGCTACAGC AGCGCGGGGC

```

```

701 ATGTCTATTC GGTCCGCACT TATCTGTGGA TGTTTGCCAT AAGTTTGGAC
751 GACGTGCCGC GATTGGTCGA ACAATATTCC AATTGAAAG ACATCGGACA
801 ACGGATAGAG TGGTCGAAAC GGAACATCAA AGCCGGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 36; ORF 006-1.a>:

```

a006-1.pep (partial)
  1 ..SQNHRKRLIG TFFLVGLENL LMLVYPVFGG WAINAVIAGQ AWQALLYALV
 51 VLLMWLVGAA RRIADTRTFT RIYTEIAVPV VLEQRQRQVP HSAVTARVAL
101 SREFVSFFEE HLPAAATSVV SIFGACIMLL VLEFWVGVS VGLALFLWL
151 LPRFAAISEN LYFRLKNSLE RDNHFIRKGD ERQLDRHYGL LARLRVLISN
201 REAFGYLCVG TAMGILFGFA FVMMLKGY SAGHVYSVGT YLWMFAISLD
251 DVPRLVEQYS NLKDIGQRIE WSKRNIKAGT *

a006-1/m006-1 95.7% identity in 280 aa overlap

              10      20      30      40      50
a006-1.pep    SQNHRKRLIGTFFLVGLENLLMLVYPVFGGWAINAVIAGQAWQALLYALVVL
m006-1         MWKMLKHIAQTHRKLIGTFSLVGLENLLMLVYPVFGGRAINAVIAGEVWQALLYALVVL
              10      20      30      40      50      60

              60      70      80      90     100     110
a006-1.pep    LMWLVGAARRIADTRTFTRIYTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL
m006-1         LMWLVGAVRRIADTRTFTRIYTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL
              70      80      90     100     110     120

              120     130     140     150     160     170
a006-1.pep    PIAATSVVSIFGACIMLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLKNSLERD
m006-1         PIAATSVVSIFGACIMLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLNNSLERD
              130     140     150     160     170     180

              180     190     200     210     220     230
a006-1.pep    NHFIRKGDERRQLDRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMLKGYSSA
m006-1         NHFIRKGDERRQLYRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMLKGYSSA
              190     200     210     220     230     240

              240     250     260     270     280
a006-1.pep    GHVYSVGTYLWMFAISLDDVPRLVEQYSNLKDIGQRIEWSKRNIKAGTX
m006-1         GHVYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX
              250     260     270     280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 37>:

```

g007.seq
  1 atgaACACAA CCCGACTGCC GACCGCCTTC ATCTTGTGCT GCCTCTGcgC
 51 CGCcGCTTCT GCCGccgaca acAGCatcat gaCaAAAGGG CAAAAAGTGT
101 ACGAATCcAa ctGCATCGCC TGCCACGGCA AGAAAGGGGA AGGGCGCGGC
151 ACTGCGtTTC CTcgcgtTTT CCggtcgGac tgtattatga acaAACCGCa
201 cgTCCTgctg cacagcatgg tcaaaggcAt cgacgggaca ttcaaagtgg
251 agcggcaaaa cctacgacgg atttatgCcc gcaaccgccca tcagcgATGC
301 GGACATTGCC GCCGTCGCCA CTTATATCAT GAACGCCTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 38; ORF 007.ng>:

```

g007.pep
  1 MNTTRLPTAF ILCCLCAAAS AADNSIMTKG QKVYESNCIA CHGKKGEGRG
 51 TAFPPLFRSD CIMNKPVL L HSMVKGIDGT FKVERQNLRR IYARNRHQRC
101 GHCRRRHLYH ERL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 39>:

This corresponds to the amino acid sequence <SEQ ID 40; ORF 007>:

m007.ppt

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 41>:

a007.seq

This corresponds to the amino acid sequence <SEQ ID 42; ORF 007.a>:

a007.pcp

m007/a007 97.3% identity over a 113 aa overlap

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 007 shows 86.7% identity over a 113 aa overlap with a predicted ORF (ORF 007.ng) from *N. gonorrhoeae*:

m007/g007

	10	20	30	40	50	60
m007.pep	MNTTRLPTALVLGCFCAAASAADNSIMTKGQKVYESNCVACHGKKGEGRGTMFPPLYRSD					
	::	:		:		:
g007	MNTTRLPTAFILCCLCAAASAADNSIMTKGQKVYESNCIACHGKKGEGRGTAFFPLFRSD					
	10	20	30	40	50	60
	70	80	90	100	110	
m007.pep	FIMKKPQVLLHSMVKGINGTIKVXRQLQRIHARNRHRQCGHCRRRHLYHERLX					
	:: :	: :	: :			

g007 CIMNKPHVLLHSMVKGIDGTFKVERQNLRRRIYARNRHQRCGHCRRRHLHYHERL
 70 80 90 100 110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 43>:

g007-1.seq (partial)

```

1  ATGAACACAA CCCGACTGCC GACCGCCTTC ATCTTGTGCT GCCTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCATCGCC TGCCACGGCA AGAAAGGGGA AGGGCGCGGC
151 ACTGCGTTTC CTCCGCTTTT CCGGTCGGAC TATATTATGA ACAAACCGCA
201 CGTCCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CAACCGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAACA GGCAAAAGGC AAAAAAAC.
```

This corresponds to the amino acid sequence <SEQ ID 44; ORF 007-1.ng>:

g007-1.pep (partial)

```

1  MNTTRLPTAF ILCLCAAAS AADNSIMTKG QKVYESNCIA CHGKKGEGRG
51 TAFPPLFRSD YIMNKPHVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKG KKN...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 45>:

m007-1.seq

```

1  ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCTTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACCGCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CAACCGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAACA GGCAAAAGC AAAAAAACT
401 AA
```

This corresponds to the amino acid sequence <SEQ ID 46; ORF 007-1>

m007-1.pep

```

1  MNTTRLPTAL VLGCFCAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKS KKN*
```

m007-1 / g007-1 91.7% identity in 133 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGCFCAAAS	AADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
		:	:			
g007-1	MNTTRLPTAFILCLCAAAS	AADNSIMTKGQKVYESNCIACHGKKGEGRG	TAFPPLFRSD			
	10	20	30	40	50	60
	70	80	90	100	110	120
m007-1.pep	FIMKKPQVLLHSMVKGINGTIKVNGKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV					
	:	:				
g007-1	YIMNKPHVLLHSMVKGINGTIKVNGKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV					
	70	80	90	100	110	120
	130					
m007-1.pep	TEKDVQAKSKKNX					
		:				
g007-1	TEKDVQAKGKKN					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 47>:

a007-1.seq (partial)

```

1  ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCCTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
```

```

151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACCGCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CCACTGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAACA GCGAAAAAC AAAAAA..

```

This corresponds to the amino acid sequence <SEQ ID 48; ORF 007-1.a>:

a007-1.pep (partial)

```

1 MNTTRLPTAL VLGCLCAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKN KK..

```

m007-1/a007-1 98.5% identity in 132 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGCLCAAAS	AAADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
a007-1	MNTTRLPTALVLGCLCAAAS	AAADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
	10	20	30	40	50	60
m007-1.pep	FIMKKPQVLLHSMVKGINGTIKVNGKTYNG	FMPATAISDADIAAVATYIMNAFDNGGGSV				
a007-1	FIMKKPQVLLHSMVKGINGTIKVNGKTYNG	FMPATAISDADIAAVATYIMNAFDNGGGSV				
	70	80	90	100	110	120
m007-1.pep	FIMKKPQVLLHSMVKGINGTIKVNGKTYNG	FMPATAISDADIAAVATYIMNAFDNGGGSV				
a007-1	FIMKKPQVLLHSMVKGINGTIKVNGKTYNG	FMPATAISDADIAAVATYIMNAFDNGGGSV				
	70	80	90	100	110	120
m007-1.pep	TEKDVQAKSKKNX					
a007-1	TEKDVQAKNKK					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 49>:

g008.seq

```

1 ATGAACAACA GACATTTTGC CGTCAtcgCC TTGGGCAGCA ACCTTGACAA
51 CCCCACACAA CAAATacgcg gcgattaga cgcgctctcg tcccatcctg
101 acatccggtc tgaaCaggtt tcctcactgt aTatgaccgc acctgtcggg
151 tacgAcaaTC agcccgATTT CATCaatgcc gTCTgcaccg TTTCCACCAC
201 CtTGGACGGC ATTGcccTGC TTGCCgaACT CAAccgTATC GAAGCCGATT
251 TCGGACGCGA aCGCAGTTTC CGCAATGCAC CGCGCACATT GGATTTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACCCCCGCC TTACCCTGCC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATACGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTTTG GGAAAATACG GAAAGGTGT CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGACA GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 50; ORF 008.ng>:

g008.pep

```

1 MNNRHFAVIA LGSNLDNPAQ QIRGALDALS SHPDIRLEQV SSLYMTAPVG
51 YDNQPDFINA VCTVSTLDG IALLAELNRI EADFRGRERSF RNAPRTLDD
101 IIDFDGISSD DPRLTLPHER AHERSFVIRP LAEILPDFIL GKYGKVVLS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 51>:

m008.seq

```

1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
51 CCCTGCTCAA CAGGTACGCG CCGCATTGGA CACGCTGTCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATTT TGTCAATGCC GTCTGCACCG TTTCCACCAC
201 TCTGGACGGC ATTGCCyTGC TTGCCGAAct CAACCGTATC GAGGCTGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GkATTTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACACsCGAC TcACcTGGCC

```

```

351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATCCGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTGTTTTTA GGAAAACACG GAAAGGTTGC CGAATTGTCA
451 AAACGGyTGG GCAATCAAGG TATCCGTCTT TTACCGGACA GGTAATT

```

This corresponds to the amino acid sequence <SEQ ID 52; ORF 008>:

```

m008.pep
  1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
 51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFRERSF RNAPRTLXLD
101 IIDFDGISSD DTRLTLPHPR AHERSFVIRP LAEILPDFVL GKHGKVAELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 53>:

```

a008.seq
  1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
 51 CCCTGCCCAA CAGGTACGCG CCGCATTGGA CACGCTGTCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATT TCGTCAATGCC GTCTGCACCG TTTCCACCAC
201 CTTGGACGGC ATTGCCCTGC TTGCCGAAC CAACCGTATC GAAGCCGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GGATTGTGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACCCCGAC TCACCCTGCC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATACGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTTTG GGAAAACACG GAAAGGTTGC CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGATA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 54; ORF 008.a>:

```

a008.pep
  1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
 51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFRERSF RNAPRTLDLD
101 IIDFDGISSD DPRLTLPHPR AHERSFVIRP LAEILPDFIL GKHGKVAELS
151 KRLGNQGIRL LPDK*

```

m008/a008 97.6% identity over a 164 aa overlap

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYNQPDFVNA					
a008	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYNQPDFVNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m008.pep	VCTVSTTLDGIALLAELNRIEADFRERSFRNAPRTLXLDDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLDGIALLAELNRIEADFRERSFRNAPRTLDLDIIDFDGISSDDPRLTLPHPR					
	70	80	90	100	110	120
	130	140	150	160		
m008.pep	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
a008	AHERSFVIRPLAEILPDFILGKHGKVAELSKRLGNQGIRLLPDKX					
	130	140	150	160		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 008 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF008.ng) from *N. gonorrhoeae*:

m008/g008

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYNQPDFVNA					
g008	MNNRHFAVIALGSNLDNPAQQIRGALDALSSHPDIRLEQVSSLYMTAPVGYNQPDFINA					

	10	20	30	40	50	60
m008.pep	70	80	90	100	110	120
	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDDIIDFDGISSDDTRLTLPHPR					
g008	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDDIIDFDGISSDDPRLTLPHPR					
	70	80	90	100	110	120
m008.pep	130	140	150	160		
	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
g008	AHERSFVIRPLAEILPDFILGKYGVVVELSKRLGNQGIRLLPDRX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 55>:

g009.seq

```

1  ATGCCCCGCG CTGCCGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51  CGAACAAAAT ACCCATCGCC GCGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAA TCAGCACACG CAGGCGCGAA ACCAGTCCGT AATGGCGGTA
151 CAGCTGCCGC TCGTCGCCTT TTCGGATAAA GTGGTTGTcg cGTTCCAAGC
201 TGTGTGTCAG GCGGAAATAC AGGTTTTTCGC TGATGGCGGC AAAACGTGGC
251 AaaaGCCATA A

```

This corresponds to the amino acid sequence <SEQ ID 56; ORF 009.ng>:

g009.pep

```

1  MPRAAVAFAER HHHKSKEQN THRRADAEIA EGFAVGNQHT QARNQSVMAV
51  QLPLVAFSDK VVVAFAQVVQ AEIQVFADGG KTWQKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 57>:

m009.seq

```

1  ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51  CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAA TCAGCACACG CAGGCGCGCA AGCAGTCCGT AATGGCGGTA
151 CAGCTGCCGC CGGTCGCCTT TTCGGATAAA GTGGTTGTTCG CGTTCCAAGC
201 TGTGTGTCAG GCGGAAATAC AGGTTTTTCGC TGATGGCGGC AAAACGTGGC
251 AAAAGCCATA A

```

This corresponds to the amino acid sequence <SEQ ID 58; ORF 009>:

m009.pep

```

1  MPRAAVAFAER HHHKSKEQN THRRADAEIA EGFAVGNQHT QARKQSVMAV
51  QLPPVAFSDK VVVAFAQVVQ AEIQVFADGG KTWQKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 009 shows 97.7% identity over a 86 aa overlap with a predicted ORF (ORF 009.ng) from *N. gonorrhoeae*:

m009/g009

	10	20	30	40	50	60
m009.pep	MPRAAVAFAERHHHKSKEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
g009	MPRAAVAFAERHHHKSKEQNTHRRADAEIAEGFAVGNQHTQARNQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
m009.pep	70	80				
	VVVAFAQVVQAEIQVFADGGKTWQKPX					
g009	VVVAFAQVVQAEIQVFADGGKTWQKPX					
	70	80				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 59>:

```
a009.seq
1  ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51  CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGAAAA TCAGCACACG CAGGCGCGCA AGCAGTCCGT AATGGCGGTC
151 CAGCTGCCGC TCGTCGCCTT TTCGGATAAA GTGGTTGTCTG CGTTCCAAGC
201 TGTTCCTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AAAAGCCATA A
```

This corresponds to the amino acid sequence <SEQ ID 60; ORF 009.a>:

```
a009.pep
1  MPRAAVAFAER HHHKSKEQN THRRADAEIA EGFVGNQHT QARKQSVMAV
51  QLPLVAFSDK VVVAFAQVLQ AEIQVFADGG KTWQKP*
```

m009/a009 97.7% identity over a 86 aa overlap

	10	20	30	40	50	60
m009.pep	MPRAAVAFAERHHHKSKEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
a009	MPRAAVAFAERHHHKSKEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
	70	80				
m009.pep	VVVAFAQVQAEIQVFADGGKTWQKPX					
	:					
a009	VVVAFAQVLQAEIQVFADGGKTWQKPX					
	70	80				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 61>:

```
g010.seq
1  ATGGGTTTTTCTGTTTCGCAA GTTTGATGCC GTGATTGTCTG GCGGTGGCGG
51  TGCAGGTTTA CGTGCAGCCC TCCAATTATC CAAATCCGGT TTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTT CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCTCTCT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGCTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGTCTG GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAAAA TTTATCAGCG
351 TCCTTTCGGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTCT TATTTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT GACGGTTTGG GCATTTGCGC CCGTGCGGGC ATTCCGTTGG
701 AAGATATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGCG GGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGATATTC TGTTGAacgc
801 cgacggcgaa cgcTTTATGG AAcgctatgc GCcgACCGta aAgaCTTGG
851 CTTCTCGCga cgtGGTTTCA CgcgcGatg CGatggaAAt ctatgaaggt
901 cgcggtctgTG GtaaAAAcAa agaCCacgtC TTAAGTAAAA TCGACcAtAt
951 cggTGCAGAA AAAATTATGG AAAAAGTACC GGGCATCCGC GAGATTTCaA
1001 TTCagtttgc cGGTATCGAT CCGATTAAAG ACCCGATTcc ggttgTGCCG
1051 ACTACCACT ATATGATGGG CCGCATTCcg aCCAATTATC ACGGTGAAGT
1101 TGTGTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGTTTGGGT
1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga
```

This corresponds to the amino acid sequence <SEQ ID 62; ORF 010.ng>:

g010.pep

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101 HMGMFPDRVE SGKIYQRPFG GHAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNVVRANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RGCGKNKDHV LLKIDHIGAE KIMEKLPGR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVPV QGDEYEVVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 63>:

```

m010.seq (PARTIAL)
1  ..nTCCAATTAT CCAAATCCGG TCTGAATTGT GCCGTTTTGT CTAAAGTGTT
51  CCCGACCCGT TCGCATACCG TAGCGGCGCA GGGCGGTATT TCCGCCTCTn
101 TGGGTAATGT GCAGGAAGAC CGTTGGGACT GGCACATGTA CGATACCGTG
151 AAAGGTTCCG ACTGTTGGG CGACCAAGAT GCGATTGAGT TTATGTGCCG
201 CGCCGCGCCT GAAGCCGTAA TTGAGTTGGA ACACATGGGT ATGCCTTTTG
251 ACCGTGTGGA AAGCGGTAAA ATTTATCAGC GTCCTTTTCG CGGCCATACT
301 GCCGAACACG GTAAACGCGC GGTAGAACGC GyCTGTGCGG TTGCCGACCG
351 TACAGGTCAT GCGATGCTGC ATACTTTGTA CCAACAAAAC GTCCGTGCCA
401 ATACGCAATT CTTTGTGGAA TGACGGCAC AAGATTTGAT TCGTGATGAA
451 AACGGCGATG TCGTCGGCGT AACCGCCATG GAAATGGAAA CCGGCGAAgT
501 TTATATTTTC CACGCTAAAG CTGTGATGTT TGCTACCGGC GCGGCGGGTC
551 GTATTTATGC GTCTTCTACC AATGCCTATA TGAATACCGG CGATGGTTTG
601 GGTATTTGTG CGCGTG CAGG TATCCCGTTG GAAGACATGG AATTCTGGCA
651 ATTCCAGCCG ACCGCGGTGG CGGGTGC GGG CGTGTGATT ACCGAA....

```

This corresponds to the amino acid sequence <SEQ ID 64; ORF 010>:

```

m010.pep (PARTIAL)
1  ..XQLSKSGLNC AVLSKVFPTR SHTVAAQGGI SASXGNVQED RWDWHMYDTV
51  KGS DWLG DQD AIEFM CRAAP EAVIELEHMG MPFDRVESGK IYQRPFGGHT
101 AEHGKRAVER XCAVADRTGH AMLHTLYQQN VRANTQFFVE WTAQDLIRDE
151 NGDVVGVTAM EMETGEVYIF HAKAVMFATG GGGRIYASST NAYMNTGDGL
201 GICARAGIPL EDMEFWQFQP TGVAGAGVLI TE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 65>:

```

a010.seq
1  ATGGGCTTTC CTGTTGCGCAA GTTTGATGCC GTGATTGTGCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GCGGTATTTT CCGCTCTCTT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCCG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGCGGCGAG GCGGATTC TGTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTA CTGAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAA ACTGCC GGGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCACT ATATGATGGG CGGTATTCG ACCAACTACC ATGGCGAAGT
1101 TGTCGTTCC TCAAGGCGACG AATACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACGAACTCCC TGCTGGACTT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAAACCT TTGCCTGCTA

```

```

1301 ATGCCGGCGA ACTGACCCGC CAACGTATCG AGCGTTTGGG CAATCAAAC
1351 GATGGTGAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TGCGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATGCCAATA CCTTGTCCTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 66; ORF 010.a>:

```

a010.pep
  1  MGFPVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKVF PTRSHTVAAQ
 51  GGISASLGNV QEDRWDWHMY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101  HMGMPFDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151  QQNV RANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201  ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251  VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301  RCGGKNKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPPIVVP
351  TTHYMMGGIP TNYHGEVVVP QGDEYEVVVK GLYAAGECAC ASVHGANRLG
401  TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT
451  DGENVDALRR ELQRSVQLHA GVFR TDEILS KGVREVM AIA ERVKRTEIKD
501  KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERDDE
551  NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY*

```

m010/a010 98.7% identity over a 231 aa overlap

```

                                10      20      30
m010.pep                                XQLSKSGLNCVLSKVF PTRSHTVAAQGGISASXGNV
                                |||||
a010      MGFPVRKFDAVIVGGGGAGLRAXLQLSKSG LNCVLSKVF PTRSHTVAAQGGISASLGNV
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m010.pep      QEDRWDWHMYDTVKGSDWLG DQDAIEFMCR AAPEAVIELEHMGMPFDRVESGKIYQRPFG
                                |||||
a010      QEDRWDWHMYDTVKGSDWLG DQDAIEFMCR AAPEAVIELEHMGMPFDRVESGKIYQRPFG
                                70      80      90      100     110     120

                                100     110     120     130     140     150
m010.pep      GHTAEHGKRAVERXCAVADR TGHAMLHTLYQQNV RANTQFFVEWTAQDLIRDENG DVVG V
                                |||||
a010      GHTAEHGKRAVERACAVADR TGHAMLHTLYQQNV RANTQFFVEWTAQDLIRDENG DVVG V
                                130     140     150     160     170     180

                                160     170     180     190     200     210
m010.pep      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGI PLEDMEFWQ
                                |||||
a010      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGI PLEDMEFWQ
                                190     200     210     220     230     240

                                220     230
m010.pep      FQPTGVAGAGVLITE
                                |:|||||
a010      FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG
                                250     260     270     280     290     300

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 010 shows 98.7% identity over a 231 aa overlap with a predicted ORF (ORF 010.ng) from *N. gonorrhoeae*:

m010.pep/g010.pep

m010.pep				10	20	30	
				XQLSKSGLNCAVL	SKVFPTR	SHTVAAQGGISASXGNV	
g010	MGFPVRKFDAVIVGGGGAGLRAAL	QLSKSG	LNC	AVL	SKVFPTR	SHTVAAQGGISASLGNV	
	10	20	30	40	50	60	
m010.pep	40	50	60	70	80	90	
	QEDRWDWHMYDTVKGSDWLGDQDAIEFMCRAAPEAVIELEHMGMFPDRVESGKIYQRPFG						
g010	QEDRWDWHMYDTVKGSDWLGDQDAIEFMCRAAPEAVIELEHMGMFPDRVESGKIYQRPFG						
	70	80	90	100	110	120	
m010.pep	100	110	120	130	140	150	
	GHTAEHGKRAVERXCAVADRTGHAMLHTLYQQNVRANTQFFVEWTAQDLIRDENGDDVVG						
g010	GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRANTQFFVEWTAQDLIRDENGDDVVG						
	130	140	150	160	170	180	
m010.pep	160	170	180	190	200	210	
	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ						
g010	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ						
	190	200	210	220	230	240	
m010.pep	220	230					
	FQPTGVAGAGVLITE						
	:						
g010	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVSRAAMEIYEG						
	250	260	270	280	290	300	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 67>:

g010-1.seq..

```

1  ATGGGTTTTTC CTGTTTCGCAA GTTTGATGCC GTGATTGTCG GCGGTGGCGG
51  TGCAGGTTTA  CGTGCGAGCCC TCCAATTATC CAAATCCGGT TTGAATTGTG
101 CCGTTTTGTC  TAAAGTGTTC CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GCGCGTATTT  CCGCCTCTCT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC  GATACCGTGA AAGGTTCCGA CTGGCTGGGC GACCAAGATG
251 CGATTGAGTT  TATGTGTGCG GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA  TGCCTTTTGA CCGCGTTGAA AGCGGCAAAA TTTATCAGCG
351 TCCTTTTCGGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT  TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG  TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT  CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC  GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG  GCGGCGGTGCT TATTTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT  GACGGTTTGG GCATTGCGCG CCGTGCGGGC ATTCCGTTGG
701 AAGATATGGA  ATTCTGGCAA TTCCACCGGA CCGGCGTGCG GGGTGCGGGC
751 GTGTTGATTA  CCGAAGGCGT ACGCGGCGAG GCGGTTATTC TGTTGAACGC
801 CGACGGCGAA  CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA  CGTGGTTTCA CGCGCGATGG CGATGGAAAT CTATGAAGGT
901 CGCGGCTGTG  GTAAAAACAA AGACCACGTC TTAAGTAAAA TCGACCATAT
951 CCGGTGCAGAA AAAATTATGG AAAAAGTGGC GGGCATCCGC GAGATTTCCA
1001 TTCAGTTTGC  CGGTATCGAT CCGATTAAAG ACCCGATTCC GGTGTGTCGG
1051 ACTACCCACT  ATATGATGGG CGGCATTCCG ACCAATTATC ACGGTGAAGT
1101 TGTTGTTCCG  CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA  GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGTTTGGGT

```

1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga

This corresponds to the amino acid sequence <SEQ ID 68; ORF 010-1.ng>:

g010-1.pep

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKV F PTRSHTVAAQ
51  GGISASLGNV QEDRWDDHMY DTVKGSDDLW DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNVRRANTQF FVEWTAQDLI RDENGDDVGV TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPT V KDLSRDVVS RAMAMEIYEG
301 RCGCKNKDHY LLKIDHIGAE KIMEKLPGR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVPK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

g010-1 / P10444

sp|P10444|DHSA_ECOLI SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT
 gnl|PID|d1015210 (D90711) Succinate dehydrogenase, flavoprotein [Escherichia coli] gi|1786942
 (AE000175) succinate dehydrogenase flavoprotein subunit [Escherichia coli] Length = 588
 Score = 1073 (495.6 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169
 Identities = 191/303 (63%), Positives = 238/303 (78%)

```

Query: 1 MGFPVRKFDAVIVXXXXXXXXXXXXXSKSLNCVLSKVFPTRSHTVAAQGGISASLGNV 60
      M PVR+FDAV++ S+SG CA+LSKVFPTRSHTV+AQGGI+ +LGN
Sbjct: 1 MKLPVREFDAVVIGAGGAGMRAALQISQSGQTCALLSKVFPTRSHTVSAQGGITVALGNT 60

Query: 61 QEDRWDDHMYDTVKGSDDLWQDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG 120
      ED W+WHMYDTVKGSDD++GDQDAIE+MC+ PEA++ELEHMG+PF R++ G+IYQRPFG
Sbjct: 61 HEDNWEWHMYDTVKGSDDYIGDQDAIEYMCCKTGPEAILEHMGMLPFSLDDGRIYQRPFG 120

Query: 121 GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRRANTQFFVEWTAQDLIRDENGDDVGV 180
      G + G R A ADRTGHA+LHTLYQQN++ +T F EW A DL++++G VVG
Sbjct: 121 GQSKNFGGEQAARTAAADRTGHALLHTLYQQNLKNTTIFSEWYALDLVKNQDGAUVGC 180

Query: 181 TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ 240
      TA+ +ETGEV F A+A + ATGG GRIY S+TNA++NTGDG+G+ RAG+P++DME WQ
Sbjct: 181 TALCIETGEVVYFKARATVLTATGGAGRIYQSTTNAHINTGDGVMAIRAGVPVQDMEMWQ 240

Query: 241 FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVS RAMAMEIYEG 300
      FHPTG+AGAGVL+TEG RGEGL LN GERFMERYAP KDLA RDVV+R++ +EI EG
Sbjct: 241 FHPTGIAGAGVLVTEGCRGEGGYLLNKHGERFMERYAPNAKDLAGRDVVARSIMIEIREG 300

Query: 301 RGC 303
      RGC
Sbjct: 301 RGC 303

```

Score = 249 (115.0 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169
 Identities = 53/102 (51%), Positives = 62/102 (60%)

```

Query: 309 HVLLKIDHIGAEKIMEKLPGIREISIQFAGXXXXXXXXXXXXTTHYMMGGIPTNYHGEVV 368
      H LK+DH+G E + +LPGI E+S FA T HYMMGGIPT G+ +
Sbjct: 310 HAKLKLDHLGKEVLESRLPGILELSRTFAHVPVKEPIPIPTCHYMMGGIPTKVTGQAL 369

Query: 369 VPQGEYEVVPKGLYAAGECACASVHGANRLGTNSLLDLVVF 410
      +V V GL+A GE AC SVHGANRLG NSLLDLVVF
Sbjct: 370 TVNEKGEDVVVPGFLFAVGEIACVSVHGANRLGNSLLDLVVF 411

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 69>:

m010-1.seq..

```

1  ATGGGTTTTTC CTGTTCGCAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCAGCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTC CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GCGGTATTT CCGCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACCGC
401 CCTGTGCGGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC

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451 CAACAAAACG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGTTC TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGCTATTC TGTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGGCGATGG CGATGGAAAT CTACGAAGGT
901 CCGGCTGCG GTAAAAACAA AGACCATGTC TTAAGTAAAA TCGACCATAT
951 CCGGCGAGAA AAAATTATGG AAAAAGTGGC GGGCATCCGC GAGATTTCCT
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCGG
1051 ACTACCCACT ATATGATGGG CCGCATTCCG ACCAATTACC ACGGCGAAGT
1101 TGTCGTTCCG CAAGGTGAAG ATTACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CCGCAGGTGA GTGCGCTTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACCAACTCCC TGTGGAAGT GGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTTAA TTCAATCAAG AGCAAGCGA CTGGAAACCT TTGCCTGCTA
1301 ATGCAGGTGA GTTGACCCGC CAACGTATCG AGCGTTTGGG CAACCAAAAC
1351 GATGGTGAAA ACGTTGATGC ATTGCGTCGC GAACTGCAAC GCTCTGTACA
1401 ACTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGAATAC CGGCGTATC GAGGCTTGG AATTGGATAA
1551 CCGATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TCGCGACGCT TCAGACGACC ATCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATATCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGATGA

```

This corresponds to the amino acid sequence <SEQ ID 70; ORF 010-1>:

m010-1.pep..

```

1  MGFPVRKFDA VIVGGGAGL RAALQLSKSG LNCAVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGS DWLG DQDAIEFMCR APEAVIELE
101 HMGMPPFDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNVVRANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RCGGKNKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPVPVP
351 TTHYMMGGIP TNYHGEVVPV QGEDYEVVPK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVFRTEILS KGVREVMAIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHFERDDE
551 NWMKHTLYHS DINTLSYKPV HTKPLSVEYI KPAKRVY*

```

m010-1 / g010-1 99.5% identity in 410 aa overlap

```

          10      20      30      40      50      60
m010-1.pep  MGFPVRKFDAVIVGGGAGLRAALQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV
          |||||
g010-1      MGFPVRKFDAVIVGGGAGLRAALQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV
          10      20      30      40      50      60

          70      80      90     100     110     120
m010-1.pep  QEDRWDWHMYDTVKGSDWLG DQDAIEFMCR APEAVIELEHMGMPFDRVESGKIYQRPFG
          |||||
g010-1      QEDRWDWHMYDTVKGSDWLG DQDAIEFMCR APEAVIELEHMGMPFDRVESGKIYQRPFG
          70      80      90     100     110     120

          130     140     150     160     170     180
m010-1.pep  GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVVRANTQFFVEWTAQDLIRDENG DVVG
          |||||
g010-1      GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVVRANTQFFVEWTAQDLIRDENG DVVG
          130     140     150     160     170     180

          190     200     210     220     230     240
m010-1.pep  TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
          |||||
g010-1      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ

```

190

	190	200	210	220	230	240
	250	260	270	280	290	300
m010-1.pep	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPT VKDLASRDVVS RAMAMEIYEG					
g010-1	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPT VKDLASRDVVS RAMAMEIYEG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m010-1.pep	RGCGKKNKDHVLLKIDHIGA EKIM EKLPGIREISIQFAGIDPIKDPIPVVPTTHYMMGGIP					
g010-1	RGCGKKNKDHVLLKIDHIGA EKIM EKLPGIREISIQFAGIDPIKDPIPVVPTTHYMMGGIP					
	310	320	330	340	350	360
	370	380	390	400	410	420
m010-1.pep	TNYHGEVVVPQGEDYEVPVKGLYAAGECACASVHG ANRLGTNSLLDLVVF GKAA GDSMK					
g010-1	TNYHGEVVVPQGEDYEVPVKGLYAAGECACASVHG ANRLGTNSLLDLVVF RPTPRX					
	370	380	390	400	410	
	430	440	450	460	470	480
m010-1.pep	FIKEQSDWKPLPANAGELTRQRIERLDNQTDGENVDALRRELQRSVQLHAGV FRTDEILS					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 71>:

a010-1.seq..

```

1  ATGGGCTTTC CTGTTGCGAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GCGGTATTTT CCGCTCTCTT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCCG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGTATTTC TGTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTACTGAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTGCC GGGCATCCGC GAGATTTCCT
1001 TTCAGTTCGC CCGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CCGTATTCCG ACCAACTACC ATGGCGAAGT
1101 TGTCGTTTCT CAAGGCGACG AATACGAAAG GCCTGTAAAA GGTCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTTCGTGAC ACGGTGCGAA CCGCTTGGGT
1201 ACGAACTCCC TGCTGGAATT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAAACCT TTGCCTGCTA
1301 ATGCCGCGCA ACTGACCCGC CAACGTATCG AGCGTTTGGG CAATCAAAGT
1351 GATGGTGAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GGCGTGTTCG TACTGATGTA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GGCGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TGCGCACGCT TCAGACGACC ATCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCG GATGCCAATA CCTGTCTCTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 72; ORF 010-1.a>:

a010-1.pep..

```

1  MGVFVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDDHMY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIQRPFG GHAEHGKRA VERACAVADR TGHAMLHTLY

```


151 QQNVRANTQF FVEWTAQDLI RDENGDVVGV TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RCGGKNKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVPV QGDEYEVVPK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVFRTEILS KGVREVMAIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPPERDE
551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY*

m010-1 / a010-1 99.3% identity in 587 aa overlap

	10	20	30	40	50	60
a010-1.pep	MGFPVRKFDIVVGGGGAGLRAXLQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV					
a010-1	MGFPVRKFDIVVGGGGAGLRALQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a010-1.pep	QEDRDWHMYDTVKGSDWLGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG					
m010-1	QEDRDWHMYDTVKGSDWLGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG					
	70	80	90	100	110	120
	130	140	150	160	170	180
a010-1.pep	GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRANTQFFVEWTAQDLIRDENGDVVGV					
m010-1	GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRANTQFFVEWTAQDLIRDENGDVVGV					
	130	140	150	160	170	180
	190	200	210	220	230	240
a010-1.pep	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ					
m010-1	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
a010-1.pep	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG					
m010-1	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG					
	250	260	270	280	290	300
	310	320	330	340	350	360
a010-1.pep	RCGGKNKDHVLLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPIPVVPTTHYMMGGIP					
m010-1	RCGGKNKDHVLLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPIPVVPTTHYMMGGIP					
	310	320	330	340	350	360
	370	380	390	400	410	420
a010-1.pep	TNYHGEVVPVQGEDYEVVPKGLYAAGECACASVHGANRLGTNSLLDLVVF GKAAGDSMIK					
m010-1	TNYHGEVVPVQGEDYEVVPKGLYAAGECACASVHGANRLGTNSLLDLVVF GKAAGDSMIK					
	370	380	390	400	410	420
	430	440	450	460	470	480
a010-1.pep	FIKEQSDWKPLPANAGELTRQRIERLDNQT DGENVDALRR ELQRSVQLHAGVFRTEILS					
m010-1	FIKEQSDWKPLPANAGELTRQRIERLDNQT DGENVDALRR ELQRSVQLHAGVFRTEILS					
	430	440	450	460	470	480
	490	500	510	520	530	540
a010-1.pep	KGVREVMAIA ERVKRTEIKDKSKVWNTARIEALELDNLIE VAKATLVSAE ARKESRGAHA					
m010-1	KGVREVMAIA ERVKRTEIKDKSKVWNTARIEALELDNLIE VAKATLVSAE ARKESRGAHA					
	490	500	510	520	530	540
	550	560	570	580		
a010-1.pep	SDDHPPERDENW MKHTLYHSDANTLSYKPVHTKPLSVEYIKPAKRVYX					

m010-1 SDDHPERDDENWMKHTLYHSDINTLSYKPVHTKPLSVEYIKPAKRVYX
550 560 570 580

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 73>:

g011.seq
1 ATGAAGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTTG CTTTTCAGAC
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA
101 GCCTGAAAAC CCGCCTTACC GAAGATATGA AAACCGCGAT GCGCGCCAAA
151 GATCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAATGCCG CCGTCAAACA
201 GTTTGAAGTA GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA
251 TCCTGACCAA AATGGTCAAA CAGCGCAAAG ACGGCGCGAA AATCTACACT
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGACGT
351 GCTGCACCGC TACCTGCCGC AAATGCTCTC CGCCGGCGAA ATCCGCACCG
401 CCGTCGAAGC AGCCGTTGCC GAAACCGGCG CGGCAGGTAT GCGGATATG
451 GGCAAAGTGA TGGTCGTATT GAAAaccGC CTCGCCGCA AAGccgATAT
501 GGGCGAAGTC AACAAATCT TGAAAaccGt aCTGACCGCC tga

This corresponds to the amino acid sequence <SEQ ID 74; ORF 011.ng>:

g011.pep
1 MKTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKTRLT EDMKTAMRAK
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDGAKIYT
101 EAGRQDLADK ENAEIDVLHR YLPQMLSAGE IRTAVEAAVA ETGAAGMADM
151 GKVMVVLKTR LAGKADMGEV NKILKTVLTA *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 75>:

m011.seq (partial)
1 ATGAGGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTTG CTTTTCAGAC
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA
101 GCCTGAAAAT CCGCCTTACC GAAGACATGA AAACCGCGAT GCGCGCCAAA
151 GACCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAACGCCG CCGTCAAACA
201 GTTTGAAGTG GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA
251 TCCTGACCAA AATGGTCAAA CAGCGAAAAG ACAGCGCGAA AATCTACACT
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGAGGT
351 ACTGCACCGC TACCTTCCCC AAATGCTTTC CGCCGGCGAA ATCCGTACCG
401 AGGTCGAAGC TGCCGTTGCC GAAACCGGCG CGGCAGGTAT GCGGATATG
451 GGTAAAGTCA TGGGGCTGCT GAAAACCCGC CTCGCAGGTA AAGCCGA...

This corresponds to the amino acid sequence <SEQ ID 76; ORF 011>:

m011.pep (partial)
1 MRTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKIRLT EDMKTAMRAK
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDSAKIYT
101 EAGRQDLADK ENAEIEVLHR YLPQMLSAGE IRTEVEAAVA ETGAAGMADM
151 GKVMGLLKTR LAGKA....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 011 shows 95.8% identity over a 165 aa overlap with a predicted ORF (ORF 011.ng) from *N. gonorrhoeae*:

m011/g011

	10	20	30	40	50	60
m011.pep	MRTHRKTCSAV	CFQFQTASKPA	VSIRHPSEDI	MSLKIRLTED	DMKTAMRAKD	QVSLGTIRL
	:	:	:	:	:	:
g011	MKTHRKTCSAV	CFQFQTASKPA	VSIRHPSEDI	MSLKTRLTED	DMKTAMRAKD	QVSLGTIRL
	10	20	30	40	50	60

	70	80	90	100	110	120
m011.pep	INAAVKQFEVD	ERTEADDAKIT	AILTKMVKQR	KDSAKIYTEA	GRQDLADKEN	AEIEVLHR
	:	:	:	:	:	:
g011	INAAVKQFEVD	ERTEADDAKIT	AILTKMVKQR	KDGAKIYTEA	GRQDLADKEN	AEIDVLHR

193

	70	80	90	100	110	120
m011.pep	130	140	150	160		
	YLPQMLSAGEIRTEVEAAVAETGAAGMADMKGVMGLLKTRLAGKA					
g011	130	140	150	160	170	180
	YLPQMLSAGEIRTAVEAAVAETGAAGMADMKGVMVVLKTRLAGKADMGEVVKILKTVLTA					
g011	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 77>:

g012.seq

```

1  ATGCTCGCCC GTCGCTATTT TTTCATATC CAACCCGGGG CGGTTTTTCAC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGCCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTGCCCC GCGTCATCA CATCCACATC AATATCATGT TTTTCAACa
201 gGcggTGGAT ATTcGgcact tccgCcacca caccaccga accgatgacc
251 gcaaacggaG CGGAAACAAT TTTATCCGcC acacacgcca tcatatagcc
301 gcCGCTTGCC GCGACCTTAT CGAcggcgac ggTCAGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTCCAATCT GAGCAGAACC TCATCTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATTT TTGCGTTTCG
551 GCAGATTTCT CCCCGCCCTC CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CTTTTTTTTC CTGATGTTTT GTCTCTTCTC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 78; ORF 012.ng>:

g012.pep

```

1  MLARRYFFNI QPGAVFTDKL LEQLMRFLQF LPEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRFRHHHTHR TDDRKRSGNN FIRHTRHHIA
101 AACRDLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS EQNLIFRLGN
151 QKHRRLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRLPAL LQTLFLCFGF
201 RLFLFLFFFF LMFCLFLA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 79>:

m012.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCCGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTGCCCC GCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GGCGGTGGAT ATTCGGTACT TCCGCCACCA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAGCAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCCGCTCGCn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
351 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
401 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
451 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
501 nnnnnnnnnn nnnnnnnnnC AACACAAAAA GGCGTGATTT nTGCGTTTCG
551 GCAGATTTCT CCCCACCCTC CTTCAAACGT TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTGT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 80; ORF 012>:

m012.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRYFRHHHTR TDNRKRSGSN FIRHTRHHIT
101 AARXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
151 XXXXXXXXXXX XXXXXXXXXXX XXXQHKKA*F XRFGRFLPTL LQTFFLCFGF
201 RLFLFLFLFF LMCLFLPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 81>:

```
a012.seq
  1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
 51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTGCGAAT
101  TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151  AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTTCACAA
201  GCGGGTGGAT ATTCGGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251  GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301  ACCGCTCGCC GCCACCTTAT CGACGGCGAC GGTGAGCGGA ATATTGCGTT
351  CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401  CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGCAAT
451  CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501  ACAAATCGCC GTCAAAATCC AACACAAAAA GCGGGGATTT TTGCGTTTCG
551  GAAGATTTCT CCCCACCCTC CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601  CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTT GCCTCTTCCC
651  CGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 82; ORF 012.a>:

```
a012.pep
  1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
 51  KFARRHHIHI NIMFFQQA VD IRYFRYNTHR TDNRKRSGNN FIRHTRHHIT
101  TARRHLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151  QKHRRLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRLPTL LQTLFLCFGF
201  RLFLFLFLFF LMFCLFPA*
```

m012/a012 64.2% identity over a 218 aa overlap

	10	20	30	40	50	60
m012.pep	MLARCHFLNIQLRAVLADKLLLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
a012	MLARCHFLNIQLRAVLADKLLLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m012.pep	NIMFFQQA VD IRYFRHHTHRTDNRKRSGSNFIRHTRHHITAARXXXXXXXXXXXXXXXXXXXX					
a012	NIMFFQQA VD IRYFRYNTHRTDNRKRSGNNFIRHTRHHITTARRHLIDGDGQRNIAFAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m012.pep	XXXQHKKAXF					
a012	PKLRSRQTVT VNHAARTFQSKQNLIFRLGNQKHRRLMTQGFGYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
	190	200	210	219		
m012.pep	XRFGRLPTLLQTFFLCFGRFLFLFLFLFLMLCLFPAX					
a012	LRFGRLPTLLQTLFLCFGRFLFLFLFLFLMLCLFPAX					
	190	200	210			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 012 shows 58.7% identity over a 218 aa overlap with a predicted ORF (ORF 012.ng) from *N. gonorrhoeae*:

m012/g012

	10	20	30	40	50	60
m012.pep	MLARCHFLNIQLRAVLADKLLLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					
g012	MLARRYFFNIQPGAVFTDKLLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					

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	10	20	30	40	50	60
m012.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYFRHHTHRTDNRKRSGSNFIRHTRHHITAARXXXXXXXXXXXXXXXXXXXX					
	: : : : : :					
g012	70	80	90	100	110	120
	NIMFFQQAVDIRHFRHHTHRTDDRKRSGNNFIRHTRHHIAAACRDLIDGDGQRNIAFAQT					
m012.pep	130	140	150	160	170	180
	XXQHKKAXF					
	:	:	:	:	:	
g012	130	140	150	160	170	180
	PKLRSRQTVTVNHAARTFQSEQNLIFRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					
m012.pep	190	200	210	219		
	XREGRFLPTLLQTFFLCFGRFLFLFLFFLMLCLFPAX					
	: : : : :					
g012	190	200	210			
	LREGRFLPALQLFLCFGRFLFLFLFFFLMFLCLFLAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 83>:

m012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGGGTGGAT ATTCGGTACT TCCGCCACCA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAGCAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCCGCTCGCC GCCACCTTAT CGACGGCGAC GGTCAGCGGA ATATTGCGTT
351 CCGCAAACG CyTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT GAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATT TGTGCTTTTCG
551 GCAGATTCTC CCCACCCCTC CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 84; ORF 012-1>:

m012-1.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRHHTH RTDNRKRSGS N FIRHTRHHIT
101 AARRHLIDGD QRNIAFAQT XKLRSRQTV T VNHAARTFQ S EQNLIFRLGN
151 QKHRRNLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRFLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFLCLFPA*

```

m012-1/g012 91.7% identity in 218 aa overlap

	10	20	30	40	50	60
m012-1.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	: : : : :					
g012	10	20	30	40	50	60
	MLARRYFFNIQPGAVFTDKLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					
m012-1.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYFRHHTHRTDNRKRSGSNFIRHTRHHITAARRHLIDGDGQRNIAFAQT					
	: : : : :					
g012	70	80	90	100	110	120
	NIMFFQQAVDIRHFRHHTHRTDDRKRSGNNFIRHTRHHIAAACRDLIDGDGQRNIAFAQT					
m012-1.pep	130	140	150	160	170	180
	XKLRSRQTVTVNHAARTFQSEQNLIFRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	: : : : :					
g012	130	140	150	160	170	180
	PKLRSRQTVTVNHAARTFQSEQNLIFRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					

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	130	140	150	160	170	180
	190	200	210	219		
m012-1.pep	LRFGRFLPTLLQTLFLCFGRFLFLFLFFLMFCLFPAX					
	: : :					
g012	LRFGRFLPALQTLFLCFGRFLFLFLFFFLMFCLFLAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 85>:

a012-1.seq

```

1   ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGGGTGGAT ATTCGGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGGCGAC GGTGAGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCCTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATT TGTGCTTTCG
551 GAAGATTCTC CCCACCCCTC CTCAAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCTTTTTC TTTTCTTTT CCTCTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 86; ORF 012-1.a>:

a012-1.pep

```

1   MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRYNTHR TDNRKRSGNN FIRHTRHHIT
101 TARRHLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151 QKHRRNLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRFLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFCLFPA*

```

a012-1/m012-1 97.2% identity in 218 aa overlap

	10	20	30	40	50	60
a012-1.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
m012-1	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
a012-1.pep	NIMFFQQAVDIRYFRYNTHRTDNRKRSGNNFIRHTRHHITTARRHLIDGDGQRNIAFAQT					
	: : :					
m012-1	NIMFFQQAVDIRYFRHHTHRTDNRKRSGSNFIRHTRHHITAARRHLIDGDGQRNIAFAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a012-1.pep	PKLRSRQTVTVNHAARTFQSKQNLIFRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					
m012-1	XKLRSRQTVTVNHAARTFQSEQNLIFRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
	190	200	210	219		
a012-1.pep	LRFGRFLPTLLQTLFLCFGRFLFLFLFFLMFCLFPAX					
m012-1	LRFGRFLPTLLQTLFLCFGRFLFLFLFFLMFCLFPAX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 87>:

g013.seq

```

1   aTgcctttga ccatgctgtg cagcaGGAcg tGCGGTTtgt tcataataca
51  gtCcgaccgG AAAagcggAG GAAaCGCAGT GCCGCGCCCT TCCCCTTTCT
101 TGCCGTGGCA GGCATGCag tTgATTTCGT AACTTTTTG CCCTTTtGtc

```

```

151 atgatGCTgt tgtcggCGGC AGAAGCgGCG GcgCAGAGGC AGCACAAGAT
201 GAAGGCGGTC GGCAGTCGGG TTGTGTtcat tGgcgTTTCC cctaattgtt
251 tgaaaccttg ttttttgatt Ttgcctttac ggggtgaaaa gtttttTtgg
301 cccaaatccg gaatttag

```

This corresponds to the amino acid sequence <SEQ ID 88; ORF 013.ng:

g013.pep

```

1 MPLTMLCSRT CGLFIIQSDR KSGGNAVPRP SPFLPWQAMQ LDSYTFCPFV
51 MMLLSAAEAA AQRQHMKAV GSRVVFIGVS PNVLKPCFLI LPLRGEKFFW
101 PKSGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 89>:

m013.seq

```

1 ATGCCTTTGA CCATGCTGTG CAGCAGCACC TCGGTTTTT TCATGATGAA
51 GTCGGAGCGG TAGAGCGGCG GAAACATGGT TCCGCGGCCT TCGCCCTTTT
101 TGCCGTGGCA GGCACGCAG TTGGATTCGT AACTTTTTTG CCCTTTTGTC
151 ATGATGCTGT TGTCGGCGGC AGAAGCGGCG GCGCAGAAGC AGCCCAAGAC
201 GAGGGCGGTC GGCAGTCGGG TTGTGTTTTC TGGTGTTCCT TTCATGTTTG
251 AAACCTTGTT GTTGATTTTG CGTAGCGGGT GAAAGATTTT TTTGCCGAAT
301 CAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 90; ORF 013>:

m013.pep

```

1 MPLTMLCSST CGFFMMKSER XSGGNMVRP SPFLPWQATQ LDSYTFCPFV
51 MMLLSAAEAA AQRQPKTRAV GSRVVFIGVS FMFETLLLLIL RSGXKIFLPN
101 Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 91>:

a013.seq

```

1 ATGCCTTTGA CCATGCTGTG CAGCAGCACC TCGGTTTTT TCATGATGAA
51 GTCGGAGCGG TAGAGCGGCG GAAACATGGT TCCGCGGCCT TCGCCCTTTT
101 TGCCGTGGCA GGCACGCAG TTGGATTCGT AACTTTTTTG CCCTTTTGTC
151 ATGATGCTGT TGTCGGCGGC AGAAGCGGCG GCGCAGAGGC AGCCCAAGAC
201 GAGGGCGGTC GGCAGTCGGG TTGTGTTTTC TGGTGTTCCT TTAATGTTTG
251 AAACCTTGTT GTTGATTTTG CGTAGCGGGT GAAAGATTTT CTTGCCGAAT
301 CGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 92; ORF 013.a>:

a013.pep

```

1 MPLTMLCSST CGFFMMKSER *SGGNMVRP SPFLPWQATQ LDSYTFCPFV
51 MMLLSAAEAA AQRQPKTRAV GSRVVFIGVS LMFETLLLLIL RSG*KIFLPN
101 R*

```

m013/a013 97.0% identity over a 101 aa overlap

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
a013	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
	10	20	30	40	50	60
	70	80	90	100		
m013.pep	AQRQPKTRAVGSRVVFIGVSFMFETLLLLILRSGXKIFLPNQX					
	: : : : :					
a013	AQRQPKTRAVGSRVVFIGVSLMFETLLLLILRSGXKIFLPNRX					
	70	80	90	100		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 013 shows 73.3% identity over a 101 aa overlap with a predicted ORF (ORF 013.ng) from *N. gonorrhoeae*:

198

m013/g013

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
	: :: :					
g013	MPLTMLCSRTCGLFIIQSDRKSGGNAVPRPSPFLPWQAMQLDSYTFCPFVMMLLSAAEAA					
	10	20	30	40	50	60
	70	80	90	100		
m013.pep	AQKQPKTRAVGSRVVFIVSF-MFETLLLILR-SGXKIFLPNQX					
	: : :: : : :					
g013	AQRQHKMKAVGSRVVFIVSPNVLKPFCFLILPLRGEKFFWPKSGIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 93>:

g015.seq

```

1  ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51  CATTTTGGTA TTCAACATCC GTTTTTCCT ACTTTGAAA AATCCAGAAA
101 AGCCCTTGGT CGGCTTTGG AAAGCACTGC CCCACCTCAA CGACACGATG
151 CTGCTGTTTA CGGGATTGTG GCTGATGAAG ATTACCCATT TCTCCCCGTT
201 CAACGCGCCT TGGCTCGGCA CAAAAATCCT GCTCCTGTTC GCCTACATCG
251 CACTGGGCAT GGTAATGATG CGCGCCCGTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTCGCTAT GTGTTGCATC GCCTGCATCG TTTACCTTGC
351 CAAAACCAAA GTCCTGCCAT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 94; ORF 015.ng>:

g015.pep

```

1  MQYLIVKYSH QIFVTITILV FNIRFFLLWK NPEKPLVGFW KALPHLNDTM
51  LLFTGLWLMK ITHFSPFNAP WLGTKILLLF AYIALGMVMM RARPRSTKFY
101 TVYLLAMCCI ACIVYLAKTK VLPF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 95>:

m015.seq (partial)

```

1  ..AAATCAGAA AAGCCTTGGC GGGCTTTTGG AAGGCACTGC CCCACCTTAA
51  CGACACCATG CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT
101 TCTCCCCGTT CAACGCGCCT TGGCTCGGTA CAAAAATCCT GCTTCTGCTC
151 GCCTATATCG CATTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTCGAC
201 CAAGTTCTAC ACCGTTTACC TGCTCGCCAT GTGTTGCGTC GCCTGCATCG
251 TTTACCTTGC CAAAACCAAA GTCCTGCCTT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 96; ORF 015>:

m015.pep (partial)

```

1  ..KIRKALAGFW KALPHLNDTM LLFTGLWLMK ITHFSPFNAP WLGTKILLLL
51  AYIALGMMM RARPRSTKFY TVYLLAMCCV ACIVYLAKTK VLPF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 97>:

a015.seq

```

1  ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51  CATTTTGGTA TTCAACATCC GTGTTTCNT ACTTTGAAA AATCCAGAAA
101 AGCCCTTGGC GGGCTTTTGG AAGGCACTGC CCCACCTTAA CGACACCATG
151 CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT TCTCCCCGTT
201 CAACGCGCCT TGGCTCGGTA CAAAAATCCT GCTTCTGCTC GCCTATATCG
251 CATTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTCGCCAT GTGTTGCCTC ACCTGCATCG TTTACCTTGC
351 CAAAACCAAA GTCCTGCCTT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 98; ORF 015.a>:

a015.pep

199

1 MQYLIVKYSH QIEVTITILV FNIRVFXLWK NPEKPLAGFW KALPHLNDTM
 51 LLFTGLWLMK ITHFSPFNAP WLGTKILLLL AYIALGMMM RARPRSTKFY
 101 TVYLLAMCCL TCIVYLAKTK VLPF*

m015/a015 96.7% identity over a 91 aa overlap

m015.pep				10	20	30
				KIRKALAGFWKALPHLNDTM	LLFTGLWLMKITH	
a015	LIVKYSHQIFVTITILVFNIRVFXLWKNPEKPLAGFWKALPHLNDTM	LLFTGLWLMKITH				
	10	20	30	40	50	60
m015.pep				40	50	60
	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTKFYTVYLLAMCCVACIVYLAKTKVLP					
a015	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTKFYTVYLLAMCCLTCIVYLAKTKVLP					
	70	80	90	100	110	120
m015.pep	FX					
a015	FX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 015 shows 94.5% identity over a 91 aa overlap with a predicted ORF (ORF 015.ng) from *N. gonorrhoeae*:

m015/g015

m015.pep				10	20	30
				KIRKALAGFWKALPHLNDTM	LLFTGLWLMKITH	
g015	LIVKYSHQIFVTITILVFNIRFFLLWKNPEKPLVGFWKALPHLNDTM	LLFTGLWLMKITH				
	10	20	30	40	50	60
m015.pep				40	50	60
	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTKFYTVYLLAMCCVACIVYLAKTKVLP					
g015	FSPFNAPWLGTKILLLLFAYIALGMVMMRRARPRSTKFYTVYLLAMCCCIACIVYLAKTKVLP					
	70	80	90	100	110	120
m015.pep	FX					
g015	FX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 99>:

g018.seq

1 atGCAGCAGG GGCagttggt tggacgcgtc gcccgcgaata AAGATATGCG
 51 GAATgctggt CTGCATggtC AGCGGATCGG CAACGGGtac gccgcgcgcg
 101 tctttgTCGA TATTGATGTT TTCCAAACCG ATATtgTCAA CGTTCGGACG
 151 GCgACCTACG GCTGCCAACA TATATTCGGC AACAAATACG CCTTTTTTCGC
 201 CATCCTGCTC CCAATGGACT tctACATTGC CGTCTGCGTC GAGTTTGACC
 251 TCGGTTTTAG CATCCAGATG CAGTTTCAAT tctTCTCCGA ACACGGCTTT
 301 CGCCTCGTCT GA

This corresponds to the amino acid sequence <SEQ ID 100; ORF 018.ng>:

g018.pep

1 MQQGQLVGRV ARNKDMRNAG LHGORIGNGY AARVFDIDV FQTDIVNVRT
 51 ATYGCQHIFG NKYAFAILL PMDFYIAVCV EFDLGFSIQM QFQFFSEHGF

101 RLV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 101>:

```
m018.seq
  1 ATGCAGCAGA GGCAGTTGGT TGGACGCATC GCCTGCGATG AAGATATGCG
 51 GAATACTGGT CTGCATGGTC AGCGGGTCGG CAACAGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATATT TTCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCCCACG GCTGCCAGCA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCATC GAGTTTGACC
251 TCGGTTTTAG CATCCAGATG CAGTTTCAAT TCTTCGCCGA ACACGGCGTT
301 CGCCTCGTCT GA
```

This corresponds to the amino acid sequence <SEQ ID 102; ORF 018>:

```
m018.pep
  1 MQQRQLVGRI ACDEDMRNTG LHGQRVGNRY AARIFFDIDI FQTDIVNVRT
 51 AAHGCQHIFG NKYAFAILL PMDFYIAVCI EFDLGFSIQM QFQFFAEHGV
101 RLV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 103>:

```
a018.seq
  1 ATGCAGCAGG GGCAGTTGGT TGGACGCGTC GCCCGCAATA AAGATATGCG
 51 GAATACTGGT CTGCATAGTC AGCGGATCGG CAACGGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATGTT TTCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCCTACG GCTGCCAGCA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCGTC GAGTTTGGCC
251 TCGGTTTTAG CATCCAAATG CAGTTTCAAT TCTTCACCGA ACACGGCTTT
301 CGCCTCGTCT GA
```

This corresponds to the amino acid sequence <SEQ ID 104; ORF 018.a>:

```
a018.pep
  1 MQQGQLVGRV ARNKDMRNTG LHSQRIGNGY AARIFFDIDV FQTDIVNVRT
 51 AAYGCQHIFG NKYAFAILL PMDFYIAVCV EFGLGFSIQM QFQFFTEHGF
101 RLV*
```

m018/a018 86.4% identity over a 103 aa overlap

	10	20	30	40	50	60
m018.pep	MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCQHIFG					
		:	::	:	:	:
a018	MQQGQLVGRVARNKDMRNTGLHSQRIGNGYAARIFFDIDVFQTDIVNVRTAAYGCQHIFG					
	10	20	30	40	50	60
	70	80	90	100		
m018.pep	NKYAFAILLPMDFYIAVCI EFDLGFSIQMQFQFFAEHGVRLVX					
		:	:	:	:	
a018	NKYAFAILLPMDFYIAVCVEFGLGFSIQMQFQFFTEHGFRLVX					
	70	80	90	100		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 018 shows 84.5% identity over a 103 aa overlap with a predicted ORF (ORF 018.ng) from *N. gonorrhoeae*:

m018/g018

	10	20	30	40	50	60
m018.pep	MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCQHIFG					
		:	::	:	:	:
g018	MQQGQLVGRVARNKDMRNAGLHGQRVGNRYAARVFDIDVFQTDIVNVRTATYGCQHIFG					
	10	20	30	40	50	60

	70	80	90	100
m018.pep	NKYAFFAILLPMDFYIAVCIEFDLGFSIQMQFFAEHGVRLVX			
	: :			
g018	NKYAFFAILLPMDFYIAVCVEFDLGFSIQMQFFSEHGFRVLX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 105>:

```

g019.seq (partial)
  1 ..ctgctggcgg ccctggtgct tgccgcgtgt tcttcgACAA ACacacTGCC
 51 AGCCGGCAAG ACCCGGCAG ACAATATAGA AActgcCgAC CTTTCGGCAA
101 GCGTCCCAC ccgcCCTGCC GAACCGGAAG GAAAAACGCT GGCAGATTAC
151 GGCGGCTACC CGTCCGCACT GGATGCAGTG AAACAGAACA ACGATGCGGC
201 AGCCGCCGCC TATTGGAAG Acgcaggaga cagCGcgatg gcGGAAAtg
251 tccgcaagga gtgGCTGa

```

This corresponds to the amino acid sequence <SEQ ID 106; ORF 019.ng>:

```

g019.pep (partial)
  1 ..LLAALVLAAC SSTNTLPAGK TPAENIETAD LSASVPTRPA EPEGKTLADY
 51 GGYPSALDAV KQNNDAAAAA YLENAGDSAM AENVRKEWL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 107>:

```

m019.seq (partial)
  1 ATGTACCTAC CCTCTATGAA GCATTCCCTG CCGCTGCTGG CGGCCCTGGT
 51 GCTTGCCGCG GTTCTTCGA CAAACACACT GCCAGCCGGC AAGACCCCGG
101 CAGACAATAT AGAAACTGCC GACCTTTCGG CAAGCGTTCC CACCCGCCCT
151 GCCGAACCCG AAAGAAAAAC GCTGGCAGAT TACGGCGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTTGG
251 AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCACGCAG ACAGTGGACG CTGTTTGCAC AGGAATACGC
351 CAAACTCGAA CCGGCAGGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCGCTG AACTGGTCAA AAATACGGGC
451 AAACTGCCTT CGGGCTGCAC CAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTTGTTGGAC GGCAACGACG CCTGGAGGCG CGTGCGCGGA CTGCTGGCCG
551 GCCGCCAAAC CACAGACGCA CGCAACCTTG CCGCCGCATT GGGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAAGAA GCACGCAAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAAGCGG TTTAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CTGCGCCCTT TGGACTATTA
801 CGGCAAGGTT GCCGACCGCC GCCAACTGAC CGACGACCAA ATCGAGTGGT
851 ACGCCCGCGC CGCCTTGCGC GCCCGACGTT GGGACGAGCT GGCCTCCGTT
901 ATCTCGCATA TGCCCGAAAA ACTGCAAAAA AGCCCGACCT GGCTCTACTG
951 GCTGGCACGC AGCCGCGCCG CAACGGGCAA CACGCAAGAG GCGGAAAAAC
1001 TTTACAAACA GCGGCGAGCG ACGGGCAGGA ATTTTATATG GGTGCTGGCA
1051 GGGGAAGAAT TGGGTCGGAA AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAAAC AGCGTCCGCC GCATGGCGGA AGACGGTGCA GTCAAACGCG
1151 CACTGGTACT GTTCCAAAAC AGCCAATCTG CCGGTGATGC AAAAATGCGC
1201 CGTCAGGCTC AGGCGGAATG GCGTTTGGC ACACGCGGCT TTGACGAAGA
1251 CAAGCTGCTG ACCGCCGCGC AAACCGCGTT CGACCACGTT TTTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCGACC GCAAACTCAA CTACACCTTG
1351 CGCTATATTT CGCCGTTTAA AGACACGGTA ATCCGCCACG CGCAAAATGT
1401 TAATGTCGAT CCGGCTTGGG TTTATGGGCT GATTCGTCAG GAAAGCCGCT
1451 TCGTTATAGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCCTGCCA CCGCGCGCGA AATCGCCGGC AAAATCGGTA TGGATGCCGC
1551 ACAACTTTAC ACCGCCGACG GG...

```

This corresponds to the amino acid sequence <SEQ ID 108; ORF 019>:

```

m019.pep (partial)
  1 MYLPSMKHSL PLLAALVLAA CSSTNTLPAG KTPADNIETA DLSASVPTRP

```

```

51  AEPERKTLAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARRQWT LFAQEYAKLE PAGRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGV
251 GHYQSQNLNV PAALDYYGKV ADRRLTDDQ IEWYARAALR ARRWDELASV
301 ISHMPEKLQK SPTWLYWLAR SRAATGNTQE AEKLYKQAAA TGRNFYAVLA
351 GEELGRKIDT RNNVPDAGKN SVRRMAEDGA VKRALVLFQN SQSAGDAKMR
401 RQAQAEWRFA TRGFDEDKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNYTL
451 RYISPFKDTV IRHAQNVNVD PAWVYGLIRQ ESRFVIGAQS RVGAQGLMQV
501 MPATAREIAG KIGMDAAQLY TADG...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 109>:

```

a019.seq
1  ATGTACCCAC CCTCTCTGAA GCATTCCCTG CCGCTGCTGG TGGNCCTGGT
51  GCTTGCCGCG TGTCTTNGA CAAACACACT GTCAGCCGAC AAGACCCCGG
101 CAGACAATAT AGAAACTGCC GACCTTTCGG CAAGCGTTCC CACCNGCCCT
151 GCCGAACCCG AANGAAAAAC GTNGGCAGAT TACGGCGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTTGG
251 AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCGCGCAG ACAGTGGACG CTGTNTGCAC ANGAATATGC
351 NAAACTCGAA CCGGCANGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCGCCG AACTGGTCAA AAATACGGGC
451 AAACTGCCTT CGGGCTGCAC CAAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTTGTTGGAC GGCAACGACG CCTGGAGGCG CGTGCGCGGA CTGCTGGCCG
551 GCCGCCAAAC CACAGACGCA CGCAACCTTG CCGCCGCATT GGGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAAGAA GCACGCAAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAAGCGG TTTAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CTGCGCCCT TGGACTATTA
801 NGGCAAGGTT GCCGACCGCC GCCAACTGAC CGACGACCAA ATCGAGTGGT
851 ACGCCCGCGC CGCNNNTNNGC NNNCGNNGTT NGNANGANN TGGCNNCCGNN
901 ANCNCGNNNN TGCNNGANAA ACNNNNNNAN AGNCNNANNT NGNTNNANTG
951 NNTGGCACGC AGCCGCGCCG CNACGGGCAA CACGCAANAN GCGGANAAAC
1001 TNTACAAACA GGCGGCAGCA NCGGGCANGA ATTTTATGC NGTGCTGNCN
1051 GGGGAAGAGT TGGGGCGCAN AATCGATACG CGCAACAATG TGCCCGATTG
1101 CGGCAAAANC AGCGTCCTCC GTATGGCGGA AGACGGCGCG ATTAAGCGCG
1151 CGCTGGTGCT GTTCCGAAAC AGCCGAACCG CCGGCGATGC GAAAATGCGC
1201 CGTCNGGCTC AGGCGGAATG GCGTTTCGCC ACACGCGGCT TCGATGAAGA
1251 CAAGCTGCTG ACCGCCGCGC AAACCGCGTT CGACCACGGT TTTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCGACC GCAAACCTCA CTACACCTTG
1351 CGCTACATTT CGNNNNNTNA NGACACGGTA ATCCGCCACG CGCAAATGT
1401 TAATGTCGAT CCGGCGTGGG TTTACGGGCT GATTCGTCAG GAAAGCCGCT
1451 CGGTTATGGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCCTGCCA CCGCGCGCGA AATCGCCGGC AAAATCGGTA TGGATGCCGC
1551 ACAACTTTAC ACCGCCGACG GCAATATCCG TATGGGGACG TGGTATATGG
1601 CGGACACCAA ACGCCGCTG CAAAACAACG AAGTCCTCGC CACCGCAGGC
1651 TATAACGCCG GTCCCGGCAG GCGCGGCCGA TGGCAGGCGG ACACGCCCTT
1701 CGAAGGCGCG GTATATGCCG AAACCATCCC GTTTTCCGAA ACGCGCGACT
1751 ATGTCAAAAA AGTGATGGCC AATGCCGCTT ACTACGCTC CCTCTTCGGC
1801 GCGCCGCACA TCCGCTCAA ACAGCGTATG GGCATTGTCC CCGCCGCTG
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 019.a>:

```

a019.pep
1  MYPPSLKHSL PLLVXLVLAA CSXTNTLSAD KTPADNIETA DLSASVPTXP
51  AEPEXKTXAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARRQWT LXAXEYAKLE PAXRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGV
251 GHYQSQNLNV PAALDYXGKV ADRRLTDDQ IEWYARAAXX XRXXXXXXXX
301 XXXXXXXXXX XXXXXXXXXAR SRAATGNTQX AXKLYKQAAA XGXNFYAVLX
351 GEELGRXIDT RNNVPDAGKX SVLRMAEDGA IKRALVLFN SRTAGDAKMR
401 RXAQAEWRFA TRGFDEDKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNYTL

```

451 RYISXXDVT IRHAQNVNVD PAWVYGLIRQ ESRFVMGAQS RVGAQGLMQV
 501 MPATAREIAG KIGMDAAQLY TADGNIRMGW WYMADTKRRL QNNEVLATAG
 551 YNAGPGRARR WQADTPLEGA VYAETIPFSE TRDYVKKVMA NAAYYASLFG
 601 APHIPLKQRM GIVPAR*

m019/a019 88.9% identity over a 524 aa overlap

m019.pep	10	20	30	40	50	60
	MYLPSMKHSLPLLAALVLAACSSTNTLPAGKTPADNIETADLSASVPTTRPAEPEKRTLAD					
a019	10	20	30	40	50	60
	MYPPSLKHSLPLLVLVLAACSXTNTLSADKTPADNIETADLSASVPTXPAEPEKXTXAD					
m019.pep	70	80	90	100	110	120
	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKS LGARRQWTLFAQEYAKLE					
a019	70	80	90	100	110	120
	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKS LGARRQWTLXAXEYAKLE					
m019.pep	130	140	150	160	170	180
	PAGRAQEVECYADSSRNDYTRAAELVKNTGKLP SGCTKLLEQAAASGLLDGNDAWRRVRG					
a019	130	140	150	160	170	180
	PAXRAQEVECYADSSRNDYTRAAELVKNTGKLP SGCTKLLEQAAASGLLDGNDAWRRVRG					
m019.pep	190	200	210	220	230	240
	LLAGRQTTDARNLAAALGSPFDGGTQGSREYALLNVIGKEARKSPNAAALLSEMESGLSL					
a019	190	200	210	220	230	240
	LLAGRQTTDARNLAAALGSPFDGGTQGSREYALLNVIGKEARKSPNAAALLSEMESGLSL					
m019.pep	250	260	270	280	290	300
	EQRSFAWGVLGHYQSQNLNVPALDYYGKVADRRQLTDDQIEWYARAALRARRWDELASV					
a019	250	260	270	280	290	300
	EQRSFAWGVLGHYQSQNLNVPALDYYGKVADRRQLTDDQIEWYARAAXXRXRXRXAXX					
m019.pep	310	320	330	340	350	360
	ISHMPEKLQKSPTWLYWLARSRAATGNTQEAELKLYKQAAATGRNFYAVLAGEELGRKIDT					
a019	310	320	330	340	350	360
	XXXXXXXXXXXXXXXXXARSRAATGNTQXAXKLYKQAAAXGXNFYAVLXGEELGRXIDT					
m019.pep	370	380	390	400	410	420
	RNNVPDAGKNSVRRMAEDGAVKRALVLFQNSQSAGDAKMRRQAQAEWRFATRGFDEDKLL					
a019	370	380	390	400	410	420
	RNNVPDAGKXSVLRMAEDGAIKRALVLFNRSTAGDAKMRRXAQAEWRFATRGFDEDKLL					
m019.pep	430	440	450	460	470	480
	TAAQTAFDHGFYDMAVNSAERTDRKLNLYTLRYISPFKDTVIRHAQNVNVDPAWVYGLIRQ					
a019	430	440	450	460	470	480
	TAAQTAFDHGFYDMAVNSAERTDRKLNLYTLRYISXXDVTIRHAQNVNVDPAWVYGLIRQ					
m019.pep	490	500	510	520		
	ESRFVIGAQSRVGAQGLMQVMPATAREIAGKIGMDAAQLYTADG					
a019	490	500	510	520	530	540
	ESRFVIGAQSRVGAQGLMQVMPATAREIAGKIGMDAAQLYTADGNIRMGWYMAADTKRRL					
a019	550	560	570	580	590	600
	QNNEVLATAGYNAGPGRARRWQADTPLEGAVYAETIPFSETRDYVKKVMANAAYYASLFG					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 019 shows 95.5% identity over a 89 aa overlap with a predicted ORF (ORF 019.ng) from *N. gonorrhoeae*:

g019/m019

		10	20	30	40	49
g019.pep		LLAALVLAACSSNTLPAGKTPADNIETADLSASVPTRPAEPEGKTLAD				
m019	MYLPSMKHSLPLLAALVLAACSSNTLPAGKTPADNIETADLSASVPTRPAEPEKTLAD					
		10	20	30	40	50
		50	60	70	80	89
g019.pep	YGGYPSALDAVKQNNDAAYLENAGDSAMAENVRKEWL					
m019	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKS LGARRQWTLFAQEYAKLE					
		70	80	90	100	110
						120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 111>:

g023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GCGATTGGGT
51  AATGCAGCGT GCGACTGCGG TTATTATGTT GATTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCCCTG CCTAAAGAAT ATCCGGCATG GCAGGCATTT
151 TTTAGTCAAG CTTGGGTAAA AGTATTACC CAAGTGAGCT TTATCGCCGT
201 ATTCTTGCAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATCA
251 AACCCTTCGG CGTGCGTTTG TTTTGCAGG TTGCCACCAT TGcttGGCTG
301 GTCGGCTGCC TCGTGTATTC AGTTAAAGTG ATTTGGGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 023.ng>:

g023.pep

```

1  MVERKLTGAH YGLRDWVMQR ATAVIMLIYT VALLVVLFLAL PKEYPAWQAF
51  FSQAWVKVFT QVSFIAVFLH AWVGIRDLWM DYIKPFGVRL FLQVATIVWL
101 VGCLVYSVKV IWG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

m023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GCGATTGGGT
51  GATGCAACGT GCGACTGCGG TTATTATGTT GATTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTCCCTG CCTAAAGAAT ATCCGGCATG GCAGGCATTT
151 TTTAGTCAAA CTTGGGTAAA AGTATTACC CAAGTGAGCT TCATCGCCGT
201 ATTCTTGCAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATCA
251 AACCCTTCGG CGTGCGTTTG TTTTGCAGG TTGCCACCAT CGTTGGCTG
301 GTCGGCTGTC TCGTGTATTC AGTTAAAGTG ATTTGGGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 023>:

m023.pep

```

1  MVERKLTGAH YGLRDWVMQR ATAVIMLIYT VALLVVLFLSL PKEYSAWQAF
51  FSQTWVKVFT QVSFIAVFLH AWVGIRDLWM DYIKPFGVRL FLQVATIVWL
101 VGCLVYSVKV IWG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

a023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GGGATTGGGC
51  GATGCAACGT GCGACCGCGG TTATTATGTT GATTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCTCTG CCTAAAGAAT ATCCGGCATG GCAGGCATTT
151 TTTAGTCAAA CTTGGGTAAA AGTATTACC CAAGTGAGCT TCATCGCCGT

```

205

201 ATTCTTGAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATNA
 251 AACCTTCGG CGTGCCTTTG TTTTTCAGG TTGCCACCAT CGTCTGGCTG
 301 GTCGGCTGCT TGGTGTATTC AATTAAAGTA ATTTGGGGGT AA

This corresponds to the amino acid sequence <SEQ ID 116; ORF 023.a>:

a023.pep
 1 MVERKLTGAH YGLRDWAMQR ATAVIMLIYT VALLVVLFL PKEYSAWQAF
 51 FSQTWVKVFT QVSFIQVFLH AWVGIRDLWM DYXKPFQVRL FLQVATIVWL
 101 VGCLVYSIKV IWG*

m023/a023 96.5% identity over a 113 aa overlap

	10	20	30	40	50	60
m023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFSLPKEYSAWQAFFSQTWVKVFT					
	: : : : :					
a023	MVERKLTGAHYGLRDWAMQRATAVIMLIYTVALLVVLFALPKEYSAWQAFFSQTWVKVFT					
	10	20	30	40	50	60
	70	80	90	100	110	
m023.pep	QVSFIQVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
	: : : : :					
a023	QVSFIQVFLHAWVGIRDLWMDYXKPFQVRLFLQVATIVWLVGCLVYSIKVIWGX					
	70	80	90	100	110	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 023 shows 97.3% identity over a 113 aa overlap with a predicted ORF (ORF 023.ng) from *N. gonorrhoeae*:

g023/m023

	10	20	30	40	50	60
g023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFALPKEYPAWQAFFSQAWVKVFT					
	: : : : :					
m023	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFSLPKEYSAWQAFFSQTWVKVFT					
	10	20	30	40	50	60
	70	80	90	100	110	
g023.pep	QVSFIQVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
	: : : : :					
m023	QVSFIQVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 117>:

g025.seq
 1 ATGTTGAAAC AAACgACACT TTTGGCAGCT TGTACCGCCG TTGCCGCTCT
 51 GTTGGGCGGT TGcgCCACCC AACAGCCTGC TccTGTCATT GCAGGCAATT
 101 CAGGTATGCA GACCGTATCG TCTGCGCCGG TTTACAATCC TTATGGCGCA
 151 ACGCCGTACA ATGCCGCTCC TGCCGCCAac gatgcGCCgT ATGTGCCGCC
 201 CGTGCAAact gcgcccgttT ATTCGCCTCC TGCTTATGTT CCGCcgTCTG
 251 CACCTGCCGT TTCGGgtaca tatgtTCCTT CTTACGCACC CgtcgACATC
 301 aacgCGGCGa cgCataCTAT TGTGCGTGGC GACACgGtgt acaACATTTc
 351 caaAcgCtAc CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA
 401 CCGACAATAC GTTGAAGCATC GGTCAGATTG TTAAAGTCAA ACCGGCaggA
 451 TATGCCGCAC CGAAAACCGC AGCCGTAGAA AGCAGGCCCG CCGTACCGGC
 501 TGCCGCGCAA ACCCTGTGA AACCgCCCGC gcaACCGCCC GTTCAGTCCG
 551 CGCCGCAACC TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCCGCCCCC
 601 GCGCCGCCCC CGCAATCTCC TGCCGCTTCG CCTTCCGGCA CGCGTTCGGT
 651 CGGCGGCATT GTTTGGCAGC GTCCGACCCA AGGTAAAGTG GTTGCCGATT

```

701 TCGGCGGCGG CAACAAGGGT GTCGATATTG CCGGCAATGC CGGACAACCC
751 GTTTTGCGCG CGGCTGACGG CAAAGTGGTT TATGCCGGTT CAGGTTTGAG
801 GGGATACGGA AACTTGGTCA TCATCCAGCA CAATTCCTCT TTCCTGACCG
851 CGTACGGGCA CAACCAAAAA TTGCTGGTCG GCGAAGGTCA GCAGGTCAAA
901 CGCGGTCAGC AGGTTGCTTT GATGGGTAAT ACCGATGCTT CCAGAACGCA
951 GCTTCATTTT GAGGTGCGTC AAAACGGCAA ACCGGTTAAC CCGAACAGCT
1001 ATATCGCGTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 025.ng>:

```

g025.pep
  1 MLKQTTLLAA CTAVAALLGG CATQQPAPVI AGNSGMQTVS SAPVYNPYGA
 51 TPYNAAPAAN DAPYVPPVQT APVYSPPAYV PPSAPAVSGT YVPSYAPVDI
101 NAATHTIVRG DTVYNISKRY HISQDDFRW NGMTDNTLSI GQIVKVKPAG
151 YAAPKTAAVE SRPAVPAQAQ TPVKPAAQPP VQSAPQPAAP AAENKAVPAP
201 APAPQSPAAS PSGTRSVGGI VWQRPTQKQV VADFGGNGKG VDIAGNAGQP
251 VLAAADGKVV YAGSGLRGYV NLVIIQHNS FLTAYGHNQK LLVGEQQQVK
301 RQQQVALMGN TDASRTQLHF EVRQNGKPVN PNSYIAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

```

m025.seq (partial)
  1 ..GTGCGCGCGG TGCAAAGCGC GCCGTTTAT ACGCCTCCTG CTTATGTTC
 51 GCCGTCTGCA CCTGCCGTTT CGGGTACATA CGTTCCTTCT TACGCACCCG
101 TCGACATCAA CGCGCGGACG CATACTATTG TGCGCGGCGA CACGGGTGAC
151 AACATTTCCA AACGCTACCA TATCTCTCAA GACGATTTC GTGCGTGGAA
201 CGGCATGACC GACAATACGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC
251 CGGCAGGATA TGCCGCACCG AAAGCCGCAG CCGTAAAAAG CAGGCCCGCC
301 GTACCGGCTG CCGCGCAACC GCCCGTACAG TCCGCACCCG TCGACATTAA
351 CGCGGCGACG CATACTATTG TGCGCGGCGA CACGGGTGAC AACATTTCCA
401 AACGCTACCA TATCTCTCAA GACGATTTC GTGCGTGGAA CGGCATGACC
451 GACAATATGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC CGGCAGGATA
501 TGCCGCACCG AAAACCGCAG CCGTAGAAAG CAGGCCCGCC GTACCGGCTG
551 CCGTGCAAAC CCCTGTGAAA CCCGCCGCGC AACCGCCTGT GCAGTCCGCG
601 CCGCAACCTG CCGCGCCCGC TGCGGAAAAT AAAGCGGTTT CCGCGCCCGC
651 CCCGCAATCT CCTGCCGCTT CGCCTTCCGG CACGCGTTCG GTCGCGGGCA
701 TTGTTTGGA GCGTCCGACG CAAGGTAAAG TGGTTGCCGA TTTCGGCGGC
751 AACAACAAGG GTGTCGATAT TGCCGTAAT GCGGGACAGC CCGTTTGGC
801 GCGGCTGAC GGCAAAGTGG TTTATGCCGG TTCAGGTTTG AGGGGATACG
851 GAAACTTGGT CATCATCCAG CATAATTCTT CTTTCCTGAC CGCATACGGG
901 CACAACCAA AATTGCTGGT CGGCGAGGGG CAGCAGGTCA AACGCGGTCA
951 GCAGGTGCT TTGATGGGCA ATACCGATGC TTCCAGAACG CAGCTTCATT
1001 TCGAGGTGCG TCAAAACGGC AAACCGGTTA ACCCGAACAG CTATATCGCG
1051 TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 025>:

```

m025.pep (partial)
  1 ..VPPVQSAPVY TPPAYVPPSA PAVSGTYVPS YAPVDINAAT HTIVRGDTVY
 51 NISKRYHISQ DDFRAWNGMT DNTLSIGQIV KVKPAGYAAP KAAAVKSRPA
101 VPAAQPPVQ SAPVDINAAT HTIVRGDTVY NISKRYHISQ DDFRAWNGMT
151 DNMLSIGQIV KVKPAGYAAP KTAAVESRPA VPAVQTPVK PAAQPPVQSA
201 PQPAAPAAEN KAVPAPAPQS PAASPSGTRS VGGIVWQRP QGKVVADFGG
251 NNKGVDIAGN AGQPVLAAD GKVYVAGSGL RYGNLVIIQ HNSSLTAYG
301 HNQKLLVGEQ QQVKGQQVA LMGNTDASRT QLHFEVRQNG KPVNPNSYIA
351 F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

```

a025.seq
  1 ATGTTGACAC CAACAACACT TTAGGTAGCT TGTACCGCCC TTGCCGCTCA
 51 GTTGGGCGGA TGCCCCACCC AACACCTTC TCCTGTCATT GCAGGCAATT
101 CAGGTATGCA GACCGTACCG TCTGCGCCGG TTTACAATCC TTATGGCGCA

```



```

151 ACGCCGTACA ATGCCGCTCC TGCCGCCAAC GATGCGCCGT ATGTGCCGCC
201 GGTGCAAAGC GCGCCGTTT ATANGCCTCC TGCTTATGTT CCGCCGTCTG
251 CACCTGCCGT TTCGGGTACA TACGTTCTT CTTACGCANC CGTCGACATC
301 AACGCGGCGA CCCATACTAT TGTGCGCGGC GACACCGTGT ACAAGATTTC
351 CAAATGCTAC CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA
401 CCGACAATAC GTTGAGCATC GGTGAGATTG TTAAAGTCAA ACCGGCAGGA
451 TATGCCGCAC CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC
501 TGCCGCGCAA CCGCTCGTAC AGTCCGCACC CGTCGACATC AACGCGGCGA
551 CGCATACTAT TGTGCGCGGC GACACGGTGT ACAACATTTC CAAACGCTAC
601 CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA CCGACAATAC
651 GTTGAGCATC GGTGAGATTG TTAAAGTCAA ACCGGCAGGA TATGCCGCAC
701 CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC TGCCGTGCAA
751 ACCCTGTGA AACC CGCGC GCAACCGCCT GTGCAGTCCG CGCCGCAACC
801 TGCCGCGCCC GTCGCGGAAA ATAAAGCGGT TCCCGCGCCC GCCCGCAAT
851 CTCCTGCCGC TTCGCCTTCC GGCACGCGTT CGGTCGCGCG CATTTGTTTG
901 CAGCGTCCGA CGCAAGGTAA AGTGGTTGCC GATTTCGGCG GCAACAACAA
951 GGGTGTGAT ATTGCAGGAA ATGCGGGACA GCGCGTTTTG GCGGCGGCTG
1001 ACGGCAAAGT GGTATTATGCA GGTTCCGGTT TGAGGGGATA CGGCAATTTG
1051 GTCATCATCC AGCATAATTC TTCCTTCTTG ACCGCATACG GGCACAACCA
1101 AAAATTGCTG GTCGGCGAAG GCCAGCAGGT CAAACGCGGG CAGCAGGTCTG
1151 CTTTGATGGG CAATACCGAG GCTTCTAGAA CGCAGCTTCA TTTCGAGGTG
1201 CGGCAAAACG GCAAACCGGT TAATCCGAAC AGCTATATCG CGTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 025.a>:

```

a025.pep
1  MLTP TTL*VA CTALAAQLGG CPTQHPSPIV AGNSGMQTVP SAPVYNPYGA
51  TPNNAAPAA DAPYVPPVQS APVYXPPAYV PPSAPAVSGT YVPSYAXVDI
101 NAATHIVRG DTVYKISKCY HISQDDFRAW NGMTDNTLSI GQIVKVKPAG
151 YAAPKAAAVK SRPAVPAAAQ PLVQSAPVDI NAATHIVRG DTVYNISKRY
201 HISQDDFRAW NGMTDNTLSI GQIVKVKPAG YAAPKAAAVK SRPAVPAAVQ
251 TPVKPAAQPP VQSAPQPAAP AAENKAVPAP APQSPAASPS GTRSVGGIVW
301 QRPTQGVVVA DFGGNNKGVD IAGNAGQPVL AAADGKVYYA GSGLRGYGNL
351 VIIQHNSFL TAYGHNQKLL VEGGQQVVRG QQVALMGNTS ASRTQLHFEV
401 RQNGKPVNPN SYIAF*

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m025/a025 97.4% identity over a 351 aa overlap

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                                     10      20      30
m025.pep                               VPPVQSAPVYTPPAYVPPSAPAVSGTYVPS
                                     |||:|||||
a025      GMQTVPSAPVYNPYGATPNNAAPANDAPYVPPVQSAPVYXPPAYVPPSAPAVSGTYVPS
               40      50      60      70      80      90

               40      50      60      70      80      90
m025.pep      YAPVDINAATHIVRGDTVYNISKRYHISQDDFRAWNGMTDNTLSIGQIVKVKPAGYAAP
               || |||:|||||
a025      YAXVDINAATHIVRGDTVYKISKCYHISQDDFRAWNGMTDNTLSIGQIVKVKPAGYAAP
               100     110     120     130     140     150

               100     110     120     130     140     150
m025.pep      KAAAVKSRPAVPAAAQPPVQSAPVDINAATHIVRGDTVYNISKRYHISQDDFRAWNGMT
               |||:|||||
a025      KAAAVKSRPAVPAAAQPLVQSAPVDINAATHIVRGDTVYNISKRYHISQDDFRAWNGMT
               160     170     180     190     200     210

               160     170     180     190     200     210
m025.pep      DNMLSIGQIVKVKPAGYAAPKTAAVESRPAVPAAVQTPVKPAAQPPVQSAPQPAAPAAEN
               || |||:|||||
a025      DNTLSIGQIVKVKPAGYAAPKAAAVKSRPAVPAAVQTPVKPAAQPPVQSAPQPAAPAAEN
               220     230     240     250     260     270

               220     230     240     250     260     270
m025.pep      KAVPAPAPQSPAASPSGTRSVGGIVWQRPTQGVVADFGGNNKGVDIAGNAGQPVLAAD
               |||:|||||

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a025      KAVPAPAPQSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLAAD
           280      290      300      310      320      330

m025.pep      280      290      300      310      320      330
GKV VYAGSGLRGYGNLVIIQHNS SFLTAYGHNQKLLVGE GQQVKRGQQVALMGNTDASRT
|||||:|||||
a025      GKV VYAGSGLRGYGNLVIIQHNS SFLTAYGHNQKLLVGE GQQVKRGQQVALMGNTASRT
           340      350      360      370      380      390

m025.pep      340      350
QLHFEVRQNGKPVNPNSYIAFX
|||||
a025      QLHFEVRQNGKPVNPNSYIAFX
           400      410

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 025 shows 75.6% identity over a 353 aa overlap with a predicted ORF (ORF 025.ng) from *N. gonorrhoeae*:

m025/g025

```

m025.pep      10      20      30
VPPVQSAPVYTPPAYVPPSAPAVSGTYVPS
|||||:|||||
g025      GMQTVSSAPVYNPYGATPYNAAPAANDAPYVPPVQTAPVYSPPAYVPPSAPAVSGTYVPS
           40      50      60      70      80      90

m025.pep      40      50      60      70      80      90
YAPVDINAATHITVRGDTVYNISKRYHISQDDFAWNGMTDNTLSIGQIVKVKPAGYAAP
|||||
g025      YAPVDINAATHITVRGDTVYNISKRYHISQDDFAWNGMTDNTLSIGQIVKVKPAGYAAP
           100     110     120     130     140     150

m025.pep      100     110     120     130     140     150
KAAAVKSRPAVPAAPAAQPPVQSAPVDINAATHITVRGDTVYNISKRYHISQDDFAWNGMT
|
g025      K-----

m025.pep      160     170     180     190     200     210
DNMLSIGQIVKVKPAGYAAPKTAAVESRPAPVPAVQTPVKPAAQPPVQSAPQPAAPAAEN
|||||:|||||
g025      -----TAAVESRPAPVPAVQTPVKPAAQPPVQSAPQPAAPAAEN
           160     170     180     190

m025.pep      220     230     240     250     260
KAVPAPAP--QSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
|||||:|||||
g025      KAVPAPAPQSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
           200     210     220     230     240     250

m025.pep      270     280     290     300     310     320
ADGKV VYAGSGLRGYGNLVIIQHNS SFLTAYGHNQKLLVGE GQQVKRGQQVALMGNTDAS
|||||
g025      ADGKV VYAGSGLRGYGNLVIIQHNS SFLTAYGHNQKLLVGE GQQVKRGQQVALMGNTDAS
           260     270     280     290     300     310

m025.pep      330     340     350
RTQLHFEVRQNGKPVNPNSYIAFX

```

g025 |||||
 RTQLHFEVRQNGKPVNPNSYIAFX
 320 330

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 113>:

g031.seq
 1 ATGGTGTCCC TCCGCTTCAG ATTCGGCAAC CACTTTAAAC GCCGACATTC
 51 TGACAATTTT CTTTCCGCC AGCCAAATAT CATGCGTATC TTTCGGTTTCG
 101 GGCTTGTTGG GCATGGCAAC CTTCAACAGC CGCGCCATCA CAGGAATCGT
 151 CGTTCCTTGA ATCAGCAGCG ACAGCACCAC CACGGCAAAC GCCACATCAA
 201 ACAGCAGGTG CGAATTGGGA ACGCCCATCA CCAGCGGCAT CATCGCCAGC
 251 GAAATCGGTA CGGCTCCTCG CAAGCCCAAC CAACTGATAT ACGCCTTTTC
 301 ACGCAGGCTG TAATTGAATT TCCACAAACC GCCGAACACT GCCAGCGGAC
 351 GCGCGACCAG CATCAGGAAC GCCGCAATCG CCAAGGCTTC CGCCGCCCTG
 401 TCCAACACGC CGGCGGGAGA AACCAGCAGA CCGAGCATGA CGAACAAAGT
 451 TGCTTGCGCC AGCCAAGCCA AACCGTCCAT CACACGCAA ACCTGTTCCG
 501 TcgCACGGTT GCGCTGGTTA CCGACAATGA TGCCGGCAAG GTAAACCGCC
 551 AAAAAGCCGC TGCCGCCTAT GGTATTGGTA AACGCAAACA CAAGCAGCCC
 601 GCGCGACACA ATCATCAGCG CGTACAGACC TTCCGtacac acctccaatt
 651 cccaatcaac gtcataagctg tctcccgtgt taaaatgttc ttcacttcag
 701 aatccccccc ttcttcccag cccgaaacct tcatgtgtta naccctgggg
 751 tgccccaacg gatttagtaa cctcccaatg actctgcttg tcgccccctt
 801 cgcccgcttt ctccttcgag gaaaacttgt tgtccccgtc ttacattaa

This corresponds to the amino acid sequence <SEQ ID 114; ORF 031.ng>:

g031.pep
 1 MVSRLRFRFGN HFKRHRSDNF LFRQPNIMRI FRFGLVGHGN LQQPRHHRNR
 51 RSLNQQRQHH HGKRHIKQV RIGNAHHQRH HRQRNRYGSS QAQPTDIRLF
 101 TQAVIEFPQT AEHCQRTRDQ HQERRNRQGF RRPVQHAGGR NQQTEHDEQS
 151 CLRQPSQTVH HTQNVFRRTV ALVTDNDAGK VNRQKAAAY GIGKRKHQKQ
 201 ARHNHQRVQT FRTHLQFPIN VIAVSRVKMF FTSESPSSQ PETFMCXTLG
 251 CPNGFSNLPM TLLVAPFARF LLPGKLVVPV LH*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

m031.seq (partial)
 1 ...CGCCTGAAGC ACGGTGTCGG ACTGCATTTC TATTCGGCTA TACGCCTTTT
 51 CACGCAGGCT GTAATTGAAT TTCCACAAAC CGCCGAACAC TGCCGACGGA
 101 CGCGCGACCA GCATCAGGAA CGCCGCAATC GCCAAGGCTT CCGCCGCCCT
 151 GTCCAACACG TTGGCAGGAG AAACCAGCAG CAAAGGCATT CCCAAACGTG
 201 CGGACAAAGT GGTCGAAACC ACGCTCAGAA ACAACAGTGC GCCACCCGGC
 251 AG....

This corresponds to the amino acid sequence <SEQ ID 116; ORF 031>:

m031.pep (partial)
 1 ...RLKHGVLHF YSAIRLFTQA VIEFPQTAEH CRRTDQHQE RNRQGFRRP
 51 VQHVGRNRQQ QRHSQTCGQS GRNHAQKQQC ATRQ....

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

a031.seq
 1 ATACGCCTTT TCACGCAGGC TGTAATTGAA TTTCCACAAA CCGCCGAACA
 51 CTGCCGCGCG ACGCGCGACC AGCATCAGGA ACGCCGCAAT CGCCAAGGCT
 101 TCCGCCGCCC CGTCCAACAC GTTGGCAGGA GAAACCAGCA GCAAAGGCAT
 151 TCCCAAACGT GCGGACAAAG TGGTCGAAAC CACGCTCAGA AACACAGTG
 201 CGCCACCCGG CAG

This corresponds to the amino acid sequence <SEQ ID 118; ORF 031.a>:

a031.pep (partial)
 1 IRLFTQAVIE FPQTAEHCRR TRDQHQERRN RQGFRFPVQH VGRNRQQQRH
 51 SQTGQSGRN HAQKQQCATR Q

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m031/a031 100.0% identity over a 71 aa overlap

	10	20	30	40	50	60
m031.pep	RLKHGVLH	FYSAIRLFTQ	AVIEFPQTAEH	CRRTDQHQ	ERRNRQGF	RFPVQHVGRNRQQ
a031		IRLFTQAVIEFPQTAEH	CRRTDQHQ	ERRNRQGF	RFPVQHVGRNRQQ	
		10	20	30	40	
	70	80				
m031.pep	QRHSQTCGQSGRNHAQKQ	QCATRQ				
a031	QRHSQTCGQSGRNHAQKQ	QCATRQ				
	50	60	70			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 031 shows 60.0% identity over a 85 aa overlap with a predicted ORF (ORF 031.ng) from *N. gonorrhoeae*:

m031/g031

		10	20	30
m031.pep		RLKHGVLH	FYSAIRLFTQ	AVIEFPQTAEH
g031	NQQRQH	HHGKRHIKQ	QVRIGNAHHQR	HRQRNRYGSSQAQPTDIRLFTQAVIEFPQTAEH
	60	70	80	90
	40	50	60	70
m031.pep	CRRTDQHQ	ERRNRQGF	RFPVQHVGRNRQQ	QRHS-QTCGQSGRNHAQKQ
g031	CQRTDQHQ	ERRNRQGF	RFPVQHAGGRNQ	QTEHDEQSLRQPSQTVHHTQN
	120	130	140	150
	160	170		
g031	TDNDAGKVN	RQKAAAYG	IGKRKHKQ	PARHNNHQRVQTFRTHLQFPIN
	180	190	200	210
	220	230		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 119>:

g032.seq

```

1  ATGCGGCGAA ACGTGCCTGC CGTCGCCGTA TTGCGCCGCC CACGATTCTGA
51  GCGGTTTTTG GATTTGCGCT TGGCTCAGGC GCGTGCCGTT CCTGCCGGTA
101 AACAGGGCTT TGCCGTCCGA TGCCGTCTGA CGCAGCGGCA GATAGTTTTT
151 CAAGGCTTCC ACGCTTTTGC CGGTCAGCGG AACCTGACGC TGCTTGCGCC
201 CTTTGCCGGT AACGTGTACC CACGCTTCGT CCAAATATAC ATCATCTGCA
251 TTCAAGCCGT GTATCTCGCT CACGCGCAAA CCGCTGCCGT ACATCAGCTC
301 GAACAGCGCG TGGTCGCGCA CCGCCAGCGG GTCGCCGCCG TCCACGGGCA
351 AATCCAACAT CCGGTTACAG CATTCCTGCG GCAGGGCTTT GGGTACGCGC
401 TCGGGCTGCT TCGGCGGTTT GATGTCGGCG GTCGGGTCGG CGCGCATCAG
451 CCCGCGTTTG ACCAGCCAGG CGCAATACTG CCGCCACGCC GACAGCTTGC
501 GCGCCAGCGT CCGACCGTCC AAACCGCGCT GCGACAGCCG CCGCAACGCC
551 GccgTAAAAAT CGCGCCGCGA CAAGTCCTGC GGCACGCcg ctcgaTCTTC
601 AGACGGCATT TGTGCCAACA GTGCAAACAG TTCTTCCAAA TCGCGCCGGT
651 ATGCCGCAAC CGTGTGCTCC GACTTGCCCT CGCGCACGAT GTTTTCCAAA
701 TAAGCGTCAA AATacgcgc AAACccgTCC AAAACCATAA CCGTCCACA
751 CAAATATCAA AAAACAGTG A

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 032.ng>:

g032.pep

```

1  MRRNVPAAVAV LRRPRFEAFD DLALAQAQAV PAGKQGFQAVR CRLTQRQIVF
51  QGFHAFAGQR NLTLLAPFAG NVYPRFVQIY IICIQAVYLA HAQTAAVHQL

```

m032.seq (partial)					
1	ATGCGGCGAA	ACGTGCMtGC	mGTCGCCGTT	kTGCGCCGCC	CATTGCGCCA
51	AACGTTTTTG	GATTTGGCGT	TGGCTCAGGC	GCGTGCCGTT	CCTGCCGGTA
101	AACAGGGCTT	TGCCGTCCGA	TGCCCTCTGA	CGCAGCGGCA	GATAGTTTTT
151	CAGGGCTTCC	ACGCTTTTGC	CGACCAGCGG	CACCTGCCCG	TgTT.GCGCC
201	CTTTGCCGAT	AAcGTGTACC	CACGcyTCGT	CCAAATAGAC	ATCATCTGCA
251	TTCAAGCCGT	GTATCTCGCT	CACGCGCAA	CCGCTGCCGT	ACATCAGTTC
301	GAACAGGGCG	TGGTCGCGCA	CCGCCAGCGG	GTCCGCCCGG	TCCACGGGCA
351	AATCCAGCAT	CCGGTTCAGC	CATTCTTGCG	GCAGGGCTTT	GGGTACGCGC
401	TCGGGCTGCT	TCGGCGGTTT	GATGTCGGCG	GTCCGGTCCG	CGTGCA TCAG
451	GCCGCGCTTT	ACCAGCGAAA	CGCAATACTG	CCGCCAAGAC	GAAAGCTTGC
501	GAGCCAGCGT	CCGTTCCCCC	AAACCGCG...		

```
m032.pep      (partial)
  1  MRRNVXAVAV XRRPLRQTFL DLAALAQARAV PAGKQGFAVR CRLTQRQIVF
51  QGFHAFADQR HLPLAXPFAD NVYPRXVQID IICIQAVYLA HAQTAAVHQF
101 QEGVVAHRQR VAAVHGQIQH PVQPFLRQGF GYALGLLRRF DVGGRVGVHQ
151 AALYQPNAIL PPRRKLASQR PFPQTA...
```

```
a032.seq
  1  ATGCGGCGAA  ACGTGCCTGC  CGTCGCCGTT  TTGCGCCGCC  CATTGCGCCA
51  AACGTTTTTG  GATTGTGGCT  TGGCTCAGGC  GCGTGCCGTT  CCTGCCGGTA
101 AACAGGGCTT  TGCCGTCCGA  TGCCGTCTGA  CGCAGCGGCA  GATAGTTTTT
151 CAGGGCTTCC  ACGCTTTTGC  CGGTACGCGG  AACCTGCCGC  TGCTTGCGTC
201 CTTTGCCGGT  AACGTGTACC  CACGCCTCGT  CCAAATATAC  ATCATCTGCA
251 TTCAAGCCGT  GTATCTCGCT  CACGCGCAA  CCGCTGCCGT  ACATCAGTTC
301 GAACAGCGCG  TGATCGCGCA  CCGCCAGCGG  GTCGCCGCCG  TCACGGGGCA
351 AATCCAGCAT  CCGGTTCCAG  CATTCTGCG  GCAGGGCTTT  GGGTACGCGC
401 TCGGGCTGCT  TCGGCGGTTT  GATGTCGGCG  CTCGGGTCTG  TATGCAGCAG
451 ACCGCGTTTG  ACCAGCCAGG  CGCAATACTG  CCGCAAGAC  GACAGCTTGC
501 GCGCCAGCGT  CCGCGCATTC  AAACCGCGCT  GCACAGCCG  CCGCAACGCC
551 GCCGTA AAA  CGCGCTGCGA  CAAGCCCTGC  GGCACGCCG  CTGCATCTTC
601 AGACGGCATT  TGTGCCAACA  GCGCAAACAG  TTCTTCCAAA  TCGCGCCGGT
651 ATGCCGCCAC  CGTGTGCTCC  GACTTGCCCT  CGCGCACGAT  GTTTTCCAAA
701 TAAGCGTCAA  AATGCGCCGC  AAACCCGTCC  AAAACCATAA  CCGCCCCACA
751 CAAATATCAA  AAAACAGGTG  A
```

```
a032.pep
  1  MRRNVPAAVAV LRRPLRQTFLL DLAALAQARAV PAGKQGFQAVR CRLTQRQIVF
 51  QGFHAFAGQR NLPLLASFAG NVYPRLVQIY IICIQAVYLA HAQTAAVHQF
101  EQRVIAHRQR VAAVHGQIQH PVQPFRLRQG GYALGLLRRF DVGGRVGMQQ
151  TAFDQPGAIL PPRRLARQR PRIQTALRQF PQRRLKIALR QALRHAACIF
201  RRHLCCQRKQ FFQIAPVCRH RVLRLALAH DVFQISVKMRR KPVQNHNRPT
251  QISKKQ*
```

```

              10      20      30      40      50      60
m032.pep  MRRNVXAVAVXRRPLRQTFLDLALAQARAVPAGKQGFVAVRCRLTQRQIVFQGFHAFADQR
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a032      MRRNVPAVAVLRRRPLRQTFLDLALAQARAVPAGKQGFVAVRCRLTQRQIVFQGFHAFAGQR
              10      20      30      40      50      60

```

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	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAHAQTAAVHQFEQGVVAHRQRVAAVHVGQIQH					
a032	NLPLASFAGNVYPRLVQIYIICIQAVYLAHAQTAAVHQFEQRVIAHRQRVAAVHVGQIQH					
	70	80	90	100	110	120
	130	140	150	160	170	
m032.pep	PVQPFRLRQGFYALGLLRRFDVGGRVGVHQAALYQPNAILPPRRKLASQRPFPQTA					
a032	PVQPFRLRQGFYALGLLRRFDVGGRVGMQQTAFDQPGAILPPRRQLARQRPRIQTALRQP					
	130	140	150	160	170	180
a032	PQRRRKIALRQALRHAACIFRRHLCQQRKQFFQIAPVCRHRVLRLLALAHDFQISVKMRR					
	190	200	210	220	230	240

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 032 shows 86.4% identity over a 176 aa overlap with a predicted ORF (ORF 032.ng) from *N. gonorrhoeae*:

m032/g032

	10	20	30	40	50	60
m032.pep	MRRNVXAVAVXRRPLRQTFLDLALAQARAVPAGKQGFVRCRLTQRQIVFQGFHAFADQR					
g032	MRRNVPAAVAVLRRPRFEAFDLALAQARAVPAGKQGFVRCRLTQRQIVFQGFHAFAGQR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAHAQTAAVHQFEQGVVAHRQRVAAVHVGQIQH					
g032	NLTLAPFAGNVYPRFVQIYIICIQAVYLAHAQTAAVHQLERQVVVAHRQRVAAVHVGQIQH					
	70	80	90	100	110	120
	130	140	150	160	170	
m032.pep	PVQPFRLRQGFYALGLLRRFDVGGRVGVHQAALYQPNAILPPRRKLASQRPFPQTA					
g032	PVQPFRLRQGFYALGLLRRFDVGGRVGAHQPAFDQPGAILPPRRQLARQRPVQTALRQP					
	130	140	150	160	170	180
g032	PQRRRKIAPRQVLRHAACIFRRHLCQQCKQFFQIAPVCRNRVLRLLALAHDFQISVKIRR					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 115>:

g033.seq

```

1  ATGGCGGCGG CGGACAAACT CTTGGGCGGC GACCGCCGCA GCGTCGCCAT
51  CATCGGAGAC GCGCGGATGA CGGCGGGGCA GCGGTTTGAA GCCTTGAATT
101 GCGCGGGCGA TATGGATGTG GATTGTCTGG TCGTCCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAAGT CGGCGCGTTG CCCAAATATC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GACTGTTGAG TACCGTCAAA GCGCAAACgg
251 GCAAGGTATT AGACAAAATA CCCGGCGCGA TGGagtTTGC CCAAAAAGTC
301 GAACAcaaa TCAAAACCCT TGCCGAAGAA GCCGAACACG CCAAACAGTC
351 GCTGTCGCTG TTTGAAAATT TCGGCTTCCG CTACACCGGC CCCGTGGACG
401 GACACAACGT CGAGAATCTG GTGGACGTAT TGAAAGACTT GCGCAGCCGC
451 AAAGGCCCTC AGTTGCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGACCCcg tcaAATACCA CGCCGTCGcC aACCTGCcta
551 AAGAAGGCGG GGCGCAAATg ccGTCTGAAA AAGAACCCAA GCCCGCCgCc
601 aaaccgACCT ATACCCAAGT ATTCGGCAA TGGCTGTGCG ACCGGGCGGC
651 GGCAGATTCC CGACTGTTG CGATTACCCC CGCATGCGC GAGGGCAGCG

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701  GACTGGTGGA GTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCGGC
751  ATCGCCGAGC AGCACGCCGT tacCTTTGCC GCGGTTTGG CGTGCGAAGG
801  CATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCCTACG
851  ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTGCCCCG TTTGTTTGCC
901  GTCGACCGTG CGGGCATCGT CGGCGCGGAC GGTCCGACCC ATGCCGGCTT
951  GTACGATTTG AGCTTCTTGC GCTGTGTGCC GAACATGATT GTTGCCGCGC
1001 CGAGCGATGA AAACGAATGC CGCCTGCTGC TTTCGACCTG CTATCAGGCG
1051 GATGCGCCCC CCGCCGTCCG CTATCCGCGC GGCACGGGTA CGGGCGCGCC
1101 GGTTCAGAC GGCATGGAAA CCGTGAAAT CCGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCC TtcatTGCCT TCGGCAGTAT GGTGCGCCAC
1201 GCATTGGCGG TTGCCGAAAA ACTGAACGCC ACCGTCGCCG ATATGCGCTt
1251 cgtcaaaccG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCACg
1301 accGCATCGT TACCCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCGGC
1351 GCGGTCTTGG AAGTGTGGC GAAACACGGC ATCTGCAAAC CCGTTTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGAACA CCGCGATCCG AAAAACTTT
1451 TGGACGATTT GGGTTTGA GTCCGAAGCGG TGAACGCCG GGTGCGCGAG
1501 TGGCTGCCGG ACCGTGATGC GGCAAATTA

```

This corresponds to the amino acid sequence <SEQ ID 116; ORF 033.ng>:

g033.pep

```

1  MAAADKLLGG DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51  MSISPNVGAL PKYLASNVR DMHLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTLAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDLKDLRSR
151 KGPQLLHVIT KKGNGYKLAE NDPVKYHAVA NLPKEGGAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRAAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPNMI VAAPSDENEC RLLSLSTCYQA
351 DAPAAVRYPR GTGTGAPVSD GMETVEIGKG IIRREGEKTA FIAFGSMVAT
401 ALAVAELKNA TVADMRVFKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGG
451 AVLEVLAKHG ICKPVLLLVG ADTVTEHGDP KKLLDDLGLS AEAVERRVRE
501 WLPDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

m033.seq

```

1  ATGGCGGCGG CAGACAACT CTTGGGCAGC GACCGCCGCA GCGTCGCCAT
51  CATCGGCGAC GCGCGGATGA CCGCGGGGCA GCGGTTTGAA GCCTTGAATT
101 GCGCaG.CGA TATGGATGTr GATTGTCTrG TCGTCCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAACGT CCGCGCGCTG CCGAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GCCTGTTGAG TACCGTCAA GCGCAAACGG
251 GCAAGGTATT AGACAAAATA CCCGCGCGCA TGGAGTTTGC CAAAAAGTC
301 GAACACAAAA TCAAAACCCT TGCCGAAGAA GCCGAACACG CCAAACAGTC
351 GCTGTCTTTG TTTGAAAAC TCGGCTTCCG CTACACCGGC CCCGTGGACG
401 GACACAACGT CGAAAATCTG GTGGACGTAT TGAAAGACTT GCGCAGCCGC
451 AAAGGCCCTC AGTTGCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGACCCCG TCAAATACCA CGCCGTCGCC AACCTGCCTA
551 AAGAAAGCGC GCGGCAAATG CCGTCTGAAA AAGAACCCAA GCCCGCCGCC
601 AAACCGACCT ATACCCAAGT GTTCGGCAAA TGGCTGTGCG ACCGGGCGGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG
701 GCTTGGTTGA GTTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCGGC
751 ATCGCCGAGC AGCACGCCGT TACCTTTGCC GCGGTTTGG CTTGCGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTACCCGT TTTGTTTGCC
901 GTCGACCGCG CGGGCATCGT CCGCGCGGAC GGCCCGACCC ATGCCGGTCT
951 GTACGATTTG AGCTTTTTGC GCTGCGTGCC GAACATGATT GTCGCCGCGC
1001 CGAGCGATGA AAACGAATGC CGCCTGTTGC TTTCGACCTG CTATCAGGCA
1051 GACGCGCCCC CCGCCGTCCG CTATCCGCGC GGCACGGGTA CGGGCGCGCC
1101 GGTTCAGAC GGCATGGAAA CCGTGAAAT CCGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCA TTCATTGCCT TCGGCAGTAT GGTGCGCCCC
1201 GCATTGGCGG TTGCCGAAAA ACTGAACGCC ACCGTCGCCG ATATGCGCTT
1251 CGTCAAACCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCACG

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1301 ACCGCATCGT TACCCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCGGC
1351 GCGGTGCTGG AAGTATTGGC GAAACACGGC ATCTGCAAAC CCGTTTGTCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATTT GGGCTTGAGT GCCGAAGCGG TGGAACGGCG TGTGCGCGCG
1501 TGGCTGTCGG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 033>:

m033.pep

```

1 MAAADKLLGS DRRSVAIIGD GAMTAGQAFE ALNCAXDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTAAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLDLRSR
151 KGPQLLHVIT KKGNGYKLAE NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPMNI VAAPSDENEC RLLSTCYQA
351 DAPAAVRYPR GTGTGAPVSD GMETVEIGKG IIRREGEKTA FIAFGSMVAP
401 ALAVAEKLNA TVADMRFVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGG
451 AVLEVLAKHG ICKPVLLLG VADTVTGHGDP KKLLDDLGLS AEAVERRVRA
501 WLSDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

a033.seq

```

1 ATGGCGGCGG CGGACAAACA GTTGGGCAGC GACCGCCGCA GCGTCGCCAT
51 CATCGGCGAC GCGCGATGA CGGCGGTCA GCGGTTTGA GCCTTGAAC
101 GCGCGGCGA TATGGATGTG GATTGCTGG TCGTCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAACGT CCGTGCGTTG CCCAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GACTGTTGAG TACCGTCAA GCGCAAACGG
251 GCAAGGTATT AGACAAATA CCCGCGCGA TGGAGTTTG CCAAAAAGTC
301 GAACATAAAA TCAAAACCCT TGCCGAAGAA GCCGAACACG CCAAACAGTC
351 ACTGTCTTTG TTTGAAACT TCGGCTTCCG CTATACCGGC CCCGTGGACG
401 GACACAACGT CGAAAATCTG GTCGATGTAT TGGAAAGACCT GCGCGGACGC
451 AAAGGCCCGC AGCTTCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGATCCCG TCAAATACCA CGCCGTCGCC AACCTGCCTA
551 AAGAAAGCGC GCGCAAATG CCGTCTGAAA AAGAACCCTA GCCCGCCGCC
601 AAACCGACCT ATACCCAAGT GTTCGGCAA TGGCTGTGCG ACCGGCGGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG
701 GCTTGGTTGA GTTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCGGC
751 ATCGCCGAGC AGCAGCGCGT TACCTTTGCC GCGGTTTGG CTTGCGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAA ACCTGCCCGT TTTGTTTGCC
901 GTCGACCGCG CGGCATCGT CGGCGCGGAC GGCCGACCC ATGCCGTTT
951 GTACGATTTA AGCTTTTTGC GCTGCATTCC GAATATGATT GTCGCCGCGC
1001 CGAGCGATGA AAATGAATGC CGCCTGCTGC TTTGACCTG CTATCAGGCA
1051 GACGCGCCCG CCGCGTCCG CTATCCGCGC GGCACGGGTA CGGGCGTGCC
1101 GGTTCAGAC GGCATGGAAT CCGTGGAAT CGGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCA TTCATTGCCT TCGGCAGTAT GGTGCCCCCT
1201 GCATTGGCGG TCGCCGAAA ACTGAACGCC ACCGTCGCCG ATATGCGCTT
1251 CGTCAAACCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCAGC
1301 ACCGCATCGT TACCCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCAGC
1351 GCGGTGCTGG AAGTGTTGGC GAAACACGGC ATCTGCAAAC CCGTCTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATTT GGGCTTGAGT GCCGAAGCGG TGGAACGGCG TGTGCGCGCG
1501 TGGCTGTCGG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 120; ORF 033.a>:

a033.pep

```

1 MAAADKQLGS DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTAAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLEDLRGR
151 KGPQLLHVIT KKGNGYKLAE NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA

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301 VDRAGIVGAD GPTHAGLYDL SFLRCIPNMI VAAPSDENEC RLLSTCYQA
 351 DAPAAVRYPR GTGTGVPVSD GMETVEIGKG IIRREGEKTA FIAFGSMVAP
 401 ALAVAGKLN TVADMRFVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGS
 451 AVLEVLAKHG ICKPVLLLG VADTVTGHGDP KKLLDDLGLS AEAVERRVRA
 501 WLSDRDAAN*

m033/a033 98.4% identity over a 509 aa overlap

m033.pep	10	20	30	40	50	60
	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAXDMDVDLLVVLNDNEMSI SPNVGAL					
a033	MAAADKQLGSDRRSVAIIGDGAMTAGQAFEALNCAGDMDVDLLVVLNDNEMSI SPNVGAL					
	10	20	30	40	50	60
m033.pep	70	80	90	100	110	120
	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL					
a033	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL					
	70	80	90	100	110	120
m033.pep	130	140	150	160	170	180
	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKG PQLLHVITKKGNGYKLAENDPVKYHAVA					
a033	FENFGFRYTGPVDGHNVENLVDVLEDLRGRKG PQLLHVITKKGNGYKLAENDPVKYHAVA					
	130	140	150	160	170	180
m033.pep	190	200	210	220	230	240
	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSR LVAITPAMREGSGLVEFEQ					
a033	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSR LVAITPAMREGSGLVEFEQ					
	190	200	210	220	230	240
m033.pep	250	260	270	280	290	300
	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNL PVLFA					
a033	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNL PVLFA					
	250	260	270	280	290	300
m033.pep	310	320	330	340	350	360
	VDRAGIVGADGPTHAGLYDLSFLRCVPNMIVAAPSDENEC RLLSTCYQADAPAAVRYPR					
a033	VDRAGIVGADGPTHAGLYDLSFLRCIPNMIVAAPSDENEC RLLSTCYQADAPAAVRYPR					
	310	320	330	340	350	360
m033.pep	370	380	390	400	410	420
	GTGTGAPVSDGMETVEIGKGIIRREGEKTA FIAFGSMVAPALAVAEKLNATVADMRFVKP					
a033	GTGTGVPVSDGMETVEIGKGIIRREGEKTA FIAFGSMVAPALAVAGKLNATVADMRFVKP					
	370	380	390	400	410	420
m033.pep	430	440	450	460	470	480
	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLG VADTVTGHGDP					
a033	IDEELIVRLARSHDRIVTLEENAEQGGAGSAVLEVLAKHGICKPVLLLG VADTVTGHGDP					
	430	440	450	460	470	480
m033.pep	490	500	510			
	KKLLDDLGLSAEAVERRVRAWLSDRDAANX					
a033	KKLLDDLGLSAEAVERRVRAWLSDRDAANX					
	490	500	510			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 033 shows 98.4% identity over a 509 aa overlap with a predicted ORF (ORF 033.ng) from *N. gonorrhoeae*:

m033/g033

m033 . pep	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAXDMDVDLLVVLNDNEMSI SPNVGAL	60
	:	
g033	MAAADKLLGGDRRSVAIIGDGAMTAGQAFEALNCAGDMDVDLLVVLNDNEMSI SPNVGAL	60
m033 . pep	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEEAEHAKQSLSL	120
g033	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEEAEHAKQSLSL	120
m033 . pep	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKGQPLLHVITKKNGYKLAENDPVKYHAVA	180
g033	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKGQPLLHVITKKNGYKLAENDPVKYHAVA	180
m033 . pep	NLPKESAAQMPSEKEPKPAKPTYTQVFGKWLCDRAAADSRSLVAITPAMREGSGLVEFEQ	240
	:	
g033	NLPKEGGAQMPSEKEPKPAKPTYTQVFGKWLCDRAAADSRSLVAITPAMREGSGLVEFEQ	240
m033 . pep	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVLF	300
g033	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVLF	300
m033 . pep	VDRAGIVGADGPTHAGLYDLSFLRCVPMIVAAPSDENECRLLLSTCYQADAPAAVRYPR	360
g033	VDRAGIVGADGPTHAGLYDLSFLRCVPMIVAAPSDENECRLLLSTCYQADAPAAVRYPR	360
m033 . pep	GTGTGAPVSDGMETVEIGKGIIRREGKTAFFIAGSMVAPALAVAELNATVADMRVFKP	420
g033	GTGTGAPVSDGMETVEIGKGIIRREGKTAFFIAGSMVATALAVAELNATVADMRVFKP	420
m033 . pep	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLGVADTVTGHGDP	480
g033	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLGVADTVTEHGDP	480
m033 . pep	KKLLDDLGLSAEAVERRVRAWLSDRDAANX	510
g033	KKLLDDLGLSAEAVERRVREWLPDRDAANX	510

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 121>:

g034 . seq

1	ATGAGCCGTT	TATGGTTTTT	TGCCGTAAAA	AACATTATAA	TCCGCCTTAT
51	TTACCTATTG	CCCAAGGAGA	CACAAATGGC	ACTCGTATCC	ATGCGCCAAC
101	TGCTTGACCA	CGCCGCCGAA	AACAGCTACG	GCCTGCCCGC	GTTCAACGTC
151	AACAACCTCG	AACAAATGCG	CGCCATTATG	GAAGCCGCCG	ACCAAGTCAA
201	CGCGCCCGTC	ATCGTACAGG	CGAGCGCAGG	TGCGCGCAAA	TACGcggGCG
251	CGCCGTTTTT	GCGCCACCTG	ATTCTGGCGG	CAGTCGAAGA	ATTTCCGCAC
301	ATCCCCGTCG	TGATGCACCA	AGACCACGGC	GCATCGCCCG	ACGTgtgCCA
351	ACGCTCCATC	CAACTGGGCT	TCTCCTCCGT	GATGATGGAC	GGCTCTTTGC
401	TCGAAGACGG	CAAAACCCCT	TCTTCTTACG	AATACAACGT	CAACGCCACC
451	CGTACCGTCG	TCAACTTCTC	CCACGCCTGC	GGCGTGTCCG	TCGAAGGCGA
501	AATCGGCGTA	TTGGGCAACC	TCGAAACCGG	CGAAGCAGGC	GAAGAAGACG
551	GAGTGGGCGC	GGCAGGCAA	CTCTCACACG	ACCAAATGCT	CACCAGCGTT
601	GAAGATGCCG	TGCGTTTTCG	TAAAGATACC	GGCGTTGACG	CATTGGCGAT
651	TGCCGTCGGC	ACCAGCCACG	GCGCATACAA	ATTCAACCGT	CCGCCACAG

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701 GCGACGTATT GCGTATCGAC CGCATCAAGG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGgctCCAGC TCCGTTCCGC AAGAatgGCT
801 GAAAGTCATC AACGAATACG GCGGCAATAT CGGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG CAAAGTCAAC
901 ATCGATACCG ACCTGCGCCT CGCTTCCACC GCGCGGTAC GCCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TTGATCCGCG CAAATACTTG GGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GTTATCTTGC GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAT CAAACCTGTT TCGTTGGAAA AAATGGCAAG
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 122; ORF 034.ng>:

g034.pep

```

1 MSRLWFFAVK NIIIRLIYLL PKETQMALVS MRQLLDHAAE NSYGLPAFNV
51 NNLEQMRAIM EAADQVNAPV IVQASAGARK YAGAPFLRHL ILAAVEEFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSSVMMD GSLEEDGKTP SSYEYNVNAT
151 RTVVNFHSHAC GVSVEGEIGV LGNLETGEAG EEDGVGAAGK LSHDQMLTSV
201 EDAVRFVKDT GVDALAIAVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKVI NEYGGNIGET YGVPVEEIVE GIKHGVRKVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPRKYL GKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMASRYA KGELNQIVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 123>:

m034.seq (partial)

```

1 ATGAGCTGTT TATGGTTTTT TGCTGTAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA wACAGCTACG GCyTGCCGGC GTTCAACGTC
151 AACAACTCG wACAGATGCG CGCCATCATG GAGGCTGCAG ACCAAGTCGA
201 CGCCCCCGTC ATCGTACAGG CGAGTGCCGG TCGCGCAAA TATGCGGGTG
251 CGCCGTTTTT ACGCCACCTG ATTTTGGCGG CTGTCAAGT ATTTCCACAC
301 ATCCCCGTCG TCATGCACCA AGACCACGGC GCATCACCCG ACGTGTGCCA
351 ACGTCCATC CAACTGGGCT TCTCCTCTGT AATGATGGAC GGCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTACG AATACAACGT CAACGCCACA
451 CGTACCGTGG TTAACCTCTC CCACGCTTGC GCGGTATCCG TTGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAAACCGG CGATGCAGGC GAAGAAGACG
551 GTGTAGGCGC AGTGGGCAAA CTTTCCCACG ACCAAATGCT GACCAGCGTC
601 GAAGATGCCG TATGTTTCGT TAAAGATACC GCGGTTGACG CATTGGCTAT
651 TGCCGTCGGC ACCAGCCACG GCGCATACAA ATTCACCCGT CCGCCCACAG
701 GCGATGTATT ACGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA C...

```

This corresponds to the amino acid sequence <SEQ ID 124; ORF 034>:

m034.pep (partial)

```

1 MSCLWFFAVK NIIIRLIYLL PKETQMALVS MRQLLDHAAE XSYGLPAFNV
51 NNLXQMRAIM EAADQVDAPV IVQASAGARK YAGAPFLRHL ILAAVEVFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFHSHAC GVSVEGEIGV LGNLETGDAG EEDGVGAVGK LSHDQMLTSV
201 EDAVCFVKDT GVDALAIAVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMH...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 125>:

a034.seq

```

1 ATGAGCCGTT TATGGTTTTT TGCCGCAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA AACAGCTACG GCCTGCCCCG GTTCAACGTC
151 AACAACTCG AACAAATGCG CGCCATTATG GAAGCCGCCG ACCAAGTCAA
201 CGCGCCCGTC ATCGTACAGG CGAGCGCAGG TCGCGCAAA TACGCGGGCG
251 CGCCGTTTTT GCGCCACCTG ATTTTGGCGG CTGTCAAGA ATTTCCGCAC
301 ATCCCCGTCG TGATGCACCA AGACCACGGC GCATCGCCCG ACGTGTGCCA
351 ACGTCCATC CAACTGGGCT TTTCTCCGT GATGATGGAC GGCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTATG AATACAACGT CAACGCCACC

```

```

451 CGTACCGTGG TTAATTTCTC CCACGCCTGC GCGGTATCCG TTGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAACTGG CGAAGCCGGC GAAGAAGACG
551 GTGTAGGCGC AGTGGGCAAA CTTTCCACG ACCAAATGCT CACCAGCGTC
601 GAAGATGCCG TCGGTTTCGT TAAAGATACC GCGGTTGACG CATTGGCGAT
651 TGCCGTCGGC ACCAGCCACG GCGGTACAA ATTCACCCGT CCGCCCACAG
701 GCGACGTGTT GCGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGGCTCCAGC TCCGTTCCGC AAGAATGGCT
801 GAAAGTCATC AACGAATACG GCGGCAATAT CGGCGAAACC TACGGCGTGC
851 CGGTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG TAAAGTCAAC
901 ATCGATACCG ACTTGCGCCT TGCTCCACC GCGCGGTAC GCCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TCGATCCGCG CAAATATTTG AGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCTCGACC GCTACCTCGC GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAT CAAACCGGTT TCCTTGAAA AAATGGCAA
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 126; ORF 034.a>:

```

a034.pep
  1 MSRLWFFAAK NIIIRLIYLL PKETQMALVS MRQLLDHAAE NSYGLPAFNV
 51 NNLEQMRAIM EAADQVNPV IVQASAGARK YAGAPFLRHL ILAAVEEFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFHAC GVSVEGEIGV LGNLETGEAG EEDGVGAVGK LSHDQMLTSV
201 EDAVRVFKDT GVDALAIAGV TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKV NEYGGNIGET YGVPVEEIVE GIKHGVRKVN
301 IDTLRLAST GAVRRYLAEN PSDFDPRKYL SKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMANRYA KGELNQIVK*

```

m034/a034 96.9% identity over a 257 aa overlap

```

              10      20      30      40      50      60
m034.pep    MSCLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNNLXQMRAIM
              || |||||:||||||||||||||||||||||||||||||||||||||||||
a034         MSRLWFFAAKNIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNNLEQMRAIM
              10      20      30      40      50      60

              70      80      90      100     110     120
m034.pep    EAADQVDAPVIVQASAGARKYAGAPFLRHLILAAVEVFPHIPVVMHQDHGASPDVCQRSI
              |||||:||||||||||||||||||||||||||||||||||||||||||
a034         EAADQVNPVIVQASAGARKYAGAPFLRHLILAAVEEFPHIPVVMHQDHGASPDVCQRSI
              70      80      90      100     110     120

              130     140     150     160     170     180
m034.pep    QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVNFHACGVSVEGEIGVLGNLETGDAG
              |||||:||||||||||||||||||||||||||||||||||||||||||
a034         QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVNFHACGVSVEGEIGVLGNLETGEAG
              130     140     150     160     170     180

              190     200     210     220     230     240
m034.pep    EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAIAGVTSHGAYKFTRPPTGDVLRID
              |||||:||||||||||||||||||||||||||||||||||||||||||
a034         EEDGVGAVGKLSHDQMLTSVEDAVRFVKDTGVDALAIAGVTSHGAYKFTRPPTGDVLRID
              190     200     210     220     230     240

              250
m034.pep    RIKEIHQALPNTHIVMH
              |||||
a034         RIKEIHQALPNTHIVMHGSSSVPQEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVRKVN
              250     260     270     280     290     300

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 034 shows 96.5% identity over a 257 aa overlap with a predicted ORF (ORF 034.ng) from *N. gonorrhoeae*:

m034/g034

m034.pep	MSCLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNNLXQMRAIM	60
g034	MSRLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNNLEQMRAIM	60
m034.pep	EAADQVDAPVIVQASAGARKYAGAPFLRHLILA AVEVFPHIPVVMHQDHGASPDVCQRSI	120
g034	EAADQVNAPVIVQASAGARKYAGAPFLRHLILA AVEEFPHIPVVMHQDHGASPDVCQRSI	120
m034.pep	QLGFSSVMMDGSLMEDGKTPSSYEYNVNATRTVVNF SHACGVSVEGEIGVLGNLETGDAG	180
g034	QLGFSSVMMDGSLLEDGKTPSSYEYNVNATRTVVNF SHACGVSVEGEIGVLGNLETGEAG	180
m034.pep	EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAI AVGTSHGAYKFTRPPTGDVLRID	240
g034	EEDGVGAAGKLSHDQMLTSVEDAVRFVKDTGVDALAI AVGTSHGAYKFTRPPTGDVLRID	240
m034.pep	RIKEIHQALPNTHIVMH	257
g034	RIKEIHQALPNTHIVMHGSSSVPQEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVRKVN	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 127>:

g036.seq

1	ATGCTGAAGC	CGTGTTCGGT	ATACAGTGCC	TGTGCGGCGG	cgttgCCTGC
51	GCGGACTTCG	AGCAGCAGGC	GTTGCGTGCC	TTCGGGCAGA	TGTGCGTACC
101	AATATTCGAG	CAGGGCGGAC	GCAACGCCCC	GTCGGCGGCA	TTCGGGCGCG
151	GTGGCAATCA	GGTGCAGTTC	GGATTCGTTC	GGCAGGTTCT	GCCAAACGAT
201	AAAGGCGGCA	ATCCTGCCGT	CTTTTCCGC	AAGGAAAACC	TGTTCCGACG
251	CGGAAACAAG	CGCGGACTCA	AATTGGCGTT	GCGTCCACGC	GGACGGGTG
301	CAGACGGTAT	CGAGCGCGGC	CAGTGCAGCG	CAGTCCGACG	GTGAGGCTGG
351	GCGGATGTTT	ATGTTCGTGC	CTTCCGTTC	GCCTGTCTT	TGGCAGTCAG
401	GGCGATTTC	TTGCGGACGT	AGAGCAGTTC	GGCGTGTGCC	GCGCCAGTTG
451	CGGGATAGCC	GCCGCCGAGG	GCGAGCGCGA	GAAAATCGGC	GGCGGTCGCG
501	ATATCGGGTT	TGCCTGAGAA	GGGCGGACGG	TTTTCCAGTG	CGAACGCACT
551	GCCGATGCCG	TCTGAAAAGA	CGTACCCCTC	GGGGAGGGCA	ATGTCTGCCG
601	CCCTACCGAC	TTGATAATCG	CTCAAACGGC	GGCGGTTTCA	CGTGTCTGAA
651	CACGCATAAA	ACACTTCGCC	CATACGCGCG	TCCGCAGCGG	CGAGTATGCA
701	GCTTTGCGGC	GGCGGCAGCG	AGGCGGCGGC	ATCGAGCGTG	GGGATGCCGA
751	TTAAAGGCGT	GTCGAACGGC	GTTGCCAAAC	CTTGCGCCAC	GCCGATGCCG
801	ATACGCAGTC	CGGTAA			

This corresponds to the amino acid sequence <SEQ ID 128; ORF 036.ng>:

g036.pep

1	MLKPCLVYSA	CAAALPARTS	SSRRCVPSGR	CAYQYSSRAD	ATPRRRHSGA
51	VAIRCSSDSS	GRFCQTIKAA	ILPSFSARKT	CSDGETSADS	NWRCVHADGL
101	QTVSSAASAA	QSDGEAGRMF	MFVPSVPPVL	WQSGRFCCGR	RAVRRVPRQL
151	RDSRRRGRAR	ENRRRSAYRV	CLRRADGFPV	RTHCRCLKR	RTPRGGQCLP
201	PYRLDNRSNG	GGACRTTHK	TLRPYARPQR	RVCSFAAAAA	RRRHRAWGCR
251	LKACRTALPN	LAPRRCRYAV	R*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 129>:

m036.seq

1	ATGCTGAAGC	CGTGCGCCGT	GTACAGTGCC	TGTGCGGCGG	TGTTGCCTGC
51	ACGGACTTCG	AGCAGCAGGC	GTTGCGTGTC	TTCGGGCAGA	TGTGTGAACC
101	AATATTCGAG	CAGGGCGGAC	GCAATTCCTT	GGCGGCGGCA	TTCGGGCGCG
151	GTGGCAATCA	GGTGCAGTTC	GGATTCGTTC	GGCAGGTTCT	GCCAAACGAT
201	AAAGGCGGCA	ATCCCg.CGT	CTTTTCCGC	AAGGAAAACC	TGTTCCGACG
251	GCGAAACCAG	TGCGGACTCA	AATTGGCGTT	GCGTCCATGC	GGACGGGTG
301	CAGACGGCAT	CGAGTGCGGC	CAGCTCCTCA	CAATCGGCAC	AAACGGCACG

```

351 GCGGATGTTT ACGGGCGCGC TCTCCGTTTC GCCTGTTCTT TGGCAGTCAG
401 GCGGATTTTG TTGCGGACGT AGAGCAAACC GCGGTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTTGGCT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601 CCCGCCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA AACTTCGCC CATAAGAGCG TCCGTAGCGG CAAGGATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGGGGT ATCAAACGGC GTTGCCAAAC CCTGAGCTAC ACCGATGCCG
801 ATACGCAGTC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 130; ORF 036>:

```

m036.pep
1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPXSFSAARKT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNRPWLEPMR ESRRQSAYPV CLRTAELLPA RTRCLCRLKR RIPPAAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*R QGCSFAAAAA RRRHRARVRR
251 LRGYQTALPN PELHRCRYAV R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 131>:

```

a036.seq
1 ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTTCCTGCG
51 ACGGACTTCG AGCAGCAGGC GTTGCGTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GCGGCGGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCCGCCGT CTTTTCCGC AAGGAAAACC TGTTCGGACG
251 GCGAAACCAG TGCGGACTCA AATTGGCGTT CCGTCCACGC GGACGGGTTG
301 CAGACGGCAT CGAGCGCGGC GAGTGCGGCG CAATCGGCAT AAACGGCGCG
351 GCGGATGTTT ACAGGCGCGC CCTCCGTTCC GCCTGTTCTT TGGCAGTCAA
401 GGCGATTTTG TTGCGGACGT AGAGCAGCTC GCGGTGTGCC GCAGCGACGG
451 CGGGAAAACC GCCTTCAGCC GCCAGATGA GGAAGTCGGC GCGGTCGGC
501 ATATCGGGTT TGCCTGAGAA GGGCGGACGG TTTTCCAGCG CGAACGCATT
551 GCCGATGCCG TCTGAAAAGG CGCATCCTTC CGGCAGCCGG ATGTCTGCCG
601 CCCGACCGAC CTGATAATCG CTCAAACGGC GCGGTTTCAG CGTGTGGAAC
651 CATGCATAAA AACTTCGCC CATAAGAGCG TCCGCAGCGG CAAGGATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGAGT ATCAAACGGC GTTGCCAAAC CTTGCGCCAC GCCGATGCCG
801 ATACGCAGTC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 132; ORF 036.a>:

```

a036.pep
1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPPSFSARKT CSDGETSADS NWRCVHADGL
101 QTASSAASAA QSA*TARRMF TGAPSVPPVL WQSRRFCCGR RAARRVPQRR
151 RENRLQPPD* GSRRRSAYRV CLRRADGFPA RTHCRCLKR RILPAAGCLP
201 PDRPDNRSNG GGSACRTMHK TLRPYVRPQR QGCSFAAAAA RRRHRARVRR
251 LKEYQTALPN LAPRRCRYAV P*

```

m036/a036 85.6% identity over a 270 aa overlap

```

          10      20      30      40      50      60
m036.pep MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAIIPWRRHSGAVAIRCSSDSS
|||||
a036      MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAIIPWRRHSGAVAIRCSSDSS
          10      20      30      40      50      60

          70      80      90     100     110     120
m036.pep GRFCQTIKAAIPXSFSAARKTCS DGETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF
|||||
a036      GRFCQTIKAAIPPSFSARKTCS DGETSADSNWRCVHADGLQTASSAASAAQSAXTARRMF
          70      80      90     100     110     120

```

221

	130	140	150	160	170	180
m036.pep	TGALSVRPVLWQSGRFCCGRRANRRVRHGRQDNRFWLPMPRESRRQSAYPVCLRTAELLPA					
a036	TGAPSVPPVLWQSGRRFCCGRRRAARVPQRRRENRLQPPDXGSRRRSAYRVCLRRADGFPA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m036.pep	RTRCLCRLKRRIPPAAGCLPPARPDNRSNGGSSAYRTMHKTLRPYERXPXQGCSTFAAAAA					
a036	RTHCRCLKRRILPAAGCLPPDRPDNRSNGGSSACRTMHKTLRPYVRPQXQGCSTFAAAAA					
	190	200	210	220	230	240
	250	260	270			
m036.pep	RRRHRARVRRRLRGYQTALPNPELHRCRYAVRX					
a036	RRRHRARVRRRLKEYQTALPNLAPRRCRYAVPX					
	250	260	270			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 036 shows 74.9% identity over a 271 aa overlap with a predicted ORF (ORF 036.ng) from *N. gonorrhoeae*:

m036/g036

	10	20	30	40	50	60
m036.pep	MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAI PWRRHSGAVAIRCSSDSS					
g036	MLKPCLVYSACAAALPARTSSSRRCVPSGRCAYQYSSRADATPRRRHSGAVAIRCSSDSS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m036.pep	GRFCQTIKAAIPXSFSARKTCS DGETSADSNWRCVHADGLQTASSAASSSSQSAQTARRMF					
g036	GRFCQTIKAAILPSFSARKTCS DGETSADSNWRCVHADGLQTVSSAASAAQSDGEAGRMF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m036.pep	TGALSVRPVLWQSGRFCCGRRANRRVRHGRQDNRFWLPMPRESRRQSAYPVCLRTAELLPA					
g036	MFVPSVPPVLWQSGRFCCGRRARVRPQRLDSRRRGRARENRRRSAYRVCLRRADGFV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m036.pep	RTRCLCRLKRRIPPAAGCLPPARPDNRSNGGSSAYRTMHKTLRPYERXPXQGCSTFAAAAA					
g036	RTHCRCLKRRTPRGGQCLPPYRLDNRSNGGSSACRTTHKTLRPYARPQRRVCSFAAAAA					
	190	200	210	220	230	240
	250	260	270			
m036.pep	RRRHRARVRRRLRGYQTALPNPELHRCRYAVRX					
g036	RRRHRAWGCRLKACRTALPNLAPRRCRYAVRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 133>:

m036-1.seq

```

1  ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTTCCTGTC
51  ACGGACTTCG AGCAGCAGGC GTTGCCTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCCCTCGT CTTTTCCGC AAGGAAAACC TGTTCGGACG
251 CGGAAACAG TGCGGACTCA AATTGGCGTT GCGTCCATGC GGACGGGTTG
301 CAGACGGCAT CGAGTGCGGC CAGCTCCTCA CAATCGGCAC AAACGGCAGC

```

222

```

351 GCGGATGTTT ACGGGCGCGC TCTCCGTTTC GCCTGTTCTT TGGCAGTCAG
401 GGCATTTTGT TTGCGGACGT AGAGCAAACC GCGGTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTTGGCT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601 CCCGCCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA ACACTTCGCC CATACGAGCG TCCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 134; ORF 0036-1>:

```

m036-1.pep
  1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
 51 VAIRCSSDSS GRFCQTIKAA IPPSFSARKT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNRPLPMR ESRRQSAYPV CLRTAELLPA RTRCLCRLKR RIPPAAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*

```

m036-1/g036 76.8% identity in 228 aa overlap

	10	20	30	40	50	60
m036-1.pep	MLKPCAVYSACA	AVLPARTSSS	RRCVSSGR	CVNQYSSRAD	AIPWRRHSGA	VAIRCSSDSS
		:				
g036	MLKPCLVYSACA	ALPARTSSS	RRCVPSGR	CAYQYSSRAD	ATPRRRHSGA	VAIRCSSDSS
	10	20	30	40	50	60
	70	80	90	100	110	120
m036-1.pep	GRFCQTIKAA	IPPSFSARKT	CSDGETSADS	NWRCVHADGL	QTASSAASSS	QSAQTARRMF
g036	GRFCQTIKAA	ILPSFSARKT	CSDGETSADS	NWRCVHADGL	QTVSSAASAA	QSDGEAGRMF
	70	80	90	100	110	120
	130	140	150	160	170	180
m036-1.pep	TGALSVRPVL	WQSGRFCCGR	RANRRVRHGR	QDNRPLPMR	ESRRQSAYPV	CLRTAELLPA
	:				:	:
g036	MEVPSVPVL	WQSGRFCCGR	RAVRRVPR	QLRDSRRR	GRARENRRR	SAYRVCLRRADGFPV
	130	140	150	160	170	180
	190	200	210	220	229	
m036-1.pep	RTRCLCRLK	RRIPPAAGCL	PPARPDNRS	NGGSSAYRT	MHKTLRPYER	XPX
	:					
g036	RTHCRCLK	RRTPRGGQCL	PPYRLDNRS	NGGGSACR	THKTLRPYAR	PQRRVCSFAAAAA
	190	200	210	220	230	240
g036	RRRHRAWGC	RKLACRTAL	PNLAPRRC	RYAVRX		
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 135>:

```

g038.seq
  1 ATGACTGATT TCCGCCAAGA TTCTCTCAA TTCTCCCTCG CCCAAATGT
 51 TTTGAAATTC GGCGAATTTA CCACCAAAGC CGGACGGCGG TCGCCCTATT
101 TCTTCAATGC CGGCCTCTTC AACGACGGCG CGTCCACGCT GCAACTGGCA
151 AAATTCTATG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201 GTTCGGCCCC GCCTACAAAG GCATTATTTT GCGCGCGGCA ACCGCGATGA
251 TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301 GCCAAAGACC GCGGCGAAGG CGGCGTGTG GTCGGCGCGC CGCTTAAAGG
351 GCGCGTGCTG ATTATCGACG ACGTGATTC CGCCGGCACA TCCGTACGCG
401 AATCAATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGCG CGGTGTGCGC
451 ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTAAATTGT CCGCCGTTCA
501 GGAAGTGGAA AAACAATACG GCCTGCCCGT CGCCCCATC GCCAGCCTGA
551 ACGATTTGTT TATCCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601 GAACCCGTCC GCACCTACCG CCGGCAGTAC GCGGTAGAAT AA

```


This corresponds to the amino acid sequence <SEQ ID 136; ORF 038.ng>:

```
g038.pep
  1  MTDFRQDFLK FSLAQNVLFK GEFTTKAGRR SPYFFNAGLF NDGASTLQLA
  51  KFYAQSIIES GIRFDMFLFGP AYKGIILAAA TAMMLAEKGV NVPPFAYNRKE
 101  AKDRGEGGVL VGAPLKGRVL IIDVISAGT SVRESIKLIE AEGATPAGVA
 151  IALDRMEKGT GKLSAVQEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
 201  EPVRTYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 137>:

```
m038.seq
  1  ATGACCGATT TCCGCCAAGA TTCTCCTCAA TTCTCCCTCG CCCAAAATGT
  51  TTTGAAATTC GGCGAATTCA CCACCAAGGC AGGACGGCGG TCGCCCTATT
 101  TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
 151  AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
 201  GTTCGGTCCC GCCTACAAAG GCATTATTTT GCGGCGGCA ACCGCGATGA
 251  TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
 301  GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGGCGCGC CGCTTAAAGG
 351  GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
 401  AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGC CGGTGTCGCC
 451  ATCGCGCTCG ATCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
 501  GGAAGTGGAA AAACAATACG GCTGCCCCGT CGCCCCCATC GCCAGCCTGA
 551  ACGATTTGTT TATTCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
 601  GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 138; ORF 038>:

```
m038.pep
  1  MTDFRQDFLK FSLAQNVLFK GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
  51  KFYAQSIIES GIRFDMFLFGP AYKGIILAAA TAMMLAEKGV NVPPFAYNRKE
 101  AKDHGEGGVL VGAPLKGRVL IIDVISAGT SVRESIKLIE AEGATPAGVA
 151  IALDRMEKGT GELSAVQEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
 201  EPVRAYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 139>:

```
a038.seq
  1  ATGACCGATT TCCGCCAAGA TTCTCCTCAA TTCTCCCTCG CCCAAAATGT
  51  TTTGAAATTC GGCGAATTCA CCACCAAGGC CGGACGGCGG TCGCCCTATT
 101  TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
 151  AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
 201  GTTCGGCCCC GCCTACAAAG GCATTATTTT GCGGCGGCA ACCGCGATGA
 251  TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
 301  GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGGCGCGC CGCTTAAAGG
 351  GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
 401  AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGC CGGTGTCGCC
 451  ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
 501  GGAAGTGGAA AAACAATACG GCCTGCCCCGT CGCCCCCATC GCCAGCCTGA
 551  ACGATTTGTT TATTCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
 601  GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 140; ORF 038.a>:

```
a038.pep
  1  MTDFRQDFLK FSLAQNVLFK GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
  51  KFYAQSIIES GIRFDMFLFGP AYKGIILAAA TAMMLAEKGV NVPPFAYNRKE
 101  AKDHGEGGVL VGAPLKGRVL IIDVISAGT SVRESIKLIE AEGATPAGVA
 151  IALDRMEKGT GELSAVQEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
 201  EPVRAYRRQY GVE*
```

m038/a038 100.0% identity over a 213 aa overlap

```

          10          20          30          40          50          60
m038.pep  MTDFRQDFLK FSLAQNVLFK GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA KFYAQSIIES
```

224

```

|||||
a038      MTDFRQDFLKFSLAQNVLKFGFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
          10      20      30      40      50      60

          70      80      90      100     110     120
m038.pep  GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
          |||||||
a038      GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
          70      80      90      100     110     120

          130     140     150     160     170     180
m038.pep  IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
          |||||||
a038      IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
          130     140     150     160     170     180

          190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
          |||||||
a038      ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
          190     200     210

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 038 shows 98.1% identity over a 213 aa overlap with a predicted ORF (ORF 038.ng) from *N. gonorrhoeae*:

m038/g038

```

          10      20      30      40      50      60
m038.pep  MTDFRQDFLKFSLAQNVLKFGFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
          |||||||
g038      MTDFRQDFLKFSLAQNVLKFGFTTKAGRRSPYFFNAGLFNDGASTLQLAKFYAQSIIES
          10      20      30      40      50      60

          70      80      90      100     110     120
m038.pep  GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
          |||||||
g038      GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDRGEGGVLVGAPLKGRVL
          70      80      90      100     110     120

          130     140     150     160     170     180
m038.pep  IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
          |||||||
g038      IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGKLSAVQEVEKQYGLPVAPI
          130     140     150     160     170     180

          190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
          |||||||
g038      ASLNDLFILLQNNPEFGQFLEPVRTYRRQYGVEX
          190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 141>:

```

g039.seq
1  ATGCCGTC CG AACCACCTGC CGCTTCAGAC GGCATCAAAC CGACACACAC
51 CGAGAAAACA TCATGCCCCG CTGTTTCTGT CCGCACTGCA AAACCCGCTT
101 CTGGGTCAA GAAAccagC TCAAcgtCgC ccaagGCTTC GTCGTCTgcc
151 aaAAAtgcga agGGCTgttt aaAgcctaaaG accAtctggc aaGcacGAAA
201 gaacctatat tcaacgattg gcccgaagct gtttcgggat gTcaaaCTCG

```

```

251 TCcaccgcAT cggcagcgac gccattagca aGAaacagat gtccccgcgac
301 gaaatCgccc atatacctcaa cggcggtaca acCCTGCACG ATACGCCGCC
351 CGCAACCGCC GCTGCCGCac ctGCCGCCGC ACCGCaggTT TCCGTACCGC
401 CCGCCCGTCA GGAAGGGCTC AACTGGACTA TTGCAACCCT GTTCGCACTT
451 ATCGTCCTCA TTATGCAGCT TTCCTACCTC TTCATCCTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 142; ORF 039.ng>:

```

g039.pep
  1 MPSEPPAASD GIKPTHTEKT SCPPVSVRTA KPASGSKKPS STSPKASSSA
 51 KNAKGCLKPK TIWQARKNLY STIGPKLFRD VKLVHRIGTH AISKKQMSRD
101 EIADILNGGT TLHDTTPATA AAAPAAAPQV SVPPARQEGT NWTIATLFAL
151 IVLIMQLSYL FIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 143>:

```

m039.seq
  1 ATGCCGTCCG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
 51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCACTGCA AAACCGTCT
101 CTGGGTCAAA GAAACCCAAC TCAATGTCGC CGnnnnnnnnn nnnnnnnnnn
151 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
201 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnCCC GAGGCTGTTT
251 CGGATGTCAA ACTCGTTCAC CGTATCGGCA CGCGCGCCAT CGGCAAGAAA
301 CAGATTTCCC GTGACGAAAT CGCCGGCATC CTCAACGGCG GTACAACCCA
351 GCCCCGATAT CCGCCCGCAA CCGCCGCCAC CCCTGCTGCC GCACCGCAGG
401 TTACCGTACC GCCCGCCGCG CCCGCCCGTC AGGATGGGTT CAACTGGACG
451 ATTGCAACCC TGTGTGCCCT TATCGTCCTC ATTATGCAGC TTTCTACCT
501 CGTCATCCTA TGA

```

This corresponds to the amino acid sequence <SEQ ID 144; ORF 039>:

```

m039.pep
  1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPXXXXXX
 51 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX EAVSDVKLVH RIGTRAIGKK
101 QISRDEIAGI LNGGTTQPD I PPATAATPAA APQVTVPAA PARQDGFNWT
151 IATLFALIVL IMQLSYLVIL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 145>:

```

a039.seq
  1 ATGCCGTCTG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
 51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCACTGCA AAACCGTCT
101 CTGGGTCAAA GAAACCCAAC TCAATGTCGC CCAAGGCTTC GTCGTCTGCC
151 AAAAATGCGA AGGAATGTTT AAAGCCAAAG ACCATCTGGC AAGCACGAAA
201 GAACCCATAT TCAACGATT. TGCCCGAAGC TGTTCGGAT GTCAAACCTG
251 TTCACCGCAT CGGCACGAGC GCCATCGGCA AGAAACAGAT TTCCCGTGAC
301 GAAATCGCCG GCATCCTCAA CGGCGGCACA ACCCAGCCCG ATATTCCGCC
351 CGCAACCGCC GCCACCCCTG CTGCCGCACC GCAGGTACC GTACCGCCCG
401 CCGCGCCCGC CCGTCAGGAT GGGTTCAACT GGACGATTGC AACCTGTTT
451 GCCCTTATCG TCCTCATTAT GCAGCTTTC TACCTCGTCA TCCTATGA

```

This corresponds to the amino acid sequence <SEQ ID 146; ORF 039.a>:

```

a039.pep
  1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPKASSSA
 51 KNAKECLKPK TIWQARKNPY STIXPEAVSD VKLVHRIGTS AIGKKQISR
101 EIAGILNGGT TQPDIPPATA ATPAAAPQVT VPPAAPARQD GFNWTIATLF
151 ALIVLIMQLS YLVL*

```

m039/a039 79.4% identity over a 170 aa overlap

	10	20	30	40	50	60
m039.pep	MPSEPPYASDGIKPDTHEEIPCPPVSAPTAKPVSGSKKPNMSMPXXXXXXXXXXXXXXXXXX					
a039	MPSEPPYASDGIKPDTHEEIPCPPVSAPTAKPVSGSKKPNMSMPKASSAKNAKECLKPK					

```

      10      20      30      40      50      60
      70      80      90     100     110     120
m039.pep  XXXXXXXXXXXXXXXXXXXXPEAVSDVKLVHRIGTRAI GKKQISRDEIAGILNGGTTQPD
:          : |          |||||          |||||          |||||          |||||
a039      TIWQARKNPYSTIX-----PEAVSDVKLVHRIGTSAIGKKQISRDEIAGILNGGTTQPD
      70      80      90     100     110
      130     140     150     160     170
m039.pep  PPATAATPAAAPQVTVPPAAPARQDGFNWTIATLFALIVLIMQLSYLVILX
          |||||          |||||          |||||          |||||          |||||
a039      PPATAATPAAAPQVTVPPAAPARQDGFNWTIATLFALIVLIMQLSYLVILX
      120     130     140     150     160

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 039 shows 60.8% identity over a 171 aa overlap with a predicted ORF (ORF 039.ng) from *N. gonorrhoeae*:

m039/g039

```

                                10          20          30          40          50          60
m039.pep  MPSEPPYASDGIKPDTHEEIPCPPVSAPTAKPVSGSKKPNMSPPXXXXXXXXXXXXXXXXXXXX
          ||||| ||||| | : ||||| : ||||| : ||||| : ||
g039      MPSEPPAASDGIKPTHTEKTS CPPVSVRTAKPASGSKKPSSTSPKASSSAKNAKGCLKPK
                                10          20          30          40          50          60

                                70          80          90          100         110         120
m039.pep  XXXXXXXXXXXXXXXXXXXXXPEAVSDVKLVHRIGTRAIGKKQISRDEIAGILNGGTTQPD
          :          :          | : ||||| ||||| : || : || : ||||| ||||| |
g039      TIWQARKNLYSTIG-----PKLFRDVKLVHRIGTHAISKKQMSRDEIADILNGGTTLHDT
                                70          80          90          100         110

                                130         140         150         160         170
m039.pep  PPATAAT-PAAAPQVTVPPAAPARQDGFNWTIATLFALIVLIMQLSYLVILX
          ||||| : ||||| : ||||| || : ||||| : ||||| : ||||| : |||||
g039      PPATAAAAPAAAPQVSVPPA---RQEGLNWTIATLFALIVLIMQLSYLFILX
                                120         130         140         150         160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 147>:

g040.seq

1	ATGAACGCGC	CCGACAGCTT	TGTCGCCCAC	TTCGCGAAG	CCGCCCCCTA
51	CATCCGCCAA	ATGCGCGGCA	CGACACTGGT	CGCCGGCATA	GAaggCCGCC
101	TGCTCGAAGG	CGGCACCTTA	AATAAGCTCG	CCGCCGACAT	CGGGCTGTTG
151	TCGCAACTGG	GCATCCGACT	CGTCCTCATC	CACGGCGCGT	ACCACTTCCT
201	CGAccgCCTC	CGCGCCGCGC	AAGgcGCAC	GCCGCATTAT	TGCCGggggt
251	tGCGCGTTAC	CGACGAaACc	tcGctcgGAC	AGGCCGACGA	GtttGCCGCG
301	AccgTCCGCA	GCCGTTTTGA	agcCGCATTG	tgcggcagCG	tttcaggatt
351	cgcgCGCGCG	CCTTCCGTCC	CGCTCGTAtc	gggcaacttc	ctgacCGCCC
401	GTcCgatggg	cgtgattgac	ggaACCGata	tggaatacgc	gggggttatc
451	cgcaaaaccg	ACACCGCCGC	CCTCCGTTTC	CAACTCGACG	CGGGCAATAT
501	CGCTATGGAT	CCGCGCGCTG	GGCATTCTTA	CGGCGGCAAA	ACCTTCAATC
551	TCGATATGGT	GCAGGCCGCG	GCTTCGCTCG	CCGTCCTGCT	TcAGGCCGAA
601	AAACTcGTTT	ACCTGACCCT	TTCAGACGGC	ATTTCCCGCC	CCGACGGCAC
651	GCTCGCCGAA	ACCCTCTCGG	CACAGGAAGC	GCAATCGCTG	GCGGAACACG
701	CCGCCAGCGA	AACCCGACGA	CTGATTTCGT	CCGCCGTTGC	CGCGCTCGAA
751	GGCGGCGTGC	ATCGCGTCCA	AATCCTCAAC	GGGGCCGCCG	ACGCAGCCTT
801	GCTGCAAGAA	CTCTTCACCC	GCAACGGCAT	CGGCACGTCC	ATTGCCAAAG
851	AAGCCTTCGT	CTCCATCCGG	CAGGCGCAC	CGGGCGACAT	CCCGCACATC
901	GCGCCCTCPA	TCCGCCCGCT	GGAAGAACAG	GGGTCCTAT	TGCACCGCAG
951	CCGCGAATAC	CTCGAAAACC	ACATTTTCCGA	ATTTTCCATC	CTCGAACACG

```

1001 ACGGCGACCT GTACGGCTGT GCCGCACTCA AAACCTTTGC CGAAGCCGAT
1051 TCGGGCGAAA TCGCCTGCCT TGCCGTCTCG CCGCAGGCAC AGGACGGCGg
1101 ctACGGCGAA CGCCTGCTTG CCCACATTAT CGATAAGGCG CGCGGCATAG
1151 GCATAAGCAG GCTGTTGCA CTGTCCACAA ATACCGGCGA ATGGTTTGCC
1201 GAACGCGGCT TTCAGACGGC ATCGGAAGAC GAGCTGCCCG AAACGCGGCG
1251 CAAAGACTAC CGCAGCAACG GACGAAACCC GCATATTCTG GTGCGTCGCC
1301 TGCACCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 148; ORF 040.ng>:

g040.pep

```

1 MNAPDSFVAH FREAAPYIRQ MRGTTLVAGI DGRLLGGTL NKLAADIGLL
51 SQLGIRLVLI HGAYHFLDRL AAAQGRTPHY CRGLRVTDET SLGQAQQFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPMGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWM PPLGHSYGGK TFNLDMVQAA ASVAVSLQAE
201 KLVYLTLSDG ISRPDGTAE TLAQEAQSL AEHAASETRR LISSAVAAL
251 GGVHRVQILN GAADGSLQLE LFTRNGIGTS IAKEAFVSIR QAHSGDIPHI
301 AALIRPLEEQ GVLLHRSREY LENHISEFSI LEHDGDLYGC AALKTFEAD
351 CGEIACLAVS PQAQDGGYGE RLLAHIIDKA RGIGISRLEA LSTNTGEWFA
401 ERGFQTASED ELPETRRKDY RSNRNPIL VRRLHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 149>:

m040.seq

```

1 ATGAGCGCGC CCGACCTCTT TGTCGCCAC TTCCGCGAAG CCGTCCCCTA
51 CATCCGCCAA ATGCGCGGCA AAACGCTGGT CGCCGGCATA GACGACCGCC
101 TGCTCGAAGG TGATACCTTA AACAAGCTCG CCGCCGACAT CGGGCTGTTG
151 TCGCAACTGG GCATCAGGCT CGTCCTCATC CACGGCGCGC GCCACTTCCT
201 CGACCGCCAC GCGCCGCTC AAGGCCGCAC GCCGCATTAT TGCCGGGGCT
251 TGCGCGTTAC CGACGAAACC TCGCTCGAAC AGGCGCAgCA GTTTGCCGGC
301 ACCGTCCGCA GCCGTTTGA AGCCGCATTG TGCGGCAGCG TTTCCGGGT
351 CGCGCGGCGC CCTTCCGTCC CGCTCGTATC GGGCAACTTC CTGACCGCCC
401 GTCCGATAGG TGTGATTGAC GGAACCGATA TGGAATACGC GGGCGTTATC
451 CGAAAACCG ACACCGCCGC CCTCCGTTTC CAACTCGACG CGGGCAATAT
501 CGTCTGGCTG CCGCCGCTCG GACATTCCTA CAGCGGCAAG ACCTTCTATC
551 TCGATATGCT TCAAACCGCC GCCTCCGCCG CCGTCTCGCT TCAGGCCGAA
601 AAACCTCGTTT ACCTGACCCT TTCAGACGGC ATTTCCCGCC CCGACGGCAC
651 GCTCGCCGAA ACCCTCTCGG CACAGGAAGC GCAATCGCTG GCGGAACACG
701 CCGGCGGGCA AACGCGACGG CTGATTTCGT CCGCCGAACT CTTACCCGC
751 AACGGCATCG GCACGTCCAT TGCCAAAGAA GCCTTCGTCT CCATCCGGCA
801 rGCGCAywgG G.CGACATCC CGCACATCGC CGCCCTCATC CGCCCGCTGG
851 AAGAACAGGG CATCCTGCTG CACCGCAs.c GCGAATACCT CGAAAACCAC
901 ATTTCCGAAT TTTCATCCT CGAACACGAC GGCAACCTGT ACGGTGCGC
951 CGCCCTGAAA ACCTTTGCCG AAGCCGATTG CGGCGAAATC GCCTGCCTTG
1001 CCGTCTCGCC GCag.cACAG GACGGCGGCT ACGGCGAACG CnTGCTTGCC
1051 CACATTATCG ATAAGCGCGC CGGCATAGGC ATAAGCAGGC TGTTTCGACT
1101 GTCCACAAAT ACCGGCGAAT GGTGTGCCGA ACGCGGCTTT CAGACGGCAT
1151 CGGAAGACGA GTTGCCCGAA ACGCGGCGCA AAGACTACCG CAGCAACGGA
1201 CGGAACTCGC ATATTCTGGT ACGTCGCCTG CACCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 150; ORF 040>:

m040.pep

```

1 MSAPDLFVAH FREAVPYIRQ MRGKTLVAGI DDRLLEGDTL NKLAADIGLL
51 SQLGIRLVLI HGARHFLDRH AAAQGRTPHY CRGLRVTDET SLEQAQQFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPIGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWL PPLGHSYSGK TFYLDMLQTA ASAAVSLQAE
201 KLVYLTLSDG ISRPDGTAE TLAQEAQSL AEHAGGQTRR LISSAELEFTR
251 NGIGTSIAKE AFVSIRQAHX XDIPHIAALI RPLEEQGILL HRXREYLENH
301 ISEFSILEHD GNLYGCAALK TFAEADCGEI ACLAVSPQXQ DGGYGERXLA
351 HIIDKARGIG ISRLFALSTN TGEWFAERGF QTASEDELPE TRRKDYRSNG
401 RNSHILVRRLL HR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 151>:

a040.seq

```

1   ATGATCGTGC CCGACCTCTT TGTCGCCCAC TTCCGCGAAG CCGCCCCCTA
51  CATCCGCCAA ATGCGCGGCA AAACGCTGGT CGCCGGCATA GACGACCGCC
101 TGCTCGAAGG TGATACCTTA AACAAAGTTCG CCGCCGACAT CGGGCTTTTG
151 TCGCAACTGG GCATCAGGCT CGTCCTCATC CACGGCGCGC GCCACTTCCT
201 CGACCGCCAC GCCGCCGCGC AAGGCCGCAC GCCGCATTAT TGCCGGGGCT
251 TGC GCGTTAC CGACGAAACC TCGCTCGAAC AGGCGCAGCA GTTTGCCGGC
301 ACCGTCCGCA GCCGTTTTGA AGCCGCATTG TGCGGCAGCG TTTCCGGGTT
351 CGCGCGCGCG CCTCCGTCC CGCTCGTATC GGGCAACTTC CTGACCGCCC
401 GTCCGATAGG TGTGATTGAC GGAACCGATA TGAATACGC GGGCGTTATC
451 CGCAAACCG ACACCGCCGC CCTCCGTTTC CAACTCGACG CGGGCAATAT
501 CGTCTGGCTG CCGCGCTCG GACATTCCTA CAGCGGCAAG ACCTTCCATC
551 TCGATATGCT TCAAACCGCC GCCTCCGTCT CCGTCTCGCT TCAGGCCGAA
601 AAACCTCGTTT ACCTGACCCT TTCAGACGGC ATTTCCCGCC CCGACGGCAC
651 GCTCGCCGTA ACCCTCTCGG CACAGGAAGC GCAATCGCTG GCGGAACACG
701 CCGCGCGCGA AACGCGACGG CTGATTTCTG CCGCCGTTCG CGCGCTCGAA
751 GGCGGCGTGC ATCGCGTCCA AATCCTCAAC GGAGCCGCCG ACGGCAGCCT
801 GCTGCAAGAA CTCTTCACCC GCAACGGCAT CGGCACGTCC ATTGCCAAAG
851 AAGCCTTCGT CTCCATCCGG CAGGCGCACA GCGGCGACAT CCCGCACATT
901 GCCGCCCTCA TCCGCCCGCT GGAAGAACAG GGCATCCTGC TGCACCGCAG
951 CCGCGAATAC CTCGAAAACC ACATTTCCGA ATTTTCCATC CTCGAACACG
1001 ACGGCAACCT GTACGGTTGC GCCGCCCTGA AAACCTTTGC CGAAGCCGAT
1051 TCGCGCGAAA TCGCCTGCCT TGCCGTCTCG CCGCAGGCAC AGGACGGCGG
1101 CTACGGCGAA CGCCTGCTTG CCCACATTAT CGATAAGGCG CGCGGCATAG
1151 GCATAAGCAG GCTGTTTCGA CTGTCCACAA ATACCGGCGA ATGGTTTGCC
1201 GAACGCGGCT TTCAGACGGC ATCGGAAGAC GAGTTGCCCG AAACGCGCGG
1251 CAAAGACTAC CGCAGCAACG GACGGAATC GCATATTCTG GTGCGTCGCC
1301 TGCACCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 152; ORF 040.a>:

a040.pep

```

1   MIVPDLFVAH FREAAPYIRQ MRGKTLVAGI DDRLLEGDTL NKFAADIGLL
51  SQLGIRLVLI HGARHFLDRH AAAQGRTPHY CRGLRVTDET SLEQAQQFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPIGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWL PPLGHSYSGK TFHLDMLQTA ASVAVSLQAE
201 KLVYLTLSDG ISRPDGT LAV TLAQEAQSL AEHAGGETRR LISSAVALAE
251 GGVHRVQILN GAADGSLLOE LFTNRGIGTS IAKEAFVSIR QAHSGDIPHI
301 AALIRPLEEQ GILLHRSREY LENHISEFSI LEHDGNLYGC AALKTFEAD
351 CGEIACLAVS PQAQDGGYGE RLLAHIIDKA RGIGISRLFA LSTNTGEWFA
401 ERGFQTASED ELPETRRKDY RSNRNSHIL VRRLHR*

```

m040/a040 91.5% identity in 436 aa overlap

	10	20	30	40	50	60
m040.pep	MSAPDLFVAHFREAVPYIRQMRGKTLVAGIDDRLLEGDTLNKLAADIGLLSQLGIRLVLI					
a040	MIVPDLFVAHFREAAPYIRQMRGKTLVAGIDDRLLEGDTLNKFAADIGLLSQLGIRLVLI					
	10	20	30	40	50	60
m040.pep	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA					
a040	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA					
	70	80	90	100	110	120
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYSGK					
a040	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYSGK					
	130	140	150	160	170	180
m040.pep	TFYLDMLQTAASAAVSLQAEKLVYLTLSDGISRPDGT LAETLSAQEAQSLAEHAGQTRR					
a040	TFHLDMLQTAASVAVSLQAEKLVYLTLSDGISRPDGT LAVTLSAQEAQSLAEHAGGETRR					

Homology with a predicted ORF from *N. gonorrhoeae*

m040/g040

m040.pep	MSAPDLFVAHFREAVPYIRQMRGKTLVAGIDDRLLLEGDTLNKLAADIGLLSQLGIRLVLI :: :	60
g040	MNAPDSFVAHFREAAPYIRQMGRGTTLVAGIDGRLLLEGDTLNKLAADIGLLSQLGIRLVLI	60
m040.pep	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA 	120
g040	HGAYHFLDRLAAAQGRTPHYCRGLRVTDETSLGQAQQFAGTVRSRFEAALCGSVSGFARA	120
m040.pep	PSVPLVSGNFLTARPIGVIDGTMDEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYSYGK : : :	180
g040	PSVPLVSGNFLTARPMGVIDGTMDEYAGVIRKTDTAALRFQLDAGNIVWMPPLGHSYGGK	180
m040.pep	TFYLDMLQTAASAAVSLQAEKLVYLTLSDGISRPDGTLAETLSAQEAQSLAEHAGGQTRR : : : : ::	240
g040	TFNLDMVQAAASVAVSLQAEKLVYLTLSDGISRPDGTLAETLSAQEAQSLAEHAASETRR	240
m040.pep	LISSA-----ELFTRNGIGTSIAKEAFVSIRQAHXXDIPHI 	276
g040	LISSAVAALEGGVHRVQILNGAADGSLLQELFTRNGIGTSIAKEAFVSIRQAHSGDIPHI	300
m040.pep	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS :	336
g040	AALIRPLEEQGVLLHRSREYLENHISEFSILEHDGDLYGCAALKTFAEADCGEIACLAVS	360
m040.pep	PQXQDGGYGERXLAIHIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPEPTRRKDY 	396
g040	PQAQDGGYGERLLAIHIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPEPTRRKDY	420
m040.pep	RSNGRNSHILVRRLHRX 413 	
g040	RSNGRNPHILVRRLHRX 437	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 153>:

```
g041.seq
  1 ATGAGTTCGC CCAAACACAT CGGCTTGCGG GCGGCGAGCA ACGGCGGCCT
 51 GATTACCGCC GCCGCCTTCG TGCGCGAACC GCAAAGCATC GGTGCGCTGG
101 TGTGCGAAGT ACCGCTGACC GATATGATCC GTTATCCGCT GCTGTCCGCC
151 GGTTCAGATT GGACGGACGA ATACGGCAAT CCGCAGAAAT ACGAAGCCTG
201 CAAACGCCGG CTGGGCGAAT TGTCGCCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCACTC ATTACCACCA GCCTCAGCGA CGACCGCGTC
301 CATCCCGCCC ACGCGCTCAA ATTCTACGCC AAAGTGGCGG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CCCAACGCGA ATCCGCCGAC AAAGTGGCGT GCGTGTGCT GTTTTGTAAA
451 GAATTTTGG GATAA
```

This corresponds to the amino acid sequence <SEQ ID 154; ORF 041.ng>:

```
g041.pep
  1 MSSPKHIGLQ GGSNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
 51 GSSWTDEYGN PQKYEACKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSPQSW LYSPDGGGHT GNGTQRESAD KLACVLLFLK
151 EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 155>:

```
m041.seq
  1 ATCAGTTCGC CCGAACACAT CGGCTTGCGG GCGGCGAGCA ACGGCGGACT
 51 GATTACTGCC GCCGCCTTCG TGCGCGAACC GCAAAGCATC GCGCGCTGG
101 TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151 GGTTCAGCT GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201 CAAACGCCGG TTGGGCGAAT TGTCGCCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301 CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAAGTGGCGG AAACCTCCGC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CCCAACGCGA ATCCGCCGAC GAAGTGGCGT GCGTCTTGCT GTTTTGTAAA
451 GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 156; ORF 041>:

```
m041.pep
  1 ISSPEHIGLQ GGSNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
 51 GSSWTDEYGN PQKYEVCRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSQSW LYSPDGGGHT GNGTQRESAD ELACVLLFLK
151 EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 157>:

```
a041.seq
  1 ATCAGTTCGC CCGAACACAT CGGCTTGCGG GCGGCGAGCA ACGGCGGACT
 51 GATTACTGCC GCCGCCTTCG TGCGCGAACC GCAAAGCATA GCGCGCTGG
101 TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151 GGTTCAGCT GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201 CAAACGCCGG TTGGGCGAAT TGTCGCCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301 CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAAGTGGCGG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CGCAGCGCGA AGCCGCCGAC GAAGTGGCGT GCGTGTGCT GTTTTGTAAA
451 GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 158; ORF 041.a>:

```
a041.pep
  1 ISSPEHIGLQ GGSNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
 51 GSSWTDEYGN PQKYEVCRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSPQSW LYSPDGGGHT GNGTQREAAD ELACVLLFLK
```


	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGLITAAAFVRE	QSIGALVCEVPLTDMIRYP	LLSAGSSWTDEYGN			
a041	ISSPEHIGLQGGSNGLITAAAFVRE	QSIGALVCEVPLTDMIRYP	LLSAGSSWTDEYGN			
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCKRRLGELSPYHNLS	DGIDYPPALIT	SLSDDRVHPAH	ALKFYAKLRE	TS	AQSW
a041	PQKYEVCKRRLGELSPYHNLS	DGIDYPPALIT	SLSDDRVHPAH	ALKFYAKLRE	TS	PQSW
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTQRES	ADELACVLLFL	KEFLGX			
a041	LYSPDGGGHTGNGTQREA	ADELACVLLFL	KEFLGX			
	130	140	150			

m041/g041

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSN	GGGLITAAAFVRE	PQSIGALVCEVPL	TDMIRYP	LLSAGSSWTDEY	GN
	:	:				
g041	MSSPKHIGLQGGSN	GGGLITAAAFVRE	PQSIGALVCEVPL	TDMIRYP	LLSAGSSWTDEY	GN
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCKRRLGEL	SPYHNLS	DGIDYPPALIT	TSLSDDR	RVHPAHALKFY	AKLRETS
	:					
g041	PQKYEACKRRLGEL	SPYHNLS	DGIDYPPALIT	TSLSDDR	RVHPAHALKFY	AKLRETS
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGT	QRESADELACV	LLFLKEFLGX			
			:			
g041	LYSPDGGGHTGNGT	QRESADKLACV	LLFLKEFLGX			
	130	140	150			

g041-1.seq

1	ATGAAATCCT	ACCCCGACCC	CTACCGCCAT	TTTGAAAC	TCGATTCCGC
51	CGAAACGCAA	AACTTCGCTG	CTGAAGCGAA	TGCCGAAACG	CGCGCGCGTT
101	TTTTAAACAA	CGACAAGCGC	CGCGCACTTT	CAGACGGCAT	TTTGAATCAA
151	ATGCAGGACA	CGCGGCAGAT	TCCGTTTTGT	CAGGAACACC	GC
201	GTACCAATTC	CATCAGAATG	CGGAATATCC	GAAAGGCGTG	TACCGCATGT
251	GTACGCGCGC	GACCTACCGT	TCCGGCTATC	CCGAGTGGAA	AATCCTGTTT
301	TCGGTGGCGG	ATTTTCGATGA	GTTGCTCGGC	GACGATGTGT	ATTTGGGCGG
351	CGTGTGCGAC	TTGGTGAGC	AGCCCAACCG	CGCGCTGCTG	ACTTTGAACA
401	AATCGGGCGC	CGATACGGCG	TATACGCTGG	AAGTGGATT	GGAAGCAGGG
451	GAATTGGTAG	AGGCGGTTT	TCACTTCCG	GCAGGCAAAA	ACCATGTGTC
501	GTGGGCGCAT	GAACAACGCG	TGTGGGTGTG	TCGGCTTGG	GACGAACGCC
551	AGTTGACCGA	ATCGGGCTAT	CCGCGCGAAG	TGTGGCTGGT	GGAACGCGGC

```

601 AAGAGTTTCG AGGAAAGCCT GCCGGCGTAC CAAATCGATA AAGGCGCGAT
651 GATGGTAAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AGACGTATTT GCAGGTGTCTG
751 TCCGAAGGCG GGGCGAAACC GTTGAACCTG CCTAATGATT GCGATGTGGT
801 CGGCTATCTG GCGGGACATC TTTTGCTGAC GCTGCGCAAG GACTGGCACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCGT TGGTGGCGGT GAAACTGAAT
901 CGGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTTGCGCCCG ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTGGTG GCAAGCCTGC
1001 TGGAGAATGT ACAAGGCCGT CTGAAAGCGT GGCGGTTTGC CGACAGCAAA
1051 TGGCAGGAAG CCGAGTTGCC GCACCTGCCC TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGCGGCG ACGTGGTTTA TCTTGCCGCC AGCGATTTCa
1151 CCACGCCGCT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAAGTACC
1201 GTCATGCGCC TCCAGCCGCA GCAGTTTGTG TCAGACGGCA TCGAAGTGCG
1251 GCAGTTTTGG GCGGTGTCTG CCGACGGCGA ACGCATTCCT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACACGCCGA CCTTAGTCTA TGCTTACGGA
1351 GGTTTCGGCA TTCTGAATT GCCGCATTAT CTGGGCAGCG TCGGCAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GGCAAACATC CGCGGCGGCG
1451 GAGAATTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAACAC
1501 AAAAGCGTTG ATGATTGTG GGCAGTCGTG CGTGATTGTG CCGAACCGCG
1551 CATGAGTTTC CCCAAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGCC
1601 TGATTACCGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT CGGTGCGCTG
1651 GTGTGCGAAG TACCGCTGAC CGATATGATC CGTTATCCGC TGCTGTCCGC
1701 CGGTTCAAGT TGGACGGACG AATACGGCAA TCCGCAGAAA TACGAAGCCT
1751 GCAAACGCGG GCTGGGCGAA TTGTCGCCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCCGCACT CATTACCACC AGCCTCAGCG ACGACCGCGT
1851 CCATCCCGCC CACGCGCTCA AATTCTACGC CAAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACCCAACGCG AATCCGCCGA CAAACTCGCC TCGGTGTTGC TGTTTTTTGAA
2001 AGAATTTTTG GGATAA

```

This corresponds to the amino acid sequence <SEQ ID 160; ORF 041-1.ng>:

g041-1.pep

```

1 MKSYDPYRH FENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILNQ
51 MQDTRQIPFC QEHRARMYHF HQNAEYPKGV YRMCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TLNKSGGDTA YTLEVDLEAG
151 ELVEGGFHFP AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVWLVERG
201 KSFEESLPAY QIDKGAMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 SEGGAAPLNL PNDCDVVGYL AGHLLLTLRK DWHRANQSYR SGALVAVKLN
301 RGELGAAQLL FAPDETQALE SVETTKRFV ASLLENVQGR LKAWRFADSK
351 WQEAPLPHLP SGALEMTDQP WGGDVVYLAA SDFTTPLTLF ALDLNVMELT
401 VMRLQPQQFV SDGIEVRQFW AVSSDGERIP YFHVGNKNAAP DTPTLVYAYG
451 FEGIPPELPHY LGSVGKYWLE EGNAPVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLLAVV RDLSEGRMSS PKHIGLQGGG NGGLITAAAF VREPQSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEACKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQRESADKLA CVLLFLKEFL G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 161>:

m041-1.seq

```

1 ATGAAATCCT ACCCGACCC CTACCGCCAT TTTGAAACC TCGATTCCGC
51 CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAGAAAA CGACAAGGCG CGCGCGCTTT CAGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAGAT TCCGTTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTC CATCAGGACG CGGAGTATCC GAAGGGCGTG TACCGCGTGT
251 GTACCGCGGC GACGTATCGT TCCGGCTATC CCGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTGACGCA ATTGCTTGGC GACGATGTGT ATTTGGGCGG
351 CGTGTGCGAC TTGGTGGAAC AGCCCAACCG CGCGTTGTTA AACTGAGCA
401 AATTGGGCAG CGATACGGCG TACACGCTGG AAGTGGATTG GGAAGCAGGG
451 GAGTTGGTCG AAGGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG AACGAACGCC
551 AGTTGACCCA ATCGGGCTAT CCGCGCGAAG TATGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCTGTGTAT CAAATCGGCG AAGACGGCAT
651 GATGGTGAAC GCGTGGCGTT ATCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AAACCTATTG GCGGGTCTCA

```

m041-1.pap

1	MKSYPPDYRH	FENLDSAETQ	NFAAEANAET	RARFLENDKA	RALSDGILAQ
51	LQDTRQIPFC	QDHRYRMHYH	HQDAEYPKGV	YRVCTAAAYR	SGYEPWKILF
101	SVADFEDELLG	QEVRLGGVSH	LVEQPNRALL	TRSLKGSDDTA	YTYEVLLEAG
151	ELVEGGFHFP	AGKNHVSWRD	ENSVWVCPAW	NERQLTQSGY	PREVVLVRG
201	KSFEESLPVY	QIGEDGMMVN	AWRYLDPPQS	PIDLIEASDG	FYTKTYLRVS
251	AEGEAKPLNL	PNCDCVVVGL	AGHLLTLRKR	DWNRANQSY	SGALVAVLKN
301	RGELGAQQLL	FAPDETQALE	SVETTKRFV	ASLENVQGR	LKAWRFADGK
351	WQEVLEPRLP	SGALEMDQFP	WGGDVVYLAA	SDFTTPLTLF	ALDLNVMELT
401	VMRRQPQQFD	SDGINVQQFV	TTSDADGERIP	YFHVGNKNA	DMPTLVVAYG
451	GFGIPPELPHY	LGSIGKYWLE	EGNAFVLANI	RGGGFNGPRW	HQAAQGISKH
501	KSVDDLLAVV	RDLSESGISS	PEHIGLQGGG	NGGLITAAAF	VREPQSIGAL
551	VCEVPLTDMI	RYPLSDSVGSS	WTDEYGNPQK	YEVCKRRLGE	LSPYHNLSDG
601	IDYPPALITT	RLSDDRVHHA	HALKFYAKLR	ETSAQSWLVS	PDGGGHTGNG
651	TQRESADELA	CVLLFLKEFL	G*		

m041-1/g041-1 94.6% identity in 671 aa overlap

	10	20	30	40	50	60
m041-1.pep	MKSYDPYPYRHFNLD	SAETQNF	AAEANAET	RARFL	ENDKAR	ALSDGIL
g041-1	MKSYDPYPYRHFNLD	SAETQNF	AAEANAET	RARFL	NNDKAR	ALSDGIL
	10	20	30	40	50	60
	70	80	90	100	110	120
m041-1.pep	QEHRARMYHFHQDAEY	PKGVYR	VC	TAATYR	SGYPEW	KILFSV
g041-1	QEHRARMYHFHQDAEY	PKGVYR	MCTAATYR	SGYPEW	KILFSV	ADFD
	70	80	90	100	110	120
	130	140	150	160	170	180
m041-1.pep	LVEQPNRALLT	LSKLGSD	TAYTLE	VDLEAG	ELVEGG	FHF
g041-1	LVEQPNRALLT	LNKSGGD	TAYTLE	VDLEAG	ELVEGG	FHF
	130	140	150	160	170	180
	190	200	210	220	230	240
m041-1.pep	NERQLTQSGYP	PREVWL	VERGKS	FEE	SLP	VYQIG
	190	200	210	220	230	240

g041-1	DERQLTESGYPREVWLVERGKSFEESLPAYQIDKGAMMVNAWRYLDPQGSPIDLIEASDG
	190 200 210 220 230 240
m041-1.pep	FYTKTYLRVSAEGEAKPLNLPNDCDVVGYLGHLLTLRKDWNRRANQSYPSGALVAVKLN
	250 260 270 280 290 300
g041-1	FYTKTYLQVSSEGGAKPLNLPNDCDVVGYLGHLLTLRKDWHRRANQSYPSGALVAVKLN
	250 260 270 280 290 300
m041-1.pep	RGELGAAQLLFAPDETQALESVETTKRFVVASLLENVQGRKAWRFADGKWQEVELPRLP
	310 320 330 340 350 360
g041-1	RGELGAAQLLFAPDETQALESVETTKRFVVASLLENVQGRKAWRFADSKWQEAELPHLP
	310 320 330 340 350 360
m041-1.pep	SGALEMTDQPWGGDVVYLAASDFTTPTLTFALDLNVMELTMVRRQPQQFSDGINVQQFW
	370 380 390 400 410 420
g041-1	SGALEMTDQPWGGDVVYLAASDFTTPTLTFALDLNVMELTMVRLQPQQFVSDGIEVRQFW
	370 380 390 400 410 420
m041-1.pep	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIKGYWLEEGNAFVLANI
	430 440 450 460 470 480
g041-1	AVSSDGERIPYFHVGNKNAAPDPTLVYAYGGFGIPELPHYLGSVKGYWLEEGNAFVLANI
	430 440 450 460 470 480
m041-1.pep	RGGGEFGPRWHQAAQGISKHKSVDLLAVVRDLSESGISSPEHIGLQGGSNGLITAAAF
	490 500 510 520 530 540
g041-1	RGGGEFGPRWHQAAQGISKHKSVDLLAVVRDLSESGMSSPKHIGLQGGSNGLITAAAF
	490 500 510 520 530 540
m041-1.pep	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCRRRLGELSPYHNLSDG
	550 560 570 580 590 600
g041-1	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEACKRRRLGELSPYHNLSDG
	550 560 570 580 590 600
m041-1.pep	IDYPPALITTSLSDDRVPAPHALKFYAKLRETSQSWLYSPDGGGHTGNGTQRESADELA
	610 620 630 640 650 660
g041-1	IDYPPALITTSLSDDRVPAPHALKFYAKLRETSPQSWLYSPDGGGHTGNGTQRESADKLA
	610 620 630 640 650 660
m041-1.pep	CVLLFLKEFLGX
	670
g041-1	CVLLFLKEFLGX
	670

m041-1/P55577

sp|P55577|Y4NA_RHISN PROBABLE PEPTIDASE Y4NA >gi|2182536 (AE000086) Y4nA [Rhizobium sp. NGR234] Length = 726

Score = 370 bits (940), Expect = e-101

Identities = 217/682 (31%), Positives = 331/682 (47%), Gaps = 22/682 (3%)

Query: 2 KSYDPDPYRHFENLDSAETQNFAAEANAETRARFLENDKARALSDGILAQLDTRQIPFCQ 61
K DP + +D + + N T + ++ + L LQ T +I
Sbjct: 42 KDASDPRAYLNEIDGDKAMTWVEAHNLSTVDKLSKDPYSEYQADALTILQATDRIASPS 101

Query: 62 EHRARMY-HFHQDAEYKPGVYRVCTAATYRSGYPEWKILFSVADFELLDVYLGGVSH 120
R M +F QD + +G++R T +YRSG P+W+ + V + G G
Sbjct: 102 FARDGMIDNFWQDGHVQGLWRRTTWESYRSGNPQWRITLDDVDAKSAEGKTWVFEGGDC 161

Query: 121 LVEQPNRALLTSLKLGSDTAYTLEVDLEAGELVEGGFHFPAKGNHVSWRDENSVMVCPAW 180
L N L+ LS G D E D+ GE V+ GF P GK V+W DEN+++V W

Sbjct: 162 LPPTSNLCLIRLSDDGGKDADVREFDIAKGEFVKEGFVLPEGKQSVTWVDENTIYVTREW 221

Query: 181 NERQLTQSGYPREVWLVERGKSFEESLPVYQ-----IGEDGMM--VNAWRYLDPOGSP 232
 ++T SGY +V+RG+S ++++ +++ E G++ ++ +D +

Sbjct: 222 TPGEVTSSGYAYVTKVVKRGQSLDQAVEIFRGQKDVSAERGVLRDIDGKYVMDTSYRGL 281

Query: 233 DLIEASDGFYTKTYLRVSAEGEAKPLNLPNDCDVVGYLAGHLLTLRKDWNANQS-YPS 291
 D FY + + L LP GY G + L+ DW A + + +

Sbjct: 282 DFFNTELAFFYPNGH----PDTRKVVLPPLPTTAVFSGYKQAIYWLKSDWTSAGKTVFHN 337

Query: 292 GALVAVKLNRELGAQAQL----LFAPDETQALSVETTKRFVVASLLENVQGRKAWRFA 347
 GA++A L A++ LF P+E Q++ TK +V S+L NV ++++ F

Sbjct: 338 GAIADFLLAALADPARVEPLVLFMPNEHQSVAGTTQTKNRLVLSILSNVTSEVRSFDFG 397

Query: 348 DGKWQEEVELPRLPSGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTMRRQPQ 407
 G W +L + L +T D +++ + F P TLF D ++ + P

Sbjct: 398 KGGWSSFKLALPENSTLSLTSSDDESDQLFVFESEGFLEPSTLFCADAATGQVEKITSTPA 457

Query: 408 QFDSGDGINVQQFWTTSADGERIPYFHVGNKAAAP---DMPTLVYAYGGFGIPELPHYLSGI 464
 +FD+ G+ QQFW TS.DG ++PYF V + PT++YAYGGF IP P Y +

Sbjct: 458 RFDAGGLQAQQFWATSKDGTKVPYFLVARKDVKLDGNTPTILYAYGGFQIPMQPSYSAYL 517

Query: 465 GKYWLEEGNAFVLANIRGGGEFGPRWHQAAGQISKHKSVDLLAVVRDLSEGRISPEHI 524
 GK WLE+G A+ LANIRGGGEFGP+WH A ++ + DD AV +DL + ++S H+

Sbjct: 518 GKLWLEKGGAYALANIRGGGEFGPKWHADAGLKTNRQVYDDFQAVAQDLIAKVTSTPHL 577

Query: 525 GLQGGSSNGGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVC 584
 G+ GGSNGGL+ ++ P A+V +VPL DM+ + +SAG+SW EYG+P V

Sbjct: 578 GIMGSSNGGLLMGVQMIQRPDLWNAVVIQVPLDMVNFTRMSAGASWQAEYGSFDD-PVE 636

Query: 585 KRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPALHAKFYAKLRETSAQSWLYSPDGG 644
 L +SPYHN+ G+ YP TS DDRV P HA K A + + Y G

Sbjct: 637 GAFLRSISPYHNKAGVAYPEPFETSTKDDRVPVHARKMAALFEDMGLPFYYENIEG 696

Query: 645 GHTNGTQRESADELACVLLFL 666
 GH +E A A +++

Sbjct: 697 GHAAAAANLQEHARRYALEYIYM 718

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 163>:

a041-1.seq

```

1   ATGAAATCCT ACCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51  CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAAACAA CGACAAGGCA CGCGCATTGT CTGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAAAT TCCGTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTT CATCAAGATG CGGAATATCC GAAAGGCGTG TACCGCGTGT
251 GTACCGCGGC GACTTACCGT TCGGGCTATC CTGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTGACGCA ATTGCTCGGT GACGATGTAT ATCTAGGCGG
351 CGTGTCGCAC CTGGTGGAAC AGCCCAACCG CGCGTTGTTA AACTGAGCA
401 AATCGGGCGG CGATACCGCG TACACGCTGG AAGTGGATT T GGAAGCAGGG
451 GAGTTGGTAG AAGGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG GACGAACGCC
551 AGTTGACCGA ATCGGGCTAT CCGCGCGAGG TGTGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCGGTGTAC CAAATTGCTG AAGACGGCAT
651 GATGGTGAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCTGACGGT TTTTACACCA AAACCTATTT GCAGGTCTCA
751 GCCGAAGGCG AAGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTAGT
801 CGGCTATCTG GCCGGACATC TTTTGCTGAC CTGCGTAAA GACTGGCACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCAT TGGTAGCAGT AAAATTAAAC
901 CGCGGCGAAT TGGGCGCGCG GCAGCTTTTG TTTGCGCCCA ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTCTG GCGAGCCTGC
1001 TGGAAAACGT ACAGGGTCGT CTGAAAGCGT GGCCTTTTAC TGATGGCAAA
1051 TGGCAGGAAA CCGAGTTGCC GCGCCTGCCT TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGGGGCG ACGTAGTTTA CCTTGCCGCC AGCGATTTC
1151 CCACGCCGCT GACGCTGTTT GCATTGGATT TGAACGTGAT GGAACGTACC
1201 GTCATGCGCC GCCAGCCGCA GCAGTTTGAT TCAGACGGCA TTAACGTGCA
1251 GCAGTTTGG ACGACTTCGG CTGACGGCGA GCGCATTCCT TATTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCCTACGGC
1351 GGTTCGGCA TTCCCGAATT GCCGCATTAT CTGGGCAGCA TTGGCAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GGCGAACATC CGCGGCGGCG

```

```

1451 GCGAGTTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAACAT
1501 AAAAGCGTTG ATGATTATT GGCAGTCGTG AGCGATTTGT CCGAACGCGG
1551 TATCAGTTCG CCCGAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGAC
1601 TGATTACTGC CGCCGCTTC GTGCGCGAAC CGCAAAGCAT AGGCGCGCTG
1651 GTGTGCGAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGTCTCCGC
1701 CGGTTCAAGC TGGACAGACG AATACGGCAA TCCGCAAAAA TACGAAGTCT
1751 GCAAACGCCG GTTGGGCGAA TTGTCGCCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCCGCGCT CATTACCACC AGCCTGTCCG ACGATCGCGT
1851 CCATCCCGCC CACGCGCTCA AGTTCTACGC CAAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACGCAGCGCG AAGCCGCCGA CGAACTCGCC TCGTGTTGC TGTTTTGTAA
2001 AGAGTTTTTG GGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 164; ORF 041-1.a>:

a041-1.pep

```

1  MKSYDPYRHFENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILAQ
51  LQDTRQIPFC QEHRARMYHF HQDAEYPKGV YRVCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TSKSGGDTA YTLEVDLEAG
151 ELVEGGFHFP AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVWLVERG
201 KSFEESLPVY QIAEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 AEGEAKPLNL PNDCDVVGYL AGHLLLTLRK DWHRANQSYPS GALVAVKLN
301 RGE LGAAQLL FAPNETQALE SVETTKRFVV ASLLENVQGR LKAWRFTDGK
351 WQETELPRLP SGALEMTDQP WGGDVVYLA SDFTPPLTLF ALDLNVMELT
401 VMRRQPQQFD SDGINVQQFW TTSADGERIP YFHVGNKNAAP DMPTLVYAYG
451 GFGIPELPHY LGSIGKYWLE EGNAFVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLLAVI SDLSESGISS PEHIGLQGGG NGGLITAAAF VREPQSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEVCRRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQREAADELA CVLLFLKEFL G*

```

a041-1/m041-1 97.9% identity in 671 aa overlap

	10	20	30	40	50	60
a041-1.pep	MKSYPDPYRHFENLDSAETQ NFAAEANAET RARFLNNDKARALSDGILAQ LQDTRQIPFC					
	:					
m041-1	MKSYPDPYRHFENLDSAETQ NFAAEANAET RARFLNNDKARALSDGILAQ LQDTRQIPFC					
	10	20	30	40	50	60
	70	80	90	100	110	120
a041-1.pep	QEHRARMYHFHQDAEYPKGVYRVCTAATYRSGYPEWKILFSVADFDELLGDDVVYLGGVSH					
	:					
m041-1	QEHRARMYHFHQDAEYPKGVYRVCTAATYRSGYPEWKILFSVADFDELLGDDVVYLGGVSH					
	70	80	90	100	110	120
	130	140	150	160	170	180
a041-1.pep	LVEQPNRALLT LSKSGGDTAYTLEVDLEAGELVEGGFHFPAGKNHVSWRDENS VVWVCPAW					
	:					
m041-1	LVEQPNRALLT LSKLGS DTA YTLEVDLEAGELVEGGFHFPAGKNHVSWRDENS VVWVCPAW					
	130	140	150	160	170	180
	190	200	210	220	230	240
a041-1.pep	DERQLTESGYPREVWLVERGKSFEESLPVYQIAEDGMMVN AWRYLDPQGS PIDLIEASDG					
	: :					
m041-1	NERQLTQSGYPREVWLVERGKSFEESLPVYQIGEDGMMVN AWRYLDPQGS PIDLIEASDG					
	190	200	210	220	230	240
	250	260	270	280	290	300
a041-1.pep	FYTKTYLQVSAEAEAKPLNLPNDCDVVGYLAGHLLLT LRKDWHRANQSYPS GALVAVKLN					
	:					
m041-1	FYTKTYLRVSAEAEAKPLNLPNDCDVVGYLAGHLLLT LRKDWNRANQSYPS GALVAVKLN					
	250	260	270	280	290	300
	310	320	330	340	350	360
a041-1.pep	RGE LGAAQLL FAPNETQALE SVETTKRFVVASLLENVQGR LKAWRFTDGK WQETELPRLP					
	:					
m041-1	RGE LGAAQLL FAPDETQALE SVETTKRFVVASLLENVQGR LKAWRFADGK WQEVLPRLP					
	310	320	330	340	350	360

237

	370	380	390	400	410	420
a041-1.pep	SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTMRRQPQQFDSGINVQQFW					
m041-1	SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTMRRQPQQFDSGINVQQFW					
	370	380	390	400	410	420
	430	440	450	460	470	480
a041-1.pep	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
m041-1	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
	430	440	450	460	470	480
	490	500	510	520	530	540
a041-1.pep	RGGGEFGPRWHQAAQGISKHKSVDLLAVVSDLSESGISSPEHIGLQGGSNGLITAAAF					
m041-1	RGGGEFGPRWHQAAQGISKHKSVDLLAVVRDLSESGISSPEHIGLQGGSNGLITAAAF					
	490	500	510	520	530	540
	550	560	570	580	590	600
a041-1.pep	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRLGELSPYHNLSDG					
m041-1	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRLGELSPYHNLSDG					
	550	560	570	580	590	600
	610	620	630	640	650	660
a041-1.pep	IDYPPALITTSLSDDRVPAPAHALKFYAKLRETSQSWLYSPDGGGHTGNGTQREAADELA					
m041-1	IDYPPALITTSLSDDRVPAPAHALKFYAKLRETSQSWLYSPDGGGHTGNGTQRESADELA					
	610	620	630	640	650	660
	670					
a041-1.pep	CVLLFLKEFLGX					
m041-1	CVLLFLKEFLGX					
	670					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 165>:

g042.seq

```

1  ATGACGATGA TTTGCTTGCG CTTCCAagcG TTCGTGCCGC ATACCAGCGC
51  GTTATCCAAC ACTTCCACGG CAGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TCGGGTCGAT GATGAAAATC CAGCCGGGGT TTTTCTCTTT GATGTATTCG
151 AAGGAAACGG GCTGCCCGTG CCCTTCGTTG CGTAAAGATT CGTCCACGGG
201 CGGCAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GATTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCGTAACCG ACAGCACCAG CCCGCGTCTT
301 TTGCCTTTGG cggCTTCGCG CTTTGGGCG AACAGCGCGT CAATCTGCGC
351 ATTCAATTCC GCCACGCGCG CTCCTTACC GAAATCCGC GACAGGGTCT
401 CCATCTGCTT CTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAAA
451 TCTATGgtgG TCGCGTTTTT CGCCAACGTG TCATACGCTT CCGCACCCGG
501 CCCGCCGGTA ATGACAAACT GCGGATTGTG GCGGTGCAGG GATTGCGCAAT
551 CGGGCTCAAA CAGCGTCCCC ACCGTTGCCG CTTGTGCAAA TGCAGGCTGC
601 AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 166; ORF 042.ng>:

g042.pep

```

1  MTMICLRFQA FVPHTSALSN TSTAAGPSCP MAAVRSMMKI QPGFFSLMYS
51  KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTDSSTPRP
101 LPLAASRFWA NSASICAFNS ATRASLPKIR DRVSICFSPL VRILPLSTVK
151 SMVVAFFANC SYASAPGPPV MTNCGLWRCR DSQSGSNSVP TVAALSNAGC
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 167>:

m042.seq

```

1  ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAmT ACTTCGACAG CCGcCGGCCy TTCyTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 168; ORF 042>:

m042.pep

```

1  MTMICLRFQA FVPRTSALSX TSTAAGXSCP MAAVRSMMKI QSGFFSLMYS
51  KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTDSSTPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTSXGLXRCR ASXSGSNSVP TVAALSNAGC
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 169>:

a042.seq

```

1  ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCCAACGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 170; ORF 042.a>:

a042.pep

```

1  MTMICLRFQA FVPRTSALSX TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51  KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTDSSTPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*GL*RCR AS*SGSNSVP TVAALSNAGC
201 K*

```

m042/a042 99.0% identity over a 201 aa overlap

	10	20	30	40	50	60
m042.pep	MTMICLRFQAFVPRTSALSXTSTAAGXSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
a042	MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
	10	20	30	40	50	60
m042.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSSTSPRPLPLAASRVWANSASICAFNS					
a042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
m042.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSSTSPRPLPLAASRVWANSASICAFNS					
a042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSSTSPRPLPLAASRVWANSASICAFNS					
	130	140	150	160	170	180
m042.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					

239

```

a042      |||||
          AARASLPKIRAKVSICFSPPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
          130      140      150      160      170      180

          190      200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
          |||||
a042      ASXSGSNSVPTVAALSNAGCKX
          190      200

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 042 shows 93.0% identity over a 201 aa overlap with a predicted ORF (ORF 042.ng) from *N. gonorrhoeae*:

m042/g042

```

          10      20      30      40      50      60
m042.pep  MTMICLRFQAFVPRTSALSXTSTAAGXSCPMMAVRSMMKIQSGFFSLMYSKETGCPCPSL
          |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g042      MTMICLRFQAFVPHTSALSNTSTAAGPSCPMMAVRSMMKIQPGFFSLMYSKETGCPCPSL
          10      20      30      40      50      60

          70      80      90      100     110     120
m042.pep  RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g042      RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRFWANSASICAFNS
          70      80      90      100     110     120

          130     140     150     160     170     180
m042.pep  AARASLPKIRAKVSICFSPPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
          |:||||| :||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g042      ATRASLPKIRD RVSICFSPPLVRILPLSTVKSMVVAFFANC SYASAPGPPVMTNCGLWRCR
          130     140     150     160     170     180

          190     200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g042      DSQSGSNSVPTVAALSNAGCKX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 171>:

m042-1.seq

```

1  ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACAG GCTGCCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACG ACAGCACCAG CCCGCGTCTT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCCCTTGC GAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 172; ORF 042-1>:

m042-1.pep

```

1  MTMICLRFQA FVPRTSALSN TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51  KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVT DSTSPR
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSP LVRILPLSTV
151 SMVVAFFANC SYASAPGPPV MTS*

```

m042-1/g042 95.4% identity in 173 aa overlap

240

	10	20	30	40	50	60
m042-1.pep	MTMICLRFQAFVPTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
	:					
g042	MTMICLRFQAFVPTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042-1.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
g042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	
m042-1.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX					
	: : : : : :					
g042	ATRASLPKIRDRVSICFSPLVRILPLSTVKSMVVAFFANC SYASAPGPPVMTNCGLWRCR					
	130	140	150	160	170	180
g042	DSQSGSNSVPTVAALSNAGCKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 173>:

a042-1.seq

1	ATGACGATGA	TTTGCTTGCG	CTTCCAAGCG	TTCGTGCCGC	GTACCAGCGC
51	GTTATCCAAT	ACTTCGACAG	CCGCCGGCCC	TTCCTGCCCG	ATGGCGGCGG
101	TACGGTCGAT	GATGAAAATC	CAATCGGGGT	TTTTCTCTTT	GATGTATTCG
151	AAGGAAACAG	GCTGCCCGTG	CCCCTCGTTG	CGTAAAGATT	CGTCTACAGG
201	CGGTAGGCCG	ATGTCGCCGT	GTATCCAAC	TGCCAACCGC	GA CTGCGTGC
251	CGAAGGCGGA	CACCTTGTG	CCCGTAACCG	ACAGCACCAG	CCCGCGTCCT
301	TTGCCTTTGG	CGGCTTCGCG	CGTTTGGGCG	AACAGCGCGT	CAATCTGCGC
351	CTTCAATTCC	GCCGCGCGCG	CTTCCTTGCC	GAAAATCCGC	GCCAAGGTCT
401	CCATCTGCTT	TCGCGCGCTG	GTGCGGATAT	TGCCGTTGTC	CACCGTCAGA
451	TCTATGGTGG	TCGCGTTTTT	CGCCAACGTG	TCATACGCTT	CCGCGCCCGG
501	CCCGCCGGTA	A			

This corresponds to the amino acid sequence <SEQ ID 174; ORF 042-1.a>:

a042-1.pep

1	MTMICLRFQA	FVPTSALSN	TSTAAGPSCP	MAAVRSMMKI	QSGFFSLMYS
51	KETGCPCPSL	RKDSSTGGRP	MSPCIQLANR	DCVPKADTLL	PVT DSTSPRP
101	LPLAASRVWA	NSASICAFNS	AARASLPKIR	AKVSICFSPL	VRILPLSTVR
151	SMVVAFFANC	SYASAPGPPV	MTS*		

m042-1/a042-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
m042-1.pep	MTMICLRFQAFVPTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
a042-1	MTMICLRFQAFVPTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042-1.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
a042-1	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	
m042-1.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX					
a042-1	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 175>:

g043.seq

```

1 ATGGTTGTTT CAAATCAAAA TATCTATGCC GTCGGCCCAT CAGCACTTTT
51 TCACATCCGA AGGCAAAAAT CCGTAATGCC GCCTGAACGC TTCgttgaAC
101 CGTCCCGCGT ggcggtagcc gcAAAAGTGC ATcGCGGCTT GGATGGTGCT
151 GCCCGATTCTG ATGAGGGGcga gcGCGTGTTT CAGCCGCAGG CGGCGCAGGC
201 GTCCGGCGAC GGTTCGCGC GTTTGCGCTT TGAAATAGCG TTTCAGGTAG
251 CATTCGTTCA GCCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGGCG
301 GGCGAATTCG CTGTCAAAA TATCGGCGGC TTCGTCTATG CGCCGGCGGC
351 GGTAGCCGTT GTCGTGGCGG CGGAAGGTGA AGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 176; ORF 043.ng>:

g043.pep

```

1 MVVSNQNIYA VGPSALFHIR RQKSVMPER FVEPSRVAVA AKVHRGLDGA
51 ARFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AGDFDGDGQRA
101 GEFVQNIGG FVYAPAAVAV VVAEAGEA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 177>:

m043.seq

```

1 ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCCT CAGCACTTCT
51 TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101 CGTCCCGCGT GCGGGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT
151 GCCCGATTCTG ATGAGGGGCGA GCGCGTGTTT CAGCCGCAGG CGGCGCAGGC
201 ATCCGGCGAC GGTTCGCGC GTTTGCGCTT TGAAATAGCG TTTCAGGTAG
251 CATTCGTTCA GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GGCGAATTCG TGTTCAGGA TGTGCGCGC TTCGTCTATG CGCCGACGGC
351 GGTAACCGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 178; ORF 043>:

m043.pep

```

1 MVVSNQNIYA AGPSALLHIR RQKSVMPER FVEPSRVAVA AKVHGGLDGA
51 AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AGDFDGDGQRT
101 GEFVLQDVGG FVYAPTAVTV VVAEAGEAQ*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 043 shows 89.8% identity over a 128 aa overlap with a predicted ORF (ORF043.a) from *N. gonorrhoeae*:

m043/g043

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPSERFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
	: : : : : : :					
g043	MVVSNQNIYAVGPSALFHIRRQKSVMPSERFVEPSRVAVAAKVHRGLDGAARFDEGERVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFDGDGQRTGEFVLQDVGGFVYAPTAVTV					
	: : : : : : :					
g043	QPQAAQASGDGFAGLRFEIAFQVAFVQPDAAAGDFDGDGQRAGEFAVQNIGGFVYAPAAVAV					
	70	80	90	100	110	120
	130					
m043.pep	VVAEAGEAQX					
g043	VVAEAGEAAX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 179>:

a043.seq

```

1 ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCCT CAGCACTTCT
51 TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101 CGTCCCGCGT GCGGGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT

```

242

```

151 GCCGGATTCG ATGAGGGCGA GCGCGTGTTT CAGCCGCAGG CGGCGCAGGC
201 ATCCGGCGAC GGTTTCGCCG GTTTCGCGTT TGAAATAGCG TTTCAGGTAG
251 CATTCGTTCA GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GGCGAATTCG TGTTCAGGA TGTCGGCGGC TTCGTCTATG CGCCGACGGC
351 GGTAACCGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 180; ORF 043.a>:

```

a043.pep
1  MVVSNQNIYA AGPSALLHIR RQKSVMPSEF FVEPSRVAVA AKVHGGLDGA
51  AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AGDFGDGQRT
101 GEFVLQDVGG FVYAPTAVTV VVAAEGEAQ*

```

m043/a043 100.0% identity in 129 aa overlap

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPSEFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
a043	MVVSNQNIYAAGPSALLHIRRQKSVMPSEFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
a043	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
	70	80	90	100	110	120
	130					
m043.pep	VVAAEGEAQX					
a043	VVAAEGEAQX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 181>:

```

g044.seq
1  ATGCTGCCCC ACCAGAGCGT CGAGTTCTTG CCACAAGTCG TCGTTTTTGA
51  CGGGCTGTTT GGCGGCGGTT TTCCAGCCGT TGCGCTTCCA ACCGTGTATC
101 CAGTTTTTCCA TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTTGAGCG ATTTACAGCC TTGATAACG GCGGTCAGCT
201 CCATGCGGTT GTTGGTGGTT TGCGCTTCGC CGCCGAAAAG TTCTTTTTTCG
251 CGGCTGCCGT AGCGCATTA

```

This corresponds to the amino acid sequence <SEQ ID 182; ORF 044.ng>:

```

g044.pep
1  MLPDQSVEFL PQVVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
51  GAAAFERFQP FDNGGQLHAV VGGLRFAAEK FFFAAVAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 183>:

```

m044.seq
1  ATGCCGTCCT ACTAGAGCGT CGAGTTCTTT CCAGAAGTCG TCGTTTTTGA
51  CGGGCTGTTT GGAGGCGGTT TTCCAGCCGT TGCGCTTCCA ACCGTGTATC
101 CAGTTTTTCCA TGCCATTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTTGAGCG ATTTACAGTC TTGATGACG GCAGTCAGTT
201 CCATGCGGTT GTTGGTGGTT TGCGCTTCGC CGCCGAAAAG TTCTTTTTTCG
251 TGGCTACCGT AGCGCAyTAa

```

This corresponds to the amino acid sequence <SEQ ID 184; ORF 044>:

```

m044.pep
1  MPSDXSVEFF PEVVVFDGLF GGGFPAVALP TVYPVFHAI F DVLRVGADDD
51  GAAAFERFQS FDDGSQFHAV VGGLRFAAEK FFFVATVAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 185>:

```
a044.seq
1  GTGCCGTCCG ACCAGCGCGT CGAGTTCTTT CCACAAGTCG TCGTTTTTGA
51  CGGGCTGTTT GGCGCGGGT TTCCAGCCGT TGCCTTCCA ACCGTGTATC
101 CAGTTTTCCA TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTTGAGCG ATTTAGTCC TTCGATGACG GCGGTCAGTT
201 CCATACGGTT GTTGGTGGT TGCCTTCGC CGCCGAAAAG TTCTTTTTCG
251 TGGCTGCCGT AGCGCATTA
```

This corresponds to the amino acid sequence <SEQ ID 186; ORF 044.a>:

```
a044.pep
1  VPSDQRVEFF PQVVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
51  GAAAFERFQS FDDGGQFHTV VGGLRFAAEK FFFVAVAH*
```

m044/a044 91.0% identity over a 89 aa overlap

	10	20	30	40	50	60
m044.pep	MPSDXSVEFFPEVVVFDGLFGGGFPAVALPTVYPVFHAI FDVLRVGADDDGAAAFERFQS					
	: : : : : :					
a044	VPSDQRVEFFPQVVVFDGLFGGGFPAVALPTVYPVFHAVFDVLRVGADDDGAAAFERFQS					
	10	20	30	40	50	60
	70	80	90			
m044.pep	FDDGSQFHAVVGGLRFAAEKFFVATVAHX					
	: :					
a044	FDDGGQFHTVVGGLRFAAEKFFVAAVAHX					
	70	80	90			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 044 shows 86.5% identity over a 89 aa overlap with a predicted ORF (ORF 044.ng) from *N. gonorrhoeae*:

m044/g044

	10	20	30	40	50	60
m044.pep	MPSDXSVEFFPEVVVFDGLFGGGFPAVALPTVYPVFHAI FDVLRVGADDDGAAAFERFQS					
	: : : :					
g044	MLPDQSVEFLPQVVVFDGLFGGGFPAVALPTVYPVFHAVFDVLRVGADDDGAAAFERFQP					
	10	20	30	40	50	60
	70	80	90			
m044.pep	FDDGSQFHAVVGGLRFAAEKFFVATVAHX					
	: : :					
g044	FDNGGQLHAVVGGLRFAAEKFFFAA VAHX					
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 187>:

```
g046.seq
1  ATGTCGGCAA TGCTGCGTCC GACAAGCAGC CCGCCGcgcc gCGCCTGTAT
51  GATGACCATC CGCACGCGGT CGTCTGCAA ACGTAAACCG TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
151 CTGATGGTTT CGGTTATGCC gaATATGGAA AGGCTGCCGt TTTcGTTGTT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TtcgctGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG
301 ATGTTGGTTT CGTCGCTGCG GGagaGCGCG AGcagcaagt cggcatcttC
351 CgcgcggcgG Cgttataatg tgAAGGGGGA TGCGccgttg ccgaAAACGG
401 TTTGGacatc gaggcggctg CCTGTTTCCT GCAATGCTTT TTCGTCGATG
451 TCGATAAcgg TTACGTCGTT GTTGGTGATG GCGGCAAGGT TTTGCGCGAC
```

501 GGTAAGACCT ACCTGCCCCGT TGCCTAAAAT GAGGATTTTC ACGGTATGGG
551 TCGCCGGGTG A

This corresponds to the amino acid sequence <SEQ ID 188; ORF 046.ng>:

g046.pep
1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
101 MLVSSLRESA SSKSASSAPA RYNVKGDAPL PKTVWTSRRL PVSCNAFSSM
151 SITVTSLLVM AARFCATVEP TCPLPKMRIF TVWVAG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 189>:

m046.seq
1 ATGTCGGCAA TGCTGCGTCC GACAAGCAst CCGC.r.sGC gCGcCTGTAT
51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCTGGGG
151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTCGTTGTT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG
301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC
351 CGCGCCGGCG CGTTCTAATG TGAAGGGGGA TCGCGCGTTG CCGAAAACGG
401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG
451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC
501 GGTAAGACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG
551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 190; ORF 046>:

m046.pep
1 MSAMLRPTSX PXXRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM
151 SITVTSLLGM AARFCATVEP TCPLPKMRIF TVWVAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 191>:

a046.seq
1 ATGTCGGCAA TGCTGCGTCC GACAAGCAGT CCGCCGCGCC GCGCCTGTAT
51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCTGGGG
151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTCGTTGTT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG
301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC
351 CGCGCCGGCG CGTTCTAATG TGAAGGGGGA TCGCGCGTTG CCGAAAACGG
401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG
451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC
501 GGTAAGACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG
551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 192; ORF 046.a>:

a046.pep
1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM
151 SITVTSLLGM AARFCATVEP TCPLPKMRIF TVWVAE*

m046/a046 98.4% identity over a 186 aa overlap

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXXRACMMTIRTRSSAKRKT CNAPGQSIRP ASCSVTSCSG LMVSVMPNME					
a046	MSAMLRPTSSPPRRACMMTIRTRSSAKRKT CNAPGQSIRP ASCSVTSCSG LMVSVMPNME					

245

	10	20	30	40	50	60
m046.pep	70	80	90	100	110	120
	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSATLQATMLVSSLRESASSKSASSAPA					
a046						
	70	80	90	100	110	120
	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSATLQATMLVSSLRESASSKSASSAPA					
m046.pep	130	140	150	160	170	180
	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
a046						
	130	140	150	160	170	180
	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
m046.pep	TVWVAEX					
a046						
	TVWVAEX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 046 shows 97.3% identity over a 185 aa overlap with a predicted ORF (ORF 046.ng) from *N. gonorrhoeae*:

m046/g046

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXRXRACMMTIRTRSSAKRKTCNAPGQSIRPASCSTSCSGLMVSVMPNME					
g046						
	10	20	30	40	50	60
	MSAMLRPTSSPPRRACMMTIRTRSSAKRKTCNAPGQSIRPASCSTSCSGLMVSVMPNME					
m046.pep	70	80	90	100	110	120
	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSATLQATMLVSSLRESASSKSASSAPA					
g046						
	70	80	90	100	110	120
	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSATLQATMLVSSLRESASSKSASSAPA					
m046.pep	130	140	150	160	170	180
	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
g046						
	130	140	150	160	170	180
	RYNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLVMAARFCATVEPTCPLPKMRIF					
m046.pep	TVWVAEX					
g046						
	TVWVAGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 193>:

g047.seq

```

1  ATGGTCATCA TACAGGCGcg gcGCGGCGGG CTGCTTGTCG GACGCAGCAT
51  TGCCGACATC GCCCAAGATT TGCCGACGG GGCCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CCGCGCCGCA AACCGTCATC
151 ATCGAAGGCG ACGAAATCCT GTTTGCCGCC GCCGCCGAAA ACATCGGGGC
201 GGTACATACCc gaATTGCGCC CCAAAGAAAC CAGCACCCGC CGCATCATGA
251 TTGCCGGCGG CGGCAACATc tgctACCGCC TCGCCAAGCA GCTCGAACAC

```

```

301 GCATAcaacG TCAAAATCAT CGAATGCCGG CCGCGCcggtg ccgaATGGAT
351 AGCCGAAAAAC ctcgAcaacCA CCTCGTCCT GCAAGGTTTCG Gcaaccgacg
401 aAaccctgct cgAcaacgaa tacatcgacg aaatcgaCGT ATTCTGCGCC
451 CTGACCAACG ACGACGAAAG CAACATTatg tCCGCCCTTT TGGCGAAAAA
501 CCTcggcgCG AAGCgcggtca tcggCATCGT CAACCGCTCA AGCTACGTCTG
551 ATTTGCTCGA AGGCAACAAA ATCGACATCG TCGTCTCCCC CCACCTCATC
601 ACCATCGGCT CGATACTCGC CCACATCCGG CGCGGCGACA TCGTTGCCGT
651 CCACCCCATC CGGCGCGGCA CGGCGGAAGC CATCGAAGTC GTCGCGCACG
701 GCGACAAAAA AACTTCCGCC ATCATCGGCA GGCGCATCAG CGGCATCAAA
751 TGGCCCGAAG GCTGCCACAT TGCCGCCGTC GTCCGCCCGG GAACCGGCGA
801 AACCATTATG GGACACCATA CCGAAACCGT CATCCAAGAC GGTGACCACA
851 TCATCTTTTT CGTCTCGCGC CGGCGCATCC TGAACGAACT GGAGAACTC
901 ATCCAAGTCA AAATGGGCTT TTTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 194; ORF 047.ng>:

g047.pep

```

1 MVIIQARRGG LLVGRSIADI AQDLPGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETSTR RIMIAGGGNI CYRLAKQLEH
101 AYNVKIIECR PRRAEWIAEN LDNTLVLQGS ATDETLDDNE YIDEIDVFCA
151 LTNDDESIM SALLAKNLGA KRVIGIVNRS SYVDLLEGNK IDIVVSPHLI
201 TIGSILAHIR RGDIVAVHPI RRGTAEAIEV VAHGDKKTSA IIGRRISGIK
251 WPEGCHIAAV VRAGTGETIM GHHTETVIQD GDHIIFFVSR RRILNELEKL
301 IQVKMGFFG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 195>:

m047.seq

```

1 ATGGTCATCA TACAGgCGcG C..syGCGGA sTGCTTGTCG GACGCAGCAT
51 TGCCGACATC GCCCAAGATT TGCCCGACGG GGCCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTATCGTCC CCGCGCCGCA AACCGTCATC
151 ATCGAAGGCG ACGAAATCCT ATTTGCCGCC GCCGCCGAAA ACATCGGCGC
201 GGTCAATACC GAATTGCGCC CCAAAGAAAC CCAAAGAAAC CAGCcCmgmm
251 GcATCATGAT TkCCGCGCGC GGCAACATCG GCTACCGTCT CGCCAAGCAG
301 CTCGAACACG CATAAACGT yAAAATCATC GAATGCCGGC CGCGCCGTGC
351 CGAATGGATA GCCGAAAACC TCGACAACAC CCTCGTCyTG CAAGGTTTCGG
401 CAACCGACGA AACCTGCTC GACAACGAAT ACATCGACGA AATCGACGTA
451 TTCTGCGCCC TGACCAACGA CGACGAAAGC AACATTATGT CCGCCCTTTT
501 GGCGAaAAAC CTCGCGCGCA AGCGCGTCAT CGGCATCGTC AACCGCTCAA
551 GCTACGTCGA TTTGCTCGAA GGCAACAAAA TCGACATCGT CGTCTCCCCC
601 CACCTCATCA CCATCGGCTC GATACTCGCC CACATCCGGC GCGGCGACAT
651 CGTTGCCGTC CACCCCATCC GGCGCGGCAC GGCGGAAGCC ATCGAAGTCG
701 TCGCACACGG CGACAAAAA ACTTCCGCCA TCATCGGCAG GCGCATCAGC
751 GGCATCAAAT GGCCCGAAGG CTGCCACATT GCCGCCGTGC TCCGCGCCGG
801 AACCGGCGAA ACCATTATGG GACACCATAC CGAAACCGTC ATCCAAGACG
851 GCGACCACAT CATCTTTTTC GTCTCGCGCC GGCGCATCCT GAACGAACTG
901 GAAAAACTCA TCCAGGTCAA AATGGGCTTT TTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 196; ORF 047>:

m047.pep

```

1 MVIIQARXXG XLVGRSIADI AQDLPGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETQRN QPXXIMIXGG GNIGYRLAKQ
101 LEHAYNVKII ECRPRRAEWI AENLDNTLVL QGSATDETL DNEYIDEIDV
151 FCALTNDDES NIMSALLAKN LGAKRVIGIV NRSSYVDLLE GNKIDIVVSP
201 HLITIGSILA HIRRGDIVAV HPIRRGTAEI IEVVAHGDKK TSAIIGRRIS
251 GIKWPEGCHI AAVVRAGTGE TIMGHHTETV IQDGDHIIFF VSRRLNEL
301 EKLIQVKMGF FG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 197>:

a047.seq

```

1 ATGGTCATCA TACAGGCGCG GCGCGGCGGA CTGCTTGTCG GACGCAGCAT

```


a047.pep

1	MVIIQARRGG	LLVGRSIADI	AQDLPDGADC	QICAVYRNNR	LIVPAQPTVI
51	IEGDEILFAA	AAENIGAVIP	ELRPKETSTR	RIMIAGGGNI	GYRLAKQLEH
101	AYNVKIIECR	PRRAEWIAEN	LDNTLVLQGS	ATDETLLDNE	YIDEIDVFCA
151	LTNDDESNIM	SALLAKNLGA	KRVIGIVNRS	SYVDLLEGNK	<u>IDIVVSPHLI</u>
201	<u>TIGSILAHIR</u>	RGDIVAVHPI	RRGTAEAEIV	VAHGDKKTS	IIGRRISGIK
251	WPEGCHIAAV	VRAGTGETIM	GHHETETVIQD	GDHIIFVFSR	RRILNELEKL
301	IQVKGMGFE*				

m047/a047 96.5% identity over a 312 aa overlap

	10	20	30	40	50	60
m047.pep	MVIIQARXXGXLVGRSIADIAQDLPGADCQICAVYRNNRLIVPAPQTVIIIEGDEILFAA					
a047	MVIIQARRGGLLVGRSIADIAQDLPGADCQICAVYRNNRLIVPAPQTVIIIEGDEILFAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m047.pep	AAENIGAVIPELRPKETQRNQPPXIMIXGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI					
			:	:		
a047	AAENIGAVIPELRPKETSTRR---IMIAGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI					
	70	80	90	100	110	
	130	140	150	160	170	180
m047.pep	AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV					
a047	AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV					
	120	130	140	150	160	170
	190	200	210	220	230	240
m047.pep	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEIVVAHGDKK					
a047	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEIVVAHGDKK					
	180	190	200	210	220	230
	250	260	270	280	290	300
m047.pep	TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRRILNEL					
a047	TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRRILNEL					
	240	250	260	270	280	290
	310					
m047.pep	EKLIQVKMGFFGX					

a047 EKLIQVKMGFFGX
 300 310

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 047 shows 96.2% identity over a 312 aa overlap with a predicted ORF (ORF 047.ng) from *N. gonorrhoeae*:

m047/g045

m047.pep	MVIIQARXXGXLVGRSIADIAQDLPGADCQICAVYRNNRLIVPAPQTVIIIEGDEILFAA	60
g047	MVIIQARRGGLLVGRSIADIAQDLPGADCQICAVYRNNRLIVPAPQTVIIIEGDEILFAA	60
m047.pep	AAENIGAVIPELRPKETQRNQPPXIMIXGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI	120
	: :	
g047	AAENIGAVIPELRPKETSTR---IMIAGGGNICYRLAKQLEHAYNVKIIIECRPRRAEWI	117
m047.pep	AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV	180
g047	AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV	177
m047.pep	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK	240
g047	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK	237
m047.pep	TSIIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRIILNEL	300
g047	TSIIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRIILNEL	297
m047.pep	EKLIQVKMGFFGX 313	
g047	EKLIQVKMGFFGX 310	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 199>:

g048.seq

```

1  ATGCTCGACA AAGGCGAGGA GTTGCCCGTC GATTTCACCA ACCGCCTGAT
51  TTACTACGTc ggcCCcgTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCCG
101 CAGGTCCGAC CACAGCCACC CGCATGGACA AATTACCCG CCAAATGCTC
151 AAACAAACCG GCCTCTTGGG CATGATCGGC AAATCCGagc gcgGcgcggc
201 cacctGCGAA GCcatCGCCG ACAACAAGGC CGTGTAACCTC ATGGCAGTCG
251 GCGGCGCGGC ATACCTCGTG GCAAAGCCA TCAAATCTTC CAAAGTCTTG
301 GCGTTCCCCG AATTGGGTAT GGAAGCCGTT TACGAATTG AAGTCAAAGA
351 TATGCCCGTA ACCGTCGCCG TGGACAGCAA AGGCGAATCC ATCCACGCCA
401 CCGCCCGCG CAAATGGCAG GCGAAAATCG GCATCATCCC CGTCGAGTCT
451 TGA

```

This corresponds to the amino acid sequence <SEQ ID 200; ORF 048.ng>:

g048.pep

```

1  MLDKGEELPV DFTNRLIYYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML
51  KQTGLLMIG KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPELGMEAV YEFVKDMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 201>:

m048.seq

```

1  ATGCTCAACA AAGGCGAAGA ATTGCCCGTC GATTTCACCA ACCGCCTGAT
51  TTACTACGTC GGCCCCGTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCCG

```

```
m048.pep
  1 MLNKGEELPV DFTNRLIIYV GPVDPVGDEV VGPAGPTTAT RMDKFTQML
  51 EQTDLLGMIG KSERGVATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPELGMEAI YEFEVKDMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151 *
```

```
a048.seq
  1  ATGCTCGACA AAGGCGAAGA ATTGCCGCTC GATTTCACCA ACCGCCTGAT
51  TTA CTACGTG GGGCCCCGTC ATCCGGTCGG CGACGAAATC GTCGGGCCAG
101 CAGGTC CCGAC CACCGCCACC CGCATGGACA AATTCACCCG CCAAATGCTC
151 GAACAA AACC GACCTCTTGG CATGATCGGC AAATCCGAGC CGGGCGCGCG
201 CACCTG CGAA GCCATCGCCG ACAACA AAGC CGTGTA CCTC ATGGCAGTGC
251 GCGGCG CGGC GTATCT CGTG GCAAAAGCCA TCAAATCTTC CAAAGTCTTG
301 GCGTTC CCGG AATTGG GCAT GGAAGCCATT TACGAATTTG AAGTCAAAGA
351 CATGCC CGTA ACCGTC GCGG TAGACAGCAA AGGCGAATCC ATCCACGCCA
401 CCGCCCCG CCAATGGCAG GCGAAAATCG GCATCATCCC CGTCAAATCT
451 TGA
```

a048.pep

1	MLDKGEELPV	DFTNRLIIYV	GPVDPVGDEI	VGPAGPTTAT	RMDKFTRQML
51	EQTDLGMIG	KSERGAATCE	AIADNKAVYL	MAVGGAAYLV	<u>AKAIKSSKVL</u>
101	AFPELGMEAI	YEFEVKDMPV	TVAVDSKGES	IHATAPPQWQ	AKIGIIPVKS
151	*				

	10	20	30	40	50	60
m048.pep	MLNKGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLEQTDLLGMIG					
	: :					
a048	MLDKGEELPVDFTNRLIYYVGPVDPVGDEIVGPAGPTTATRMDKFTRQMLEQTDLLGMIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m048.pep	KSERGVATCEAIADNKAVYLMVAVGGAAYLVAKAIKSSKVLAFPELGMEAIYEFVVKDMPV					
	:					
a048	KSERGAATCEAIADNKAVYLMVAVGGAAYLVAKAIKSSKVLAFPELGMEAIYEFVVKDMPV					
	70	80	90	100	110	120
	130	140	150			
m048.pep	TVAVDSKGESIHATAPRKWQAKIGIIPVESX					
	:					
a048	TVAVDSKGESIHATAPPQWQAKIGIIPVKSX					
	130	140	150			

ORF 048 shows 96.4% identity over a 150 aa overlap with a predicted ORF (ORF 048.ng) from *N. gonorrhoeae*:

250

m048/g048

	10	20	30	40	50	60
m048 . pep	MLNKGEELPVDFTNRLIYYVGPVDPVGVDEVVGPAGPTTATRMDKFTRQMLEQTDLLGMIG					
	:					
g048	MLDKGEELPVDFTNRLIYYVGPVDPVGVDEVVGPAGPTTATRMDKFTRQMLKQTGLLGMIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m048 . pep	KSERGVATCEAIADNKAVYLMVGGAAAYLVAKAIKSSKVLAFPELGMEAIYEFVVKDMPV					
	:					
g048	KSERGAATCEAIADNKAVYLMVGGAAAYLVAKAIKSSKVLAFPELGMEAVYEFVVKDMPV					
	70	80	90	100	110	120
	130	140	150			
m048 . pep	TVAVDSKGESIHATAPRKQWQAKIGIIPVESX					
g048	TVAVDSKGESIHATAPRKQWQAKIGIIPVESX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 205>:

g049 . seq

1	ATGCGGGCGC	AGGCGTTTGA	TCAACCGTTC	GGTCAGCTCC	TGTTCCGACA
51	GGCAGAACAC	TTGCGCCCGG	TTGACGGCTT	TCGGGTTCAG	GATATTGATT
101	TGGACGGGCA	TCAACGCCTC	TTCCGCACCG	CCTTCGCCGT	TTTCCGCAAC
151	CCCGTCTGCC	GCCGTACCGG	ATTCTGCCGC	ATCGCGGTTT	TCCCGCCCT
201	CAATCTGTGC	GGTTTCAAAT	TCGGCACTGT	CTTTTTTGGC	ATCGAACCGG
251	ATTCTCCGCC	GCGATTCGAT	GTGTTTTTCC	GAAAccggca	tTTGCAGGGA
301	AGCCTGcgcg	TTGAGCCAGT	TTTCTGAAG	GACGATCATC	GGGTCGGTTT
351	CGACTTCCTC	GCCGCAATCG	GCAACGGGcg	tGTTGTGTTT	TTCCTGCCAT
401	TTCTTCAGAT	ACGCCTTTAA			

This corresponds to the amino acid sequence <SEQ ID 206; ORF 049.ng>:

g049 . pep

1	MRAQAFDQPF	GQLLFGQAEH	FAPVDGFRVQ	DIDLGHQRL	FRTAFVFRN
51	PVCRRTGFCR	IGVFPALNLC	GFKFGTVFFG	IEPDSPPRFD	VFFRNRHLQG
101	SLRVEPVFLK	DDHRVGFDL	AAIGNGAVVF	FLPFLQIRL*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 207>:

m049 . seq (partial)

1	ATGCGGGCGC	AGGCGTTTGA	TCAGCCGTTC	GGTCAGCTCC	TGTTCCGACA
51	GGCAGAACAC	TTGCGCCCGG	TTGACGGCTT	TCGGGTTCAG	GATATTGATT
101	TGGACGGGCA	TCAACGTTTC	TTCCGCATCG	TTTTCCCCGT	TTTCCGAAAC
151	CGCCGGCTCA	TTGCTGCCGG	ATTCTGCCTC	GTCGGCGTTT	TCCCGCTTT
201	CAATCTGTCC	GGTTTCAAAT	TCGACACTGT	CTTTTTTGGT	ATCAAACCGG
251	ATTCTCCGCC	GCGATTCGAT	GTGTTTTTCC	GAAACCGACA	TTTGCAGGGA
301	AGCCTGCGCG	TTGAGCCAGT	TTTCTGAAG	GACGATCATC	GGGTCGGTTT
351	CGACTTCCTC	GCCGCAATCG	GCAACGGCGG	CATTGTGTTT	CTCCTGCCAT
401	TTTTTCAGAT	ACGCCTT...			

This corresponds to the amino acid sequence <SEQ ID 208; ORF 049>:

m049 . pep (partial)

1	MRAQAFDQPF	GQLLFGQAEH	FAPVDGFRVQ	DIDLGHQRF	FRIVFPVFRN
51	RRLIRAGFCL	VGVPFANLS	GFKFDTVFFG	IKPDSPPRFD	VFFRNRHLQG
101	SLRVEPVFLK	DDHRVGFDL	AAINGGIVF	LLPFFQIRL...	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 209>:

a049 . seq

251

```

1  ATGCGGGCGC AGGCGTTTGA TCAGCCGTTT GGTCTAGCTCC TGTTCGGACA
51  GGCAGAACAC TTCGCGCCGG TTGACGGCTT TCGGGTTTCT AATATTGATT
101 TGGACGGGCA TCAACGCTTC TTCCGCACCG CCTTCGCCGT TTTCCGCAAC
151 CCCGTCTGCC GCCGTACCCG ATTCTGCCGC ATCGGCGTTT TCCCCGCCTT
201 CAATCTGTCC GGTTCCTCAAT TCGGCACTGT CTTTTTTTGGC ATCAAACCGG
251 ATTCTCCGCC GCGATTTCGAT GTGTTTTTCC GAAACCGACA TTTGCAGGGA
301 AGCCTGCGCG TTGAGCCAGT TTTCTGAAG GACGATCATC GGGTCGGTTT
351 CGACTTCCTC GCCGCAATCG GCAACGGCGG CATTGTGTTC CTCCTGCCAT
401 TTTTTCAGAT ACGCCTT

```

This corresponds to the amino acid sequence <SEQ ID 210; ORF 049.a>:

```

a049.pep
1  MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ NIDLDGHQRF FRTAFVFRN
51  PVCRRTRFCR IGVFFAFNLS GFKFGTVFFG IKPDSPPRFD VFFRNRHLQG
101 SLRVEPVFLK DDHRVGFDL AAIGNGGIVF LLPFFQIRL

```

m049/a049 90.6% identity over a 139 aa overlap

```

              10      20      30      40      50      60
m049.pep      MRAQAFDQPFQQLLFGQAEHFAPVDGFRVQDIDLDGHQRFRRIVFPVFRNRRLIRAGFCL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a049           MRAQAFDQPFQQLLFGQAEHFAPVDGFRVQNIDLDGHQRFRTAFVFRNPVCRRTRFCR
              10      20      30      40      50      60

              70      80      90     100     110     120
m049.pep      VGVFFAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRHLQGSRLRVEPVFLKDDHRVGFDL
              :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a049           IGVFFAFNLSGFKFGTVFFGIKPDSPPRFDVFFRNRHLQGSRLRVEPVFLKDDHRVGFDL
              70      80      90     100     110     120

              130     139
m049.pep      AAIGNGGIVFLLPFFQIRL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a049           AAIGNGGIVFLLPFFQIRL
              130

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 049 shows 86.3% identity over a 139 aa overlap with a predicted ORF (ORF 049.ng) from *N. gonorrhoeae*:

```

m049/g049
              10      20      30      40      50      60
m049.pep      MRAQAFDQPFQQLLFGQAEHFAPVDGFRVQDIDLDGHQRFRRIVFPVFRNRRLIRAGFCL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g049           MRAQAFDQPFQQLLFGQAEHFAPVDGFRVQDIDLDGHQRLFRTAFVFRNPVCRRTGFCR
              10      20      30      40      50      60

              70      80      90     100     110     120
m049.pep      VGVFFAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRHLQGSRLRVEPVFLKDDHRVGFDL
              :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g049           IGVFFPALNLCGFKFGTVFFGIEPDSPPRFDVFFRNRHLQGSRLRVEPVFLKDDHRVGFDL
              70      80      90     100     110     120

              130     139
m049.pep      AAIGNGGIVFLLPFFQIRL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g049           AAIGNGAVVFFLPFLQIRLX
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 211>:

```
g050.seq
  1 atgggCGCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGG
 51 cacgcccGAA AAAGccgtgt TGATGGcaaa AGAATCCCTG ATGAGCCACA
101 TCGACatCca aGaATTGCAG GAAAAAGCCG CGTccggggc ggaattgtcc
151 accaccgaAG ccCTGCGCCT cGAACTCTTT GAAAAGGTCA ACGCGCTGGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAT GCCGCCTCCA AACCGATTGC CATGATTCCC
301 AACTGTGCcg ccacCCGcca cgtcgAATTT GAATTGgACG GCTCAGgtcc
351 TGTCGAactc acgccGCcgc gtgtCGAAGA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 212; ORF 050.ng>:

```
g050.pep
  1 MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
 51 TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVED*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 213>:

```
m050.seq
  1 ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGTATCG GCATCGGCGG
 51 C..agCCgAA AAAGCCGTGC TGATGGCAAA AGAGTCCCTG ATGAGCCACA
101 TCGACATTCA AGAATTGCAG GAAAAGGCCG CGTCCGGCGC GgAATTGTCC
151 ACCACCGAAG CCCTGCGCCT CGAACTCTTT GAAAAGTCA ACGCGCTGGG
201 CATCGGCGCA CAAGGCTTGG GCGGACTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA TCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCCC
351 TGTCGAACTC ACGCCGCCGC GCGTCGAAGA TGGCCCGATT TGA
```

This corresponds to the amino acid sequence <SEQ ID 214; ORF 050>:

```
m050.pep
  1 MGAGWCPPGI LGIGIGGXAE KAVLMAKESL MSHIDIQELQ EKAASGAELS
 51 TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDGPI *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 215>:

```
a050.seq
  1 ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGG
 51 TACGCCCGAA AAAGCCGTGT TGATGGCGAA AGAATCCCTG ATGAGCCACA
101 TCGACATCCA AGAATTGCAG GAAAAGGCCG CGTCCGGCGC GGAATTGTCC
151 ACCACCGAAG CCCTGCGCCT CGAACTCTTT GAAAAGTCA ACGCGCTAGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCCC
351 TGTCGAACTC ACGCCGCCGC GCGTCGAAGA CTGGCCC
```

This corresponds to the amino acid sequence <SEQ ID 216; ORF 050.a>:

```
a050.pep
  1 MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
 51 TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDWP
```

m050/a050 97.7% identity over a 129 aa overlap

```

          10      20      30      40      50      60
m050.pep  MGAGWCPPGILGIGIGGXAEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF
          |||||: |||||: |||||: |||||: |||||: |||||:
a050       MGAGWCPPGILGIGIGGTPEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF
```

253

	10	20	30	40	50	60
m050.pep	70	80	90	100	110	120
	EKNVALGIGAQGLGGLTTVLDVKILDYPHTHAASKPIAMIPNCAATRHVEFELDGSGPVEL					
a050	EKNVALGIGAQGLGGLTTVLDVKILDYPHTHAASKPIAMIPNCAATRHVEFELDGSGPVEL					
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
a050	TPPRVEDWP					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 050 shows 98.4% identity over a 127 aa overlap with a predicted ORF (ORF 050.ng) from *N. gonorrhoeae*:

m050/g050

	10	20	30	40	50	60
m050.pep	MGAGWCPPGILGIGIGGXAEKAVLMAKESLSHIDIQELQEKAASGAELSTTEALRLLELF					
	:					
g050	MGAGWCPPGILGIGIGGTPEKAVLMAKESLSHIDIQELQEKAASGAELSTTEALRLLELF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m050.pep	EKNVALGIGAQGLGGLTTVLDVKILDYPHTHAASKPIAMIPNCAATRHVEFELDGSGPVEL					
g050	EKNVALGIGAQGLGGLTTVLDVKILDYPHTHAASKPIAMIPNCAATRHVEFELDGSGPVEL					
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
g050	TPPRVEDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 217>:

g050-1.seq

```

1  ATGACCGTTA TCAAGCAAGA AGACTTTATT CAAAGTATCT GCGATGCCTT
51  CCAATTCATC AGCTACTACC ATCCAAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AATCCGCGG CCAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCCGAA AACAACCGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCCTCAA AGTCGGTATG GATGTGCAAT
251 GGGATGCGGA CATGAGCGTG GAAAAGATGG TTAACGAAGG CGTACGCCGC
301 GCCTACACTT GGAAGGCAA CACCCTGCGC GCTTCGTCC TCGCCGATCC
351 GGCCGGCAAA CGCCAAAACA CCAAAGACAA CACCCCGCC GTCATCCACA
401 TGAGCATCGT GCCGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAGGC
451 GCGGCTCTG AAAACAATC CAAACTCGCT ATGCTCAACC CTCCGACAA
501 CATCGTCTG TGGGTATTGA AAACCATCCC GACGATGGG CCGGGCTGGT
551 GTCCTCCCG CATCTTGGG ATCGGCATCG GCGGCAcgc CGAAAAAGCC
601 GTGTTGATGG cgaAAGAATC CCTGATGAG CACATCGACA TCCAAGAATT
651 GCAGGAAAAA GCCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAAAG GTCAACGCGC TGGGCATCGG CGCGCAAGGC
751 TTGGGCGGTC TGACCACCGT GTTGACGTG AAAATCCTCG ATTACCCGAC
801 CCATGCCGCC TCCAAACCGA TTGCCATGAT TCCCAACTGT GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GTCCTGTGCA ACTCACGCCG
901 CCGCGCGTCG AAGACTGACC CGATCTGACT TACAGCCCG ACAACGGCAA
951 ACGCGTCGAT GTCGATAAGC TGACCAAAGA AGAAGTGGA AGCTGGAATA
1001 CCGGCGACGT ATTGCTGTTG AACGGCAAAA TCCTCACC GGCGGATGCC
1051 GCGCACAAC GCCTCGTCAA TATGCTCGAC AAAGGCGAGG AGTTGCCCGT
1101 CGATTTCACC AACCGCCTGA TTTACTACGT CGGCCCCGTC GATCCGGTCG
1151 CGATGAAGT CGTCGGTCCC GCAGGTCCGA CCACAGCAC CCGCATGGAC
1201 AAATTTACCC GCCAATGCT CAAACAAACC GGCTCTTG GCATGATCGG

```

```

1251 CAAATCCGAG CGCGGCGCGG CCACCTGCGA AGCCATCGCC GACAACAAGG
1301 CCGTGTACCT CATGGCAGTC GCGGCGCGG CATACTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GCGTTCCCC GAATTGGGTA TGGAAGCCGT
1401 TTACGAATTT GAAGTCAAAG ATATGCCCGT AACCGTCGCC GTGGACAGCA
1451 AAGGCGAATC CATCCACGCC ACCGCCCGC GCAAATGGCA GGCAGAAATC
1501 GGCATCATCC CCGTCGAGTC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 218; ORF 050-1.ng>:

g050-1.pap

```

1  MTVIKQEDFI QSIDAFQFI SYHHPKDYID ALYKAWQKEE NPAAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVG M DVQWDADMSV EKMVNEGVR
101 AYTWEENTLR ASVLADPAGK RQNTKDNTPA VIHMSIVPGG KVEVTCAAKG
151 GGSENKSKLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMAKESLMS HIDIQELQEK AASGAELSTT EALRLELFEK VNALGIGAQQ
251 LGGLTTVLDV KILDYPTTHA SKPIAMIPNC AATRHVEFEL DSGPVELTP
301 PRVED*PDLT YSPDNGKRVD VDKLTKEEVA SWKTGDVLLL NGKILTGRDA
351 AHKRLVNMLD KGEELPVDFE NRIIYVGPV DPVGDEVVGP AGPTTATRMD
401 KFTRQMLKQT GLLGMIGKSE RGAATCEAIA DNKAVYLMV GGAAYLVAKA
451 IKSSKVLAF ELMGEAVYEF EVKDMPTVA VDSKGESHA TAPRKWQAKI
501 GIIPVES*

```

g050-1/p14407

```

sp|P14407|FUMB_ECOLI FUMARATE HYDRATASE CLASS I, ANAEROBIC (FUMARASE)
>gi|280063|pir|B44511 fumarate hydratase (EC 4.2.1.2) fumB, iron-dependent - Escherichia coli
>gi|146048 (M27058) anaerobic class I fumarase (EC 4.2.1.2) [Escherichia coli] Length = 548
Score = 172 bits (432), Expect = 4e-42
Identities = 138/488 (28%), Positives = 216/488 (43%), Gaps = 22/488 (4%)

```

```

Query: 11 QSIDAFQFISYHHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAENNRPICQDTG 70
      Q+ DA + H K L+ E + K Q L NS + A+ P CQDTG
Sbjct: 53 QAFHDASFMLRPAHQKQVAAILHDPEASEND---KYVALQFLRNSEIAAKGVLPCTCQDTG 109

```

```

Query: 71 IATVFLKVGMDVQWDADMSVEKMVNEGVRRAITWEGNTLRASVLADPAGKRQNTKDNTPA 130
      A + K G V W E+ +++GV Y E N + A K NT N PA
Sbjct: 110 TAIIVGKKQGRV-WTGGGD-EETLSKGVNTYI-EDNLRYSQNAALDMYKEVNTGTNLPA 166

```

```

Query: 131 VIHMSIVPGGKVEVTCAAKGGGSENKSKL-----AMLNPSDNIVDWVLKTIPTMGAGWCP 185
      I + V G + + C AKGGGS NK+ L A+L P + +++++ + T+G CP
Sbjct: 167 QIDLYAVDGEYKFLCVAKGGGSANKTYLYQETKALLTPG-KLKNFLVEKMRTLGTAAACP 225

```

```

Query: 186 PXXXXXXXXXTPEKAVLMAKESLSHIDIQELQEKAAAGELSTTEALRLELFEKVNXXX 245
      P T + L + +H EL + + L EL E+
Sbjct: 226 PYHIAFVIGGTS AETNLKTVKLASAHY-YDELPTGEGNEHQAFRDVQLEQELLEEAQKLG 284

```

```

Query: 246 XXXXXXXXXXXTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGGSG---PVELTPP 301
      D++++ P H AS P+ M +C+A R+++ +++ G +E P
Sbjct: 285 LGAQFGGKYFAH-DIRVIRLPRHGASCPVGMGVSCSADRNIKAKINREGIWIEKLEHNPG 343

```

```

Query: 302 RVEDXPDLTYSYSPDNGKRVDVDKLTKE---EVASWKTGDVLLNGKILTGRDAAHKRLVNM 358
      + +VD+++ KE +++ + L L G I+ GRD AH +L +
Sbjct: 344 QYIPQELRQAGEAVKVDLNRPMKEILAQLSQYPVSTRSLTGTIIVGRDIAHAKLKL 403

```

```

Query: 359 LDKGEELPVDFE NRIIYXXXXXXXXXXXXXXXXTTATRMDKFTRQMLKQTGLLGMIGK 418
      +D G+ELP + IYY TTA RMD + + G + M+ K
Sbjct: 404 IDAGKELPQYIKDHPIIYAGPAKTPAGYPSGSLGPTTAGRMDSYVDLLQSHGSGMIMLAK 463

```

```

Query: 419 SERGAATCEAIADNKAVYLMVAVGG-AAYLVAKAIKSSKVLAFPELMEAVYEFVVDMPV 477
      R +A + YL ++GG AA L ++IK + +A+PELMEAAA EV+D P
Sbjct: 464 GNRSQQVTDACHKHGGFYLGSIIGPAAVLAQOSIKHLECVAYPELMEAIWKIEVEDFPA 523

```

```

Query: 478 TVAVDSKG 485
      + VD KG

```

```

Sbjct: 524 FILVDDKG 531

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 219>:

m050-1.seq

```

1  ATGACCGTCA TCAAACAGGA AGACTTTATC CAAAGCATTT GCGATGCCTT
51  CCAATTCATC AGCTACTATC ATCCCAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AATCCTGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCGGAA AACAAACGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCTCAA AGTCGGTATG AACGTCCAAT
251 GGGATGCGGA CATGAGCGTG GAAGAGATGG TTAACGAAGG CGTACGCCGC

```



```

301 GCCTACACTT GGGGAAGGCAA TACGCTGCGC GCTTCCGTCC TCGCCGATCC
351 GGCCGGCAAA CGCCAAAAACA CCAAAGACAA CACCCCGGCC GTCATCCATA
401 TGAGCATCGT GCCGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GGCGGCTCTG AAAACAAATC CAAACTCGCC ATGCTCAATC CTTCCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACCATGGGC GCGGGCTGGT
551 GTCTCTCCGG CATCTTGGGT ATCGGCATCG GCGGCACGCC CGAAAAAGCC
601 GTGCTGATGG CAAAAGAGTC CCTGATGAGC CACATCGACA TTCAAGAATT
651 GCAGGAAAAG GCCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAAAA GTCAACGCGC TGGGCATCGG CGCACAAGGC
751 TTGGGCGGAC TGACCACCGT GTGGACGTG AAAATCCTCG ATTATCCGAC
801 CCACGCCGCC TCCAAACCGA TTGCCATGAT TCCGAATGC GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GCCCTGTCGA ACTCACGCCG
901 CCGCGCGTCG AAGACTGGCC CGATTTGACT TACAGCCCGG ACAACGGCAA
951 ACGCGTCGAT GTCGACAAGC TGACCAAGA AGAAGTGGCA AGCTGGAAAA
1001 CCGGCGACGT ATTGCTGTTG AACGGCAAAA TCCTCACCGG CCGCGATGCC
1051 GCACACAAAC GCCTCGTCGA TATGCTCAAC AAAGCGAAG AATTGCCCGT
1101 CGATTTCACC AACCGCCTGA TTTACTACGT CGGCCCGGTC GATCCGGTCG
1151 GCGATGAAGT CGTCGGTCCG GCAGGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTCACCC GCCAAATGCT CGAACAACC GACCTCTTGG GCATGATCGG
1251 CAAATCCGAG CGCGGCGTGG CCACCTCGCA AGCCATCGCC GACACAAAG
1301 CCGTGATCCT CATGGCAGTC GCGGCGCGCG CGTATCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GGCGTTCCCC GAATTGGGCA TGGAAGCCAT
1401 TTACGAATTT GAAGTCAAAG ACATGCCCGT AACCGTCGCC GTAGATAGCA
1451 AAGGCGAATC CATCCACGCC ACCGCCCGC GCAAATGGCA GGCAGAAATC
1501 GGCATCATCC CCGTCGAATC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 220; ORF 050-1>:

m050-1.pep

```

1  MTVIKQEDFI QSIDAFQFI SYHHPKDYID ALYKAWQKEE NPAAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVGM NVQWDADMSV EEMVNEGVR
101 AYTWEGNTRL ASVLADPAGK RQNTKDNTPA VIHMSIVPGG KVEVTCAAKG
151 GGSSENKSLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMAKESIMS HIDIQELQEK AASGAELSTT EALRLELFEK VNALGIGAQG
251 LGGLTTVLDV KILDYPTTHA SKPIAMIPNC AATRHVEFEL DSGSPVELTP
301 PRVEDWPDLT YSPDNGKRVD VDKLTKEEVA SWKTGDVLLL NGKILTGRDA
351 AHKRLVMDLN KGEELPVDFE NRIIYVGPV DPVGDEVVGP AGPTTATRMD
401 KFTRQMLEQT DLLGMIGKSE RGVATCEAIA DNKAVYLMV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAIYEF EVKDMPTVTA VDSKGESIHA TAPRKWQAKI
501 GIIPVES*

```

m050-1/g050-1 98.2% identity in 507 aa overlap

	10	20	30	40	50	60
m050-1.pep	MTVIKQEDFIQSIDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
g050-1	MTVIKQEDFIQSIDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m050-1.pep	NNRPICQDTGIATVFLKVGMNVQWDADMSVEEMVNEGVRRAITWEGNTRLASVLADPAGK					
g050-1	NNRPICQDTGIATVFLKVGMDVQWDADMSVEKMNNEGVRRAITWEGNTRLASVLADPAGK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m050-1.pep	RQNTKDNTPAVIHMSIVPGGKVEVTCAAKGGGSENKSLAMLNPSDNIWDVWLKTIPTMG					
g050-1	RQNTKDNTPAVIHMSIVPGGKVEVTCAAKGGGSENKSLAMLNPSDNIWDVWLKTIPTMG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m050-1.pep	AGWCPPGILGIGIGGTPEKAVLMAKESLSHIDIQELQEKAASGAELSTTEALRLELFEK					
g050-1	AGWCPPGILGIGIGGTPEKAVLMAKESLSHIDIQELQEKAASGAELSTTEALRLELFEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m050-1.pep	VNALGIGAQGLGGLTTVLVDVKILDYPTTHAASKPIAMIPNCAATRHVEFELDSGSPVELTP					
g050-1	VNALGIGAQGLGGLTTVLVDVKILDYPTTHAASKPIAMIPNCAATRHVEFELDSGSPVELTP					
	250	260	270	280	290	300

256

	310	320	330	340	350	360
m050-1.pep	PRVEDWPDLTYS	PDNGKRV	VDKLTKEE	VASWKTG	VDVLLNGK	ILTGRDA
g050-1	PRVEDXPDLTYS	PDNGKRV	VDKLTKEE	VASWKTG	VDVLLNGK	ILTGRDA
	310	320	330	340	350	360
	370	380	390	400	410	420
m050-1.pep	KGEELPVDF	TNRLIYY	VGPVDP	VGDEVV	GPA	GPTTAT
g050-1	KGEELPVDF	TNRLIYY	VGPVDP	VGDEVV	GPA	GPTTAT
	370	380	390	400	410	420
	430	440	450	460	470	480
m050-1.pep	RGVATCEA	IADNKAV	YLMVGG	AAYLVAK	AIKSSK	VLAFPE
g050-1	RGVATCEA	IADNKAV	YLMVGG	AAYLVAK	AIKSSK	VLAFPE
	430	440	450	460	470	480
	490	500				
m050-1.pep	VDSKGESI	HATAPRK	WQAKIG	IIPVES	X	
g050-1	VDSKGESI	HATAPRK	WQAKIG	IIPVES	X	
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 221>:

a050-1.seq

1	ATGACCGTCA	TCAACAGGA	AGACTTTATC	CAAAGCATTT	GCGATGCCTT
51	CCAATTCATC	AGCTACTACC	ATCCCAAAGA	CTACATCGAC	GCGCTTTATA
101	AGGCGTGGCA	GAAGGAAGAA	AACCCCGCCG	CCAAAGACGC	GATGACGCAG
151	ATTTTGGTCA	ACAGCCGCAT	GTGTGCCGAA	AACAACCGCC	CCATCTGCCA
201	AGATACCGGT	ATCGCGACCG	TGTTTTTGAA	AGTCGGTATG	GATGTGCAAT
251	GGGATGCAGA	CATGAGCGTC	GAAGAGATGG	TTAACGAAGG	CGTGCGCCGC
301	GCCTACACTT	GGGAAGGCAA	TACGCTGCGC	GCTTCCGTTC	TCGCCGACCC
351	CGCCGGCAAA	CGCCAAAATA	CCAAAGACAA	CACGCCCGCC	GTCCATCCATA
401	TGAGCATCGT	GCCGGGCGAC	AAAGTCGAAG	TAACCTGCGC	GGCAAAAGGC
451	GGCGGTTCTG	AAAACAAATC	CAAACCTCGC	ATGCTCAACC	CTTCCGACAA
501	CATCGTCGAT	TGGGTATTGA	AAACCATTCC	GACCATGGGC	GCGGGCTGGT
551	GTCTTCCCGG	CATCTTGGGC	ATCGGCATCG	GCGGTACGCC	CGAAAAGGCC
601	GTGTTGATGG	CGAAAGAATC	CCTGATGAGC	CACATCGACA	TCCAAGAATT
651	GCCAGGAAAA	GCCGCGTCCG	GCGCGGAATT	GTCCACCACC	GAAGCCCTGC
701	GCCTCGAACT	CTTTGAAAAA	GTCAACGCGC	TAGGCATCGG	CGCGCAAGGC
751	TTGGGCGGTC	TGACCACCGT	GTTGGACGTG	AAAATCCTCG	ATTACCCGAC
801	CCACGCCGCC	TCCAAACCGA	TTGCCATGAT	TCCGAAGTGC	GCCGCCACCC
851	GCCAGGTCGA	ATTTGAATTG	GACGGCTCAG	GCCCTGTGCA	ACTCAGCCCG
901	CCGCGCGTCG	AAGACTGGCC	CGATTTGACT	TACAGCCCCG	ACAACGGCAA
951	ACGCGTCGAT	GTCGACAAGC	TGACCAAAGA	AGAAGTGCA	AGCTGAAAAA
1001	CCGCGCACGT	ATTGCTGTTG	AACGGCAAAA	TCCTCACCGG	CCGCGATGCC
1051	GCACAGCAAA	GCCTCGTCGA	TATGCTCGAC	AAAGGCGAAG	AATTGCCCGT
1101	CGATTTCACC	AACCGCCTGA	TTTACTACGT	CGGCCCGGTC	GATCCGGTCG
1151	GCGACGAAAT	CGTCGGCCCA	GCAGGTCCGA	CCACCGCCAC	CCGCATGGAC
1201	AAATTCACCC	GCCAAATGCT	CGAACAACCC	GACCTCTTGG	GCATGATCGG
1251	CAATCCCGAG	CGCGGCGCGG	CCACCTGCGA	AGCCATCGCC	GACAACAAAG
1301	CCGTGTACCT	CATGGCAGTC	GGCGGCGCGG	CGTATCTCGT	GGCAAAAGCC
1351	ATCAAATCTT	CCAAAGTCTT	GGCGTTCGCC	GAATTGGGCA	TGGAAGCCAT
1401	TTACGAATTT	GAAGTCAAAG	ACATGCCCGT	AACCGTCGCC	GTAGACAGCA
1451	AAGGCGAATC	CATCCACGCC	ACCGCCCCGC	CCCAATGGCA	GGCGAAAATC
1501	GGCATCATCC	CCGTCAAATC	TTGA		

This corresponds to the amino acid sequence <SEQ ID 222; ORF 050-1.a>:

a050-1.pep

1	MTVIKQEDFI	QSICDAFQFI	SYHPKDYID	ALYKAWQKEE	NPAAKDAMTQ
51	ILVNSRMCAE	NNRPICQDTG	IATVFLKVGM	DVQWDADMSV	EEMVNEGVR
101	AYTWEGNTLR	ASVLADPAGK	RQNTKDNTPA	VIHMSIVPGD	KVEVTCAAKG
151	GGSENKSKLA	MLNPSDNIVD	WVLKTIPTMG	AGWCPPGILG	IGIGGTPEKA
201	VLMAKESLMS	HIDIQELQEK	AASGAELSTT	EALRLELFKE	VNALGIGAQQ
251	LGGLTTVLVD	KILDYPHTAA	SKPIAMIPNC	AATRHVEFEL	DGSGPVELTP
301	PRVEDWPDLT	YSPDNGKRV	VDKLTKEEVA	SWKTGDVLLL	NGKILTGRDA
351	AHKRLVDMLD	KGEELPVDF	TNRLIYYVGP	DPVGDEIVGP	AGPTTATRMD
401	KFTRQMLEQT	DLGMIKSE	RGAAATCEAIA	DNKAVYLMV	GGAAYLVAKA
451	IKSSKVLAFP	ELGMEAIYEF	EVKDMPVTVA	VDSKGESIHA	TAPPQWQAKI
501	GIIPVKS*				

a050-1/m050-1 98.4% identity in 507 aa overlap

```

      10      20      30      40      50      60
a050-1.pep MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE
          |||
m050-1      MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE
          |||
      10      20      30      40      50      60

      70      80      90     100     110     120
a050-1.pep NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAYTWEGNTRLASVLADPAGK
          |||
m050-1      NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAYTWEGNTRLASVLADPAGK
          |||
      70      80      90     100     110     120

      130     140     150     160     170     180
a050-1.pep RQNTKDNTPAVIHMSIVPGDKVEVTCAAKGGGSENKSKLAMLNPSDNIVDWVLKTIPTMG
          |||
m050-1      RQNTKDNTPAVIHMSIVPGDKVEVTCAAKGGGSENKSKLAMLNPSDNIVDWVLKTIPTMG
          |||
      130     140     150     160     170     180

      190     200     210     220     230     240
a050-1.pep AGWCPPGILGIGIGGTPEKAVLMAKESLSMHSIDIQELQEKAASGAELSTTEALRLELFK
          |||
m050-1      AGWCPPGILGIGIGGTPEKAVLMAKESLSMHSIDIQELQEKAASGAELSTTEALRLELFK
          |||
      190     200     210     220     230     240

      250     260     270     280     290     300
a050-1.pep VNALGIGAQGLGGLTTVLVDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGS GPVELTP
          |||
m050-1      VNALGIGAQGLGGLTTVLVDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGS GPVELTP
          |||
      250     260     270     280     290     300

      310     320     330     340     350     360
a050-1.pep PRVEDWPDLTYS PDNGKRV DDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLD
          |||
m050-1      PRVEDWPDLTYS PDNGKRV DDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLN
          |||
      310     320     330     340     350     360

      370     380     390     400     410     420
a050-1.pep KGEELPVDFTNRLIYYVGPVDPVGDEIVGPAGPTTATRMDFTRQMLEQTDLLGMIGKSE
          |||
m050-1      KGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDFTRQMLEQTDLLGMIGKSE
          |||
      370     380     390     400     410     420

      430     440     450     460     470     480
a050-1.pep RGAATCEAIADNKAVYLMVGGAAYLVAKAISKSKVLAFPELGMEAIYEFV KDMPTVA
          |||
m050-1      RGVATCEAIADNKAVYLMVGGAAYLVAKAISKSKVLAFPELGMEAIYEFV KDMPTVA
          |||
      430     440     450     460     470     480

      490     500
a050-1.pep VDSKGESIHATAPPQWQAKIGIIPVKSX
          |||
m050-1      VDSKGESIHATAPRKWQAKIGIIPVESX
          |||
      490     500

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 223>:

g052.seq

```

1  ATGGCTTTGG TGGCGGAGGA AACGGAATA TCCGCGCCGT GTTTCAAAGG
51 CTGCGAGCCG ACGGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
151 AAGGGGTTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC
201 GGCGGCTTTC CATTCAATTA TATCAGTCGG CGACACGGG CTCACTCCGA
251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA
351 CGCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 224; ORF 052.ng>:

g052.pep

1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP
 51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN
 101 RLRLETTWSP ACRKVKNA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 225>:

m052.seq
 1 ATGGCTTTGG TGGCGGAGGA AACGGAAATA TCCGCGCCGT GTTTCAAAGG
 51 CTGCGAGCCG ACGGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
 101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
 151 AAGGGGTTGG ACGGCGTTTC CAAAACAGC AGTTTGGTGT TGGCTTTGAC
 201 GGCGGCTTTC CATTCATTTA TATCAGTCGG CGACACGGC CTCACTCCGA
 251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
 301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA
 351 CGCCGCCTGA

This corresponds to the amino acid sequence <SEQ ID 226; ORF 052>:

m052.pep
 1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP
 51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN
 101 RLRLETTWSP ACRKVKNA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 227>:

a052.seq
 1 ATGGCTTTGG TCGCGGAGGA AACGGAAATA TCCGCGCCGT GTTTCAAAGG
 51 CTGAGAGCCG ACAGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
 101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCTCCC
 151 AAGGGATTGG ACGGCGTTTC CAAAACAGC AGTTTGGTGT TGGCTTTGAC
 201 GGCGGCTTTC CATTCGTTTA TATCAGTCGG CGACACGTGA CTCACTTCGA
 251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
 301 AGGCTGCGGC TGGAAATCAC ATGGTCGCCC GCCTGCAAAA AGGTGAAAAA
 351 CGCCGCCTGA

This corresponds to the amino acid sequence <SEQ ID 228; ORF 052.a>:

a052.pep
 1 MALVAEETEI SAPCFKG*EP TGDSRLLSTT KSAPMPCANS AKASKSATSP
 51 KGLDGVSKNS SLVLALTAAF HSFISVGD* LTSMPLVTM LLIKPTVVPN
 101 RLRLEITWSP ACKKVKNA*

m052/a052 95.8% identity over a 119 aa overlap

	10	20	30	40	50	60
m052.pep	MALVAEETEISAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
a052	MALVAEETEISAPCFKGXEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m052.pep	SLVLALTAAFHSFISVGDTRLTPMPNLVTMLLIKPTVVPNRLRLETTWSPACRKVKNAAX					
a052	SLVLALTAAFHSFISVGDXTLTSMPNLVTMLLIKPTVVPNRLRLEITWSPACKKVKNAAX					
	70	80	90	100	110	120

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 052 shows 95.8% identity over a 119 aa overlap with a predicted ORF (ORF 052.ng) from *N. gonorrhoeae*:

m052/g052

	10	20	30	40	50	60
m052.pep	MALVAEETEISAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					

259

```

g052      MALVAEETEISAPCFKGCEPTGDSRLSTTKSAPMPCANSASKSATSPPKGLDGVSKNS
           10      20      30      40      50      60
           70      80      90      100     110     120
m052 .pep  SLVLALTAAFHSFISVGDTWLTSMPLNLTMLLIKPTVVPNRLRLEITWSPACKKVKNAA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g052      SLVLALTAAFHSFISVGDTRLTMPNLTMLLIKPTVVPNRLRLETTWSPACRKVKNAAX
           70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 229>:

```

g073 .seq
  1  ATGTGTATGC CATACGCAAT AAGGGTTTCA GACGGCATCT GCCGCATTTT
 51  TCCGCCGATG CCGTCTGAAA CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101  AATCGTCAAT CAAATCGCCA ACATATTCCA AACCACCAGA CAGGCGCACC
151  AGTCCGGGGC GGatacCGGC GCGGAGTTT TCTTCGGGCT GCATCCTGCC
201  GTGCGTGGTT GTCCACGGAT TGGTGATGGT CGAGCGCACG TCGCCGAGGT
251  TGGCGGTACG GGAAAAGAGT TCCACGACTT TCCACGCGGC TGCTTGGTCG
301  GCGACTTCAA AACCAGATGAC GATGCCGCCG CCGTTTGTCT GTTTGCGGAT
351  AAGCTCCGCC TCGGATGGT CGGGCAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 230; ORF 073.ng>:

```

g073 .pep
  1  MCMPIAIRVS DGICRIFPPM PSETRNQRAS ACFKSSIKSP TYSKPTDRRT
 51  SPGRIPAASF SSGCILPCVV VHGLVMVERT SPRLAVREKS STTFHAAAWS
101  ATSKPMTMPP PFCCLRISSA CGWSGNPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 231>:

```

m073 .seq
  1  ATGTGTATGC CATATAAGAT AAGGGTTTCA GACGGCATCT GCTGTCCAAT
 51  GCCGTCTGAA ACACGCAATC AGCGTGCGAG TGCCTGTTTC AAATCGTCAA
101  TCAAATCGCC AACATATTCC AAACCGACCG ACAGGCGCAC CAATCCGGGG
151  CGGATGTTGG CGGCGAGTTT TTCTTCGGGC TGCATCCTGC CGTGCGTGGT
201  TGTCCACGGG TGGGTAATGG TCGAGCGCAC GTCACCGAGG TTGGCGGTGC
251  GGGAAAAGAG TTCCACGCCG TCCACAACCT TCCACGCCGC TTCTTGATCG
301  GCAACTTCAA AGCCGATGAC GATGCCGCCG CCGTTTGTCT GTTTGCGGAT
351  AAGCGCCGCC TGAGGATGGT CGGACAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 232; ORF 073>:

```

m073 .pep
  1  MCMPIKIRVS DGICCPMPSE TRNQRASACF KSSIKSPTYS KPTDRRTNPG
 51  RMLAASFSSG CILPCVVVHG WVMVERTSPR LAVREKSSTP STTFHAASXS
101  ATSKPMTMPP PFCCLRISAA XGWSNPNV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 233>:

```

a073 .seq
  1  ACGTGTATGT CATATAAGAT AAGGGTTTCA GACGGCATTT GCGGTGTTTT
 51  TCCGCCGATG CCGTCTGAA. CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101  AATCGTCAAT CAAATCGCCA ACATATTCCA AACCACCAGA CAGGCGCACC
151  AATCCGGGGC GGATGTTGGC GCGGAGTTT TCTTCGGGCT GCATCCTGCC
201  GTGCGTGGTT GTCCACGGAT GGGTAATGGT CGAGCGCACG TCGCCGAGGT
251  TGCGGGTACG GGAGAAAAGT TCGACGCCGT CCACGACTTT CCACGCGGCT
301  GCTTGGTCCG GCACTTCAAA GCCGATGACG ATGCCGCCGC CGTTTGTCTG
351  TTTGCGGATA AGCTCCGCCT GAGGATGGTC GGGTAATCCG GTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 234; ORF 073.a>:

```

a073 .pep
  1  TCMSYKIRVS DGICGVFPPM PSEXNRQRAS ACFKSSIKSP TYSKPTDRRT
 51  NPGRMLAASF SSGCILPCVV VHGWVMVERT SPRLAVREKS STPTTFHAA
101  AWSATSKPMT MPPPFCLRI SSA*GWSGNP V*

```

m073/a073 92.3% identity over a 130 aa overlap

260

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICCC---PMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
a073	TCMSYKIRVSDGICGVFPMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVVHGWMVERTSPRLAVREKSSTPSTTFHAASXSATSKPMTMPPPFCCCLRI				
a073	SSGCILPCVVVHGWMVERTSPRLAVREKSSTPSTTFHAAAWSATSKPMTMPPPFCCCLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSNPNVX				
a073	SSAXGWSGNPNVX				
	130				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 073 shows 87.0% identity over a 131 aa overlap with a predicted ORF (ORF 073.ng) from *N. gonorrhoeae*:

m073/g073

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICCC---PMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
g073	MCMPIAIRVSDGICRIFPPMPSETRNQRASACFKSSIKSPTYSKPTDRRTSPGRIPAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVVHGWMVERTSPRLAVREKSSTPSTTFHAASXSATSKPMTMPPPFCCCLRI				
g073	SSGCILPCVVVHGLVMVERTSPRLAVREKSST---TFHAAAWSATSKPMTMPPPFCCCLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSNPNVX				
g073	SSACGWSGNPNVX				
	120				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 235>:

g075.seq

```

1  ATGCCGCCTT ACTTCATCAC CCTCTTAACG ATGGAAAATA CAAAAAGCGC
51  GGCGAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CGGCTTCCAA AGCGTTTITT GCCGTTTCGG GCAACGCTGC GTTTCCTGT
151 GCCGCCAAAG CCAGCGGGGC GGCTGTTACA ACAGCCAGTT TTGCGCCGTA
201 TTTACGGCAG GTGTTAATAA ATTTTCATGAT ATTTTCCTTT ACGAAATTTT
251 TAAAAAATG TGTTCGCGG CTTTGTGAAG GTTTTAGAGA CCGCTGCCG
301 GGCCTCTTAA ACTTAATCTT CTTTTCGTA GAATCCGAAA ATTACAAATT
351 CCCCCTAT CTCTTCAAT GCCGAGCTAA AAGCGTCTT ATAGCTGTCA
401 TATTTACCGG CTGA

```

This corresponds to the amino acid sequence <SEQ ID 236; ORF 075.ng>:

g075.pep

```

1  MPPYFITLLT MENTKSAKT PTTIQPASIP SAFAASKAFF AVSGNAAFAC
51  AAKASGAAVT TASFAPYLQ VLINFMIFSF TKFLKKVCG LCEGFRDLRP
101 GLLNLIFFFV ESENYKFPAY LFQCRASVSV IAVIFTG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 237>:

```
m075.seq
  1 ATGCCGTCTT ACTTCATCAC TCTCTTAACG ATGGAAAATA CAAAAAGCGC
  51 GGCGAAAATG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
 101 CGGCTTCCAA AGCGTTTTTT GCGGTATCGG GCAACGTTGC ATTTGCATGT
 151 GCGGCCAAAG CCAGGGGAGC AGCTGTTACA ACAGCCAGTT TTGCGCCGTA
 201 TTTACGGCAG GTGTTAATAA ATTTTCATGAT ATTTTCCTTC AAAAAAGTGT
 251 TGGCGGTAAT GGATGGAGCG TTTTTCAGAC GACCGCCGAA CATCCGAAAA
 301 TCAGTCTTTC AAAAATCCGA ATACGACAAA TTCGTATTGG TTGCCGATTT
 351 CTTCCAAACC TGCGTTAATC GCTTCTTCGA AGTCGTAGAA ATAATCGGCA
 401 TTGGTGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 238; ORF 075>:

```
m075.pep
  1 MPSYFITLLT MENTKSAAKM PTTIQPASIP SAFAASKAFF AVSGNVAFAC
  51 AAKARGAAVT TASFAPYLRQ VLINFMIFSF KKCLAVMDGA FFRRPPNIRK
 101 SVFQKSEYDK FVLVADFFQT CVNRFFEVEE IIGIGD*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 075 shows 65.7% identity over a 137 aa overlap with a predicted ORF (ORF 075.ng) from *N. gonorrhoeae*:

```
m075/g075

      10      20      30      40      50      60
m075.pep  MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT
          |||||||||||||||||||||||||||||||||||||||||:|||||||
g075      MPPYFITLLTMENTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNAAFACAAKASGAAVT
          10      20      30      40      50      60

      70      80      90      100     110
m075.pep  TASFAPYLRQVLINFMIFSF---KKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVAD
          ||||||||||||||||||| |||: : :| |:: : :| |:: : |
g075      TASFAPYLRQVLINFMIFSFTKFLKKVCGLCEGFRDRLPGLLNLIFFVSESENYKFPAY
          70      80      90      100     110     120

      120     130
m075.pep  FFQTCVNRFFEVEEIIIGIDX
          :|| :: | :| : |
g075      LFQCRASVFIIVIFTGX
          130
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 239>:

```
a075.seq
  1 ATGCCGTCTT ACTTCATCAC TCTCTTAACG ATGGAAAAGA CAAAAAGCGC
  51 GGCGAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
 101 CGGCTTCCAA AGCGTTTTTT GCTGTATCGG GCAACGTTGC ATTTGCATGT
 151 GCGGCCAAAG CCAGGGGAGC AGCTGTTACA ACAGCCAGTT TTGCGCCGTA
 201 TTTACGGCAG GTGTTAATAA ATTTTCATGAT ATTTTCCTTC AAAAAAGTGT
 251 TGGCGGTAAT GGATGGAGCG TTTTTCAGAC GACCGCCGAA CATCCGAAAA
 301 TCAGTCTTTC AAAAATCCGA ATACGACAAA TTCGTATTGG TTGCCGATTT
 351 CTTCCAAACC TGCGTTAATC GCTTCTTCGA AGTCGTAGAA ATAATCGGCA
 401 TTGGTGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 240; ORF 075.a>:

```
a075.pep
  1 MPSYFITLLT MEKTKSAAKT PTTIQPASIP SAFAASKAFF AVSGNVAFAC
  51 AAKARGAAVT TASFAPYLRQ VLINFMIFSF KKCLAVMDGA FFRRPPNIRK
 101 SVFQKSEYDK FVLVADFFQT CVNRFFEVEE IIGIGD*
```

m075/a075 98.5% identity over a 136 aa overlap

	10	20	30	40	50	60
m075.pep	MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
a075	MPSYFITLLTMEKTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
	10	20	30	40	50	60
m075.pep	TASFAPYLRLQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
a075	TASFAPYLRLQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
	70	80	90	100	110	120
m075.pep	TASFAPYLRLQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
a075	TASFAPYLRLQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
	70	80	90	100	110	120
m075.pep	CVNRFFEVEIIGIGDX					
a075	CVNRFFEVEIIGIGDX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 241>:

```

g080.seq
1  ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
51  CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
101 CGAATCATCT GCCCGTCAAG CAGGTGTCGC TGAAGGGCAA CCTGGTTTAT
151 TCCGATAAGA AGGCATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAAGCCTAC CGCCGGTATC
251 CGTGGATTGC GTCGGTCATG GTGCGCCGCC GTTTTCCCGA TACGGTTGAG
301 GTCGTCCTGA CCGAGCGCAA GCCGGTTGCA CGTTGGGGCG ACCATGCCTT
351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGCTTGGAC AGACCCGGAA
401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
451 TATGACGAAT TTTGCACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA
501 GATGACCTAT ACGGCACGTT CGGCGTGGAA TGTCGTTTGG GACAACGGCA
551 TCACCGTCAG GCTCGGACGG GAAAACgaGA TGAAACGCCT CCgGCTTTTT
601 ACcgAAGCGT GGCAGCATCT gttgcGTAAG AATAAAATC GGTtATCCTA
651 TGTGGATATG Aggtataagg acggatttTC agtcccccat gctCCCgACG
701 GTTTACCCGA AAAAGAATcc gAAGAATatt ggggaacaggt ttgggacata
751 ttacggcctg gcgtcggaac cggttcgacg caaatttcaa tcagttatAA
801 GGGCAGacga acaatggaac AGcagtaa
  
```

This corresponds to the amino acid sequence <SEQ ID 242; ORF 080.ng>:

```

g080.pep
1  MWDNAEAMER LTRWLLVMMA MLLAASGLVW FYNSNHLPVK QVSLKGNLVY
51  SDKKALGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDVE
101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RPGMPVFRGA EGTSAEMLRR
151 YDEFSTVLAK QGLGIKEMTY TARSANVVL DNGITVRLGR ENEMKRLRLF
201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVPH APDGLPEKES EBYWEQVWDI
251 LRPGVNGNST QISISYKGRR TMEQQ*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 243>:

```

m080.seq
1  ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
51  CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
101 CGAATCATCT GCCCGTCAAG CAGGTGTCGC TGAAGGGCAA CCTGGTTTAT
151 TCCGATAAGA AGACATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAGGCCTAC CGCCGGTATC
251 CGTGGATTGC GTCGGTCATG GTGCGCCGCC GTTTTCCCGA CACGGTTGAG
301 GTCGTCCTGA CCGAGCGCAA GCCGGTCGCG CGTTGGGGCG ACCATGCCTT
351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGCTTGGAC AGACCCGGAA
401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
451 TATGACGAAT TTTGCACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA
501 GATGACCTAT ACGGCACGTT CGGCGTGGAT TGTCGTTTGG GACAACGGCA
551 TCACCGTCAG GCTCGGACGG GAAAACGAGA TGAAACGCCT CCGGCTTTTT
  
```


601 ACCGAAGCGT GGCAGCATCT GTTGCCTAAA AATAAAAATC GGTTATCCTA
 651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTTCCGACG
 701 GTTTACCCGA AAAAGAATCC GAAGAATAG

This corresponds to the amino acid sequence <SEQ ID 2441; ORF 080>:

m080.pep
 1 MWDNAEAMER LTRWLLVMMA MLLAASGLVW FYNSNHLVPK QVSLKGNLVY
 51 SDKKTLGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDTVE
 101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RPGMPVFRGA EGTSAEMLRR
 151 YDEFSTVLAK QGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRLF
 201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY ASDGLPEKES EE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 080 shows 97.9% identity over a 242 aa overlap with a predicted ORF (ORF 080.ng) from *N. gonorrhoeae*:

m080/g080

	10	20	30	40	50	60
m080.pep	MWDNAEAMERL LTRWLLVMMA MLLAASGLVW FYNSNHLVPK QVSLKGNLVY SDKKTLGSLA					
080	MWDNAEAMERL LTRWLLVMMA MLLAASGLVW FYNSNHLVPK QVSLKGNLVY SDKKALGSLA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m080.pep	KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDTVE VVLTERKPVARWGDHALVDG					
080	KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDTVE VVLTERKPVARWGDHALVDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m080.pep	EGNVFEARLD RPGMPVFRGA EGTSAEMLRRY DEFSTVLAK QGLGIKEMTY TARSAWIVVL					
080	EGNVFEARLD RPGMPVFRGA EGTSAEMLRRY DEFSTVLAK QGLGIKEMTY TARSAWIVVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m080.pep	DNGITVRLGR ENEMKRLRLF TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY ASDGLPEKES					
080	DNGITVRLGR ENEMKRLRLF TEAWQHLLRK NKNRLSYVDM RYKDGFSVPHAPDGLPEKES					
	190	200	210	220	230	240
m080.pep	EEX					
080	EEYWEQVWDILRPGVNGSTQISISYKGRRTMEQQX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 245>:

a080.seq

1 ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
 51 CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
 101 CGAATCATCT GCCCGTCAAG CAGGTGTCGC TGAAGGGCAA CCTAGTTTAT
 151 TCCGATAAGA AAGCATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
 201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAGGCCTAC CGCCGGTATC
 251 CGTGATTGCG GTCGGTCATG GTGCGCCGCC GTTTTCCCGA CACGGTTGAG
 301 GTCGTCCTGA CCGAGCGCAA GCCGGTCGCG CGTTGGGGCG ACCATGCCTT
 351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGTTTGGAC AGACCCGGAA
 401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
 451 TATGACGAAT TTTCGACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA
 501 GATGACCTAT ACGGCACGTT CGGCGTGGAT TGTCGTTTGG GACAACGGCA

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```

551 TCACCGTCAG GCTCGGACGG GAAAACGAGA TGAAACGCCT CCGGCTTTTT
601 ACCGAAGCGT GGCAACATCT GTTGCCTAAA AATAAAAAATC GGTATCCTA
651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTCCCGACG
701 GTTTACCCGA AAAAGAATCC GAAGAATAG

```

This corresponds to the amino acid sequence <SEQ ID 246; ORF 080.a>:

a080.pep

```

1 MWDNAEAMER LTRWLLVMMA MLLAASGLVW FYN SNHLPVK QVSLKGNLVY
51 SDKKALGSLA KEYIHGNILR TDINGAQEAY RRY PWIASVM VRRRFPDVE
101 VVLTERRKPA RWGDHALVDG EGNVFEARLD RPGMPVFRGA EG TSAEMLRR
151 YDEFSTVLAK QGLGIKEMTY TARS AWIVVL DNGITVRLGR ENEMKRLRLF
201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY APDGLPEKES EE*

```

m080/a080 99.2% identity over a 242 aa overlap

	10	20	30	40	50	60
m080.pep	MWDNAEAMER	LTRWLLVMMA	MLLAASGLVW	FYN SNHLPVK	QVSLKGNLVY	SDKKTLGSLA
a080	MWDNAEAMER	LTRWLLVMMA	MLLAASGLVW	FYN SNHLPVK	QVSLKGNLVY	SDKKALGSLA
	10	20	30	40	50	60
	70	80	90	100	110	120
m080.pep	KEYIHGNILR	TDINGAQEAY	RRY PWIASVM	VRRRFPDVE	VVLTERRKPA	RWGDHALVDG
a080	KEYIHGNILR	TDINGAQEAY	RRY PWIASVM	VRRRFPDVE	VVLTERRKPA	RWGDHALVDG
	70	80	90	100	110	120
	130	140	150	160	170	180
m080.pep	EGNVFEARLD	RPGMPVFRGA	EG TSAEMLRR	YDEFSTVLAK	QGLGIKEMTY	TARS AWIVVL
a080	EGNVFEARLD	RPGMPVFRGA	EG TSAEMLRR	YDEFSTVLAK	QGLGIKEMTY	TARS AWIVVL
	130	140	150	160	170	180
	190	200	210	220	230	240
m080.pep	DNGITVRLGR	ENEMKRLRLF	TEAWQHLLRK	NKNRLSYVDM	RYKDGFSVRY	ASDGLPEKES
a080	DNGITVRLGR	ENEMKRLRLF	TEAWQHLLRK	NKNRLSYVDM	RYKDGFSVRY	APDGLPEKES
	190	200	210	220	230	240
m080.pep	EEX					
a080	EEX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 247>:

g081.seq

```

1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51 GCCGTCTGAA AACAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGATA
101 TTCGGAAGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGACGCG
151 CATGATTTTG TTGGAGGCGT ATTGTCTGCG GGCGCGGGCG CGGTTGTGGT
201 TTCGCGCGAA GATTGCGCGG CTTTGGGCGG CGCGTTGAAA GTCGATGACA
251 CGCTTGCCGC GTTGCAAACG TTGGCGAAGG CGTGGCGCGA TAATGTGAAC
301 CCGTTTGTGT TCGGCATTAC CGGTCGGGCG GCAAGACGA CGGTGAAGGA
351 GATGCTGGCT GCGGTATTGC GCCGCCGTTT CGCGCATGAT GCCGTTTCGG
401 CGACGGCAGG CAACTTCAAC AACCACAtcg gaTTGCCGCT GACTTTATTG
451 AAATtaaAcg aAAAACACCG CTATGCCGTG ATTGAAATGG GCATGAACCA
501 TTTTGGcgaa ctggcggtTt taacgcaaaT CGCCAAACCC GATGCCGCTT
551 TGGtcaACAA CGCCCTGCGC GCCCATGTCTG GATGCGGTTt cgacggagtg
601 GCGCATATTG CCAAAGcgaa aagcGAGATT TatgcagGct tATGTTcAGA
651 CGGCATGGCA CTGATTCTCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGTT TAATTTGAAT ACGTGCACTT TCGGCGTCGA TAGCGGCGAT
751 GTCCGCGCGG AAAATATCGT GCTGAAACCT TTGTCGTGCG AATTTGATT

```

```

801 GGTGTGCGGC GACGAGCGCA CTGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG CAAGGCTTCA GCAACATCAA
951 AGGCCGTCTG AACGTCAAAG CCGGCATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAATCCC GACAGTATGA AAGCCGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCCGC CATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAGGAc gaAGCCGCCG CCATGCACGC CGAagtcgGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGcggaAA AATTTGGCGC GGACGGTTTG TGGTTCGCCG CCAAAGACCC
1251 GTTGATTCAA GTGTTGAGCC ACGATTGGCC CGAACGCGCC ACCGTGTTGG
1301 TGAAAGGTTT GCGCTTTATG CAGAtggaAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTga

```

This corresponds to the amino acid sequence <SEQ ID 248; ORF 081.ng>:

g081.pep

```

1 MKPLDLNFIC QALKLPMPSE NKPVSRIVTD SRDIREGDVF FALAGGRFDA
51 HDFVGGVLSA GAAAVVVSRE DCAALGGALK VDDTLAALQT LAKAWRDNVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFDD AVSATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTQIAKP DAALVNNALR AHVGCDFDGV
201 GDIKAKSEI YAGLCSDGMA LIPQEDANMA VFKTATFNLN TCTFGVDSGD
251 VRAENIVLKP LSCEFDLVCG DERTAVVLPV PGRHNVHNA AAAALALAAG
301 LSLNDVAEGL QGFSNIKGR LNVKAGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMDGELGED EAAAMHAEVG AYARDQIEA AYFVGDNVSE
401 AAEKFGADGL WFAAKDPLIQ VLSHDLPERA TVLVKGSRFM QMEEVVEALE
451 DK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 249>:

m081.seq

```

1 ATGAAACCAC TGGACCTAAA TTTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51 GCCGTCTGAA AGCAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGAGCG GTTTGACGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCT GGTGCGGCGG CGGTTGTGGT
201 TTCGCGCGAA GATTGTGCTG CAATGGATGG CCGTGTGAAA GTCGATGACA
251 CGCTTGCCGC ATTGCAAACG CTGGCAAAGG CGTGGCGTGA AAATGTGAAT
301 CCGTTTGTGT TCGGCATTAC CGGTTCCGGC GGCAAGACGA CGGTGAAGGA
351 AATGCTGGCT GCGGTATTGC GCCGCGGTTT CGGCGATGAT GCCGTGTTGG
401 CGACGGCAGG CAACTTCAAC AACCATATCG GATTGCCGCT GACTTTGTTG
451 AAGTTAAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GCATGAACCA
501 TTTCGCGGAA CTGGCGGTTT TAACGCAMAT CGCCAAACCA AATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTCG GCTGCGGTTT CGACGGAGTG
601 GGCGATATTG CCAAAGCGAA AAGCGAGATT TACCAAGGTT TATGTTTACA
651 CGGCATTGCA CTGATTCTCT AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTTGAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTTACGCGG AAAATATTGT GCTGAAACCG TTGTCGTGCG AATTTGATTT
801 GGTGTGCGGC GATGAGCGCG CCGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCGGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCCT GACAGCATGA AAGCTGCGAT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCCGC TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAACTG GCGGAGGACG AAGCCGCCGC TATGCACGCC GAAGTCGGCG
1151 CGTATGCCCC CGACCAAGGC ATCGAAGCGG CTTATTTTGT CGGCGACAAC
1201 AGCGTCGAAG CGGCGGAAAA ATTTGGCGCG GACGGTTTGT GGTTCGCCCG
1251 CAAAGACCCG TTGATTCAAG TGTGCGCCA CGATTGCCCC GAACGCGCCA
1301 CCGTGTTGGT GAAAGGTTTC CGCTTTATGC AGATGGAAGA AGTGGTCGAG
1351 GCATTGGAGG ATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 250; ORF 081>:

m081.pep

```

1 MKPLDLNFIC QALKLPMPSE SKPVSRIVTD SRDIRAGDVF FALAGERFDA
51 HDFVEDVLAA GAAAVVVSRE DCAAMDGALK VDDTLAALQT LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFDD AVLATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTXIAKP NAALVNNAMR AHVGCDFDGV

```

201 GDIKAKSEI YQGLCSDGIA LIQEDANMA VFKTATLNLN TRTFGIDSGD
 251 VHAENIVLKP LSCEFDLVCG DERAADVLPV PGRHNVHNAA AAAALALAAG
 301 LSLNDVAEGL KGFSNIKGR LNVKSGIKGAT LIDDTYNANP DSMKAAIDVL
 351 ARMPAPRIFV MGD MGELGEL GEDEAAAMHA EVGAYARDQG IEAAYFVGDN
 401 SVEAAEKFGA DGLWFAAKDP LIQVLRHDL P ERATVLVKG S RFMQMEEVVE
 451 ALEDK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 081 shows 94.1% identity over a 455 aa overlap with a predicted ORF (ORF 081.ng) from *N. gonorrhoeae*:

m081/g081

	10	20	30	40	50	60
m081.pep	MKPLDLNFICQALKLPMPSESKPVSRIVTDSRDIRAGDVFFALAGERFDAHDFVEDVLAA					
	: : : : :					
g081	MKPLDLNFICQALKLPMPSENKPVSRIVTDSRDIREGDVFFALAGGRFDAHDFVGGVLSA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m081.pep	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
	: : : : :					
g081	GAAAVVVSREDCAALGGALKVDDTLAALQTLAKAWRDNVNPFVFGITGSGGKTTVKEMLA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m081.pep	AVLRRRFGDDAVLATAGNFNNHIGLPLTLLKLNKHYAVIEMGMNHFGE LAVLTXI AKP					
	: : : : :					
g081	AVLRRRFGDDAVSATAGNFNNHIGLPLTLLKLNKHYAVIEMGMNHFGE LAVLTQI AKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m081.pep	NAALVNNAMRAHVCGFDGVDIAKAKSEIYQGLCSDGIALIPQEDANMAVFKTATLNLN					
	: : : : : :					
g081	DAALVNNALRAHVCGFDGVDIAKAKSEIYAGLCSDGMALIPQEDANMAVFKTATFNLN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m081.pep	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGDERAAVLPVPGRHNVHNAAAAALALAAG					
	: :					
g081	TCTFGVDSGDVRAENIVLKPLSCEFDLVCGDERTAVVLPVPGRHNVHNAAAAALALAAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m081.pep	LSLNDVAEGLKGFSNIKGR LNVKSGIKGATLIDDTYNANPDSMKAAIDVLARMPAPRIFV					
	: : : : :					
g081	LSLNDVAEGLQGFSNIKGR LNVKAGIKGATLIDDTYNANPDSMKAAVDVLARMPAPRIFV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m081.pep	MGDMGELGELGEDEAAAMHA EVGAYARDQGEAAYFVGDN SVEAAEKFGADGLWFAAKDP					
	: : : : :					
g081	MGDMGELGE---DEAAAMHA EVGAYARDQGEAAYFVGDN SVEAAEKFGADGLWFAAKDP					
	370	380	390	400	410	
	430	440	450			
m081.pep	LIQVLRHDLPERATVLVKGSRFMQMEEVVEALEDKX					
	: : : : :					
g081	LIQVLSHDLPERATVLVKGSRFMQMEEVVEALEDKX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 251>:

a081.seq

```

1  ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51  GCCGTCTGAA AGCAAACCCG TGTGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGATGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCG GGTGCGGCGG CGGTTGTGGT
201 TTCGCGCGAA GATTGCGTTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTACCGC GTTGCAAATG TTGGCGAAGG CGTGGCGCGA GAATGTGAAC
301 CCGTTTGTGT TCGGTATTAC CGGCTCGGGC GGCAAGACGA CGGTGAAGGA
351 AATGTTGGCT GCGGTATTGC GCCGCCGTTT CGGCGATAAT GCCGTTTTGG
401 CGACGGCAGG CAACTTCAAC AACCACATCG GATTGCCGTT GACTTTGTTG
451 AAATTAAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GTATGAACCA
501 TTTTGGCGAA CTGGCGGTTT TGACACAAAT CGCCAAACCC GATGCCGCAT
551 TGGTCAACAA GCCCATGCGC GCCCATGTCG GCTGCGGTTT CGACGGAGTG
601 GCGGATATTG CCAAAGCGAA AAGCGAGATT TATCAAGGCT TATGTTTCTG
651 CGGCATGGCG CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTGAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTCACGCGCG AAAATATCGT GCTGAAACCG TTGTCGTGCG AATTTGATTT
801 GGTGTGCGGC AACGAGTGCG CAGCCGTGGT TCTGCCCGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCCGCCGCCG CGCTGTCTTT GGCTGCAGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCCT GACAGCATGA AAGCTGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGTGAGGAC GAAGCCGCCG CCATGCACGC CGAAGTCGGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGCGGAAA AATTTGGCGC GGACGGTTTG TGGTTCGCGC CCAAAGACCC
1251 GTTGATTCAA GTGTTGCGCC ACGATTTGCC CGAACGCGCC ACCGTGTTGG
1301 TGAAAGGTTT GCGCTTTATG CAGATGGAAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 252; ORF 081.a>:

a081.pep

```

1  MKPLDLNFIC QALKLPMPSE SKPVSRIVTD SRDIRAGDVF FALAGGRFDA
51  HDFVEDVLAA GAAVVVSRE DCVAMDGALK VDDTLTALQM LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDN AVLATAGNFN NHIGLPLTLL
151 KLNKHHRYAV IEMGMNHFGE LAVLTQIAKP DAALVNNAMR AHVCGFDGV
201 GDIKAKSEI YQGLCSDGMA LIPQEDANMA VFKTATLNLN TRTFGIDSGD
251 VHAENIVLKP LSCEFDLVCG NECAAVVLPV PGRHNVHNAA AAAALSLAAG
301 LSLNDVAEGL KGFSNIKGR LNVKSGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMGELGED EAAAMHAEVG AYARDQGIEA AYFVGDNVSE
401 AAEKFGADGL WFAAKDPLIQ VLRHDLPERA TVLVKGSRFM QMEEVVEALE
451 DK*

```

m081/a081 96.7% identity over a 455 aa overlap

	10	20	30	40	50	60
m081.pep	MKPLDLNFICQALKLPMPSESKPVSRIVTDSDIRAGDVFFALAGERFDAHDFVEDVLAA					
a081	MKPLDLNFICQALKLPMPSESKPVSRIVTDSDIRAGDVFFALAGGRFDAHDFVEDVLAA					
	10	20	30	40	50	60
m081.pep	GAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
	70	80	90	100	110	120
m081.pep	GAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
	130	140	150	160	170	180
m081.pep	AVLRRRFGDNAVLTAGNFNNHIGLPLTLLKLNKHHRYAVIEMGMNHFGEAVLTQIAKP					
a081	AVLRRRFGDNAVLTAGNFNNHIGLPLTLLKLNKHHRYAVIEMGMNHFGEAVLTQIAKP					

268

	130	140	150	160	170	180
	190	200	210	220	230	240
m081.pep	NAALVNNAMRAHVGCDFGVGDIKAKSEIYQGLCSGIALIPQEDANMAVFKTATLNLN					
a081	DAALVNNAMRAHVGCDFGVGDIKAKSEIYQGLCSGDMALIPQEDANMAVFKTATLNLN					
	250	260	270	280	290	300
m081.pep	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGDERAAVVLVPVGRHNVHNAALALAAG					
a081	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGNECAAVVLVPVGRHNVHNAALSLAAG					
	310	320	330	340	350	360
m081.pep	LSLNDVAEGLKGFSNIKGRNLNVKSGIKGATLIDDTYNANPDSMKAAIDVLARMPAPRIFV					
a081	LSLNDVAEGLKGFSNIKGRNLNVKSGIKGATLIDDTYNANPDSMKAAVDVLARMPAPRIFV					
	370	380	390	400	410	420
m081.pep	MGDMGELGELGEDEAAAMHAEVGAYARDQIEAAYFVGDNVSEAAEKFGADGLWFAAKDP					
a081	MGDMGELGE---DEAAAMHAEVGAYARDQIEAAYFVGDNVSEAAEKFGADGLWFAAKDP					
	430	440	450			
m081.pep	LIQVLRHDLPERATVLVKGSRFMQEVEVEALEDKX					
a081	LIQVLRHDLPERATVLVKGSRFMQEVEVEALEDKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 253>:

g082.seq

```

1  aTGTTGGTTGT TGAAGTTGCC TGCCGTCGCC GAAACGGCAT CATCGCCGAA
51  ACGGCGGCGC AATACCGCAG CCAGCATCTC CTTACCGTC GTCTTGCCGC
101 CCGAACCGGT AATGCCGAAC ACAAACGGGT TCACATTATC GCGCCACGCC
151 TTCGCCAACG TTTGCAACGC GGCAAGCGTG TCATCGACTT TCAACGCGCC
201 GCCCAAAGCC GCGCAATCTT CGCGCGAAAC CACAACCGCC GCCGCGCCCG
251 CAGACAATAC GCCTCCAACA AAATCATGCG CGTCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC TTCCCGAATA TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTGTTGTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGCG
401 AGATGAAATT TAGGTCCAGT GGTTTCATAT TTGCTTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTAAGAACAC AGATTATTTT CCCATTCTCA TTCGGCATT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTAGCCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGGG TCGTCGGACT GTCTGTGCAT AAAGGCAAGG TTATTGCCTT
651 CGCCCGGCAC ATCGGGGACA TTCCCCAAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTCGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 254; ORF 082.ng>:

g082.pep

```

1  MWLLKLPAVA ETASSPKRRR NTAASISFTV VLPPEPVMPN TNGFTLSRHA
51  FANVCNAASV SSTFNAPPKA AQSSRETTTA AAPADNTPTT KSCASNRPPA
101 NAKNTSPSRI SRLSVTMRDT GLFSDGIGSL RAWQMKFRSS GFIFAFVNIR
151 AADTSVAADF FIACFAVVKH RLFSHSHSAF FLYVSFFRRI FSRFAFSRIP
201 RRGVGLSVD KGKVIAFARH IGDIPPKIIA VIGQLVGFD TPTAES*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 255>:

m082.seq

```

1  ATGnnGTTGT TGAAGTTGCC TGCCGTCGCC AACACGGCAT CATCGCCGAA
51  ACGGcGGCGC AATACCGCAG CCAGCATTTT CTTACCGTC GTCTTGCCGC
101 CCGAACCGGT AATGCCGAAC ACAAACGGAT TCACATTTTC ACGCCACGCC
151 TTTGCCAGCG TTTGCAATGC GGCAAGCGTG TCATCGACTT TCAACGCGCC

```

```

201 ATCCATTGCA GCACAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCAG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CGTCAAACCG CTCGCCCCGC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CGGTACGAT
351 GCGCGACACG GGTTTGCTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGCG
401 AGATGAAATT TAGGTCCAGT GGTTTCATAT TTAATTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTA AACAC AGATTATTTT CCCATTCTCA TTCGGAATTT TTTCTGTACG
551 TATCATTTT TAGACGTATT TTAGTCGAT TTGCCTTTT CCGCATACCA
601 CGGCGCGGG TCGTCGGGCA GTCCGTCGAT AAAGCAAGG TTATTGCCTT
651 CGCCCTGCAC ATCGGGAACA TTCCCCAAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTGATAACC CGTCCAAC TG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 256; ORF 082>:

```

m082.pep
1  MXLLKLPAVA NTASSPKRRR NTAASISFTV VLPPEPVMPN TNGFTFSRHA
51  FASVCNAASV SSTFNAPSIA AQSSRETTA AAPAANTSST KSCASNRSPA
101 NAKNTSPARM SRLSVTMRDT GLLSDGIGSL RAWQMKFRSS GFIFTFVNIR
151 AADTSVAADF FIACFAVVKH RLFSHSHSXF FLYVSFFRRI FSRFAFSRIP
201 RRGVVGQSDV KGKVIAFALH IGNIPPKIIA VIGQLVGFD T RPTAESAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 082 shows 92.7% identity over a 247 aa overlap with a predicted ORF (ORF 082.ng) from *N. gonorrhoeae*:

```

m082/g082

      10      20      30      40      50      60
m082.pep  MXLLKLPAVANTASSPKRRRNTAASISFTVLPPEPVMPNTNGFTFSRHAFAVCNAASV
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082       MWLLKLPAVAETASSPKRRRNTAASISFTVLPPEPVMPNTNGFTLSRHAFAVNCNAASV
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      10      20      30      40      50      60

      70      80      90     100     110     120
m082.pep  SSTFNAPSIAAQSSRETTTAAAPAANTSSTKSCASNRSPANAKNTSPARMSRLSVTMRDT
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082       SSTFNAPPKAAQSSRETTTAAAPADNTPPTKSCASNRPPANAKNTSPSRISRLSVTMRDT
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      70      80      90     100     110     120

      130     140     150     160     170     180
m082.pep  GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSXF
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082       GLFSDGIGSLRAWQMKFRSSGFIFAFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSAF
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      130     140     150     160     170     180

      190     200     210     220     230     240
m082.pep  FLYVSFFRRIFSRFAFSRIPRRGVVGQSDKGVIAFALHIGNIPPKIIAVIGQLVGFD T
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082       FLYVSFFRRIFSRFAFSRIPRRGVVGLSVDKGVIAFARHIGDIPPKIIAVIGQLVGFD T
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      190     200     210     220     230     240

m082.pep  RPTAESAX
          | | | | |
g082       RPTAESAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 257>:

```

a082.seq
1  ATGTGGTTGT TGAAGTTGCC TGCCGTCGCC AAAACGGCAT TATCGCCGAA
51  ACGGCGGCGC AATACCGCAG CCAACATTC CTACACCGTC GTCTTGCCGC

```

```

101 CCGAGCCGGT AATACCGAAC ACAAACGGGT TCACATTCTC GCGCCACGCC
151 TTCGCCAACA TTTGCAACGC GGTAAGCGTG TCATCGACTT TCAACGCGCC
201 ATCCATTGCA ACGCAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCCG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CATCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTTCGCTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGCG
401 AGATGAAATT TAGGTCCAGT GGTTTCATAT TTACTTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTAAAACAC AGATTATTTT CCCATTCTCA TTCGGCATT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTAGTCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGGG TCGTCGGGCA GTCCGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCTGCAC ATCGGGAACA TTCCCCCAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTCGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 258; ORF 082.a>:

a082.pep

```

1 MWLLKLPAVA KTALSPKRRR NTAANISFTV VLPPEPVI PN TNGFTFSRHA
51 FANICNAVSV SSTFNAPSIA TQSSRETTA AAPAANTSST KSCASNRPPA
101 NAKNTSPARM SRLSVTMRDT GLLSDGIGSL RAWQMKFRSS GFIFTFVNIR
151 AADTSVAADF FIACFAVVKH RLFSSHSAF FLYVSFFERRI FSRFAFSRIP
201 RRGVVGQSV DKGKVI AFALH IGNIPPKIIA VIGQLVGFD T RPTAESAX

```

m082/a082 95.5% identity over a 247 aa overlap

	10	20	30	40	50	60
m082.pep	MXLLKLPAVANTASSPKRRRNTAASISFTVLPPEPVMPTNGFTFSRHAFASVCNAASV					
a082	MWLLKLPAVAKTALSPKRRRNTAANISFTVLPPEPVIPTNGFTFSRHAFANICNAVSV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m082.pep	SSTFNAPSIAAQSSRETTTAAAPAANTSSTKSCASNRSPANAKNTSPARMSRLSVTMRDT					
a082	SSTFNAPSIAATQSSRETTTAAAPAANTSSTKSCASNRPPANAKNTSPARMSRLSVTMRDT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m082.pep	GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSXF					
a082	GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSAF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m082.pep	FLYVSFFERRIFSRFAFSRIPRRGVVGQSV DKGKVI AFALHIGNIPPKIIA VIGQLVGFD T					
a082	FLYVSFFERRIFSRFAFSRIPRRGVVGQSV DKGKVI AFALHIGNIPPKIIA VIGQLVGFD T					
	190	200	210	220	230	240
m082.pep	RPTAESAX					
a082	RPTAESAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 259>:

g084.seq

```

1 ATGAAacaAT CCGcccgaat aAAAAATATG GATCAGACAT TAAAAAATAc
51 attggggcatt tGCGCGcttt tagcctTTTG TTTggcgG gccaTCGCAT
101 CAGGTTATCA CTTGGAATAT GAATACGGCT ACCGTTATTC TGCCGTGGGC
151 GCTTTGGCTT CGGTGTATT TTTATTATTA TTGGCACGCG GCTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTACGT CGGCACAACC GCCCTATATT
251 TGCCGCTCGG CTGGCTGTAT GGTGCGCCTT CTTATCAGAT AGTCGGTTCG
301 ATATTGGAAG GCAATCCTGC CGAGGCGCGT GAATTTGTGCG GCAATCTTCC
351 CGGGTCGCTT TATTTGTGTC AGGCATTATT TTTCATTTTT GGCTTGACAG

```


q084 . pep

```

1  MKQSARIKNM DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVG
51  ALASVVFLLL LARGFPRVSS VVLLIYVGT T ALYLPVGWLY GAPSYQIVGS
101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWKYCVS VGVFADVKNY
151 KRRSKIWLTI LLTLILSCAV MEKIQAGDKDW REPDAGLLN IFDLYYDLAF
201 RAGTICROAR PHFGSSKXSV NMAYPPTCAQ V*

```

m084.seq

1	ATGAAACAAT	CGCCCcGAAT	AAAa .ATATG	AATCAGACAT	TACTTTATAC
51	ATTGGGCATT	TGCGCGCTTT	TAACCTTnn	nnnnnnnnnn	nnnnnnnnnn
101	nnnnnnTATCA	CCcNGAATAT	GAATACGGCT	ACCGTTATTC	TGCCGTGGGT
151	GCTTTGGCTT	CGGTTGTATT	TTTATTATTA	TTGGCACGCG	GTTTCCCGCG
201	CGTTTCTTCA	GTGTGTTTAC	TGATTTACGT	CGGCACAACC	CGCCTATATT
251	TGCCGGTCGG	CTGGCTGTAT	GGTGCCCGCT	CTTATCAGAT	AGTCGGTTCG
301	ATATTGAAA	GCAATCCTGC	CGAGGCGCGT	GAATTTGTCT	GCAATCTTCC
351	CGGGTCGCTT	TATTTTGTGC	AGGCATTATT	TTTCATTTT	GGCTTGACAG
401	TTTGAAAATA	TTGTGTATCG	GGGGGGGTAT	TTGCTGACGT	AAAAAACTAT
451	AAACGCCGCA	GCAAAATATG	GCTGACTATA	TTATTGACTT	TGATTTTGTC
501	CTGCGCGGTG	ATGGATAAAA	TCGCCAGCGA	TAAAGATTTG	CGAGAACCTG
551	ATCGCCGGCT	GTGTGTTGAAT	ATTTTCGACC	TGTATTACGA	TTTGGCT .TC
601	CGCGCCGGCA	CAATATGCCG	CCAAGCGCGC	CCCATATTTG	GAAGCAGCAA
651	AAAAAGCGTC	AACATGGCAT	ATCCGTCATG	TTGCGCCCAA	GTATAA

m084 . pep

```

1  MKQSARIKXM  NQTLLYTLGI  CALLTFXXXX  XXXXXYHPEY  EYGYRSAVG
51  ALASVVFLLL  LARGFPRVSS  VVLLIYVGTT  ALYLPVGGWL  GAPSQIVGS
101 ILESNPAEAR  EFVGNLPGSL  YFVQALFFIF  GLTWVKYCS  GGVFADVKNY
151 KRRSKIWLTI  LTLTILSCAV  MDKIAPCKDL  REPDAGLLRN  IFDLYYDLAX
201 KRRGTCROAR  PHFGSSKXSV  NMAYSPSCAQ  V*

```

ORF 084 shows 90.5% identity over a 231 aa overlap with a predicted ORF (ORF 084.ng) from *N. gonorrhoeae*:

m084/q084

	10	20	30	40	50
m084 . pep	MKQSARIKXMNQTLTYLTGICALLTF-----YHPEYEGYRYSAVGALASVVFLLL				
	: :				
g084	MKQSARIKNMDQTLKNTLTGICALLAFCFGAAIASGYHLEYEGYRYSAVGALASVVFLLL				
	10	20	30	40	50
	60	70	80	90	100
m084 . pep	LARGFPRVSSVVLLIYVGTALYLPVGWLYGAPSYQIVGSILESNPAAEAREFVGNLPGSL				
g084	LARGFPRVSSVVLLIYVGTALYLPVGWLYGAPSYQIVGSILESNPAAEAREFVGNLPGSL				
	70	80	90	100	110
	120	130	140	150	160
m084 . pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTIILLTLILSCAVMDKIASDKDL				
	: :				
g084	YFVQALFFIFGLTVWKYCVSVGVFADVKNYKRRSKIWLTIILLTLILSCAVMEKIAGDKDW				
	130	140	150	160	170
	180				

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	180	190	200	210	220
m084 . pep	REPDAGLLLNIFDLYYDLAXRAGTICRQARPHFGSSKKSVMAYPSCCAQVX				
g084	REPDAGLLLNIFDLYYDLAFRAGTICRQARPHFGSSKKSVMAYPPTCAQVX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 263>:

a084 . seq

```

1  ATGAAACAAT CCGCCCGAAT AAAAAATATG GATCAGACAT TAAAAAATAC
51  ATTGGGCATT TGCGCGCTTT TAGCCTTTTG TTTTGGCGCG GCCATCGCAT
101 CAGGTTATCA CTTGGAATAT GAATACGGCT ACCGTTATTC TGCCGTGGGT
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GTTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCGG CTGGCTGTAT GGTGCGCCGT CTTATCAGAT AGTCGGTTCG
301 ATATTGGAAG GCAATCCTGC CGAGGCGCGT GAATTTGTCG GCAATCTTCC
351 CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTTCATTTT GGCTTGACAG
401 TTTGGAGATA TTGTGTATCG GGGGGGGTAT TTGCTGACGT AAAAACTAT
451 AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTC
501 CTGCGCGGTG ATGGATAAAA TCGCCAGCGA TAAAGATTG CGAGAACCTG
551 ATGCCGGGCT GTTGTGAAT ATTTTCGACC TGTATTACGA TTTGGCTTCC
601 .GCGCCGGCA CAATATGCCG CCAAGCGCGC CCACATTTT GAAGCAGCAA
651 AAAAAGCGTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 264; ORF 084.a>:

a084 . pep

```

1  MKQSARIKNM DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVG
51  ALASVVFLLL LARGFPRVSS VVLLIYVGT ALYLPVGWLY GAPS YQIVGS
101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWRYCVS GGVFADVKNY
151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLN IFDLYYDLAS
201 XAGTICRQAR PHFGSSKKSVMAYPSCCAQ V*

```

m084/a084 92.2% identity over a 231 aa overlap

	10	20	30	40	50	60
m084 . pep	MKQSARIKXMNQTLTYLGICALLTFXXXXXXXHYHPEYGYRYSAVGALASVVFLLL					
	: :					
a084	MKQSARIKNMDQTLKNTLGIALLAFCFGAAIASGYHLEYEYGYRYSAVGALASVVFLLL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m084 . pep	LARGFPRVSSVVLLIYVGTALYLPVGWLYGAPS YQIVGSILESNPAEAREFVGNLPGSL					
a084	LARGFPRVSSVVLLIYVGTALYLPVGWLYGAPS YQIVGSILESNPAEAREFVGNLPGSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m084 . pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL					
	:					
a084	YFVQALFFIFGLTVWRYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL					
	130	140	150	160	170	180
	190	200	210	220	230	
m084 . pep	REPDAGLLLNIFDLYYDLAXRAGTICRQARPHFGSSKKSVMAYPSCCAQVX					
a084	REPDAGLLLNIFDLYYDLASXAGTICRQARPHFGSSKKSVMAYPSCCAQVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 265>:

g085 . seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCTG CGCGACGCGT TGAAAGATAA

```

```

51  GGCAAAAGGC GTGTTCTGA TCGGCGTCGA TCGCCCGCAA ATCCGCCGCG
101  ATTTGGACGG CTGCGGCTTG AACCTGACCG ACTGCGTCAC TTTGGAAGAG
151  GCGGTTTCAGA CGGCATACGC CCAAGCCGAA GCGGGCGATA TTGTCTTGCT
201  CAGCCCCGCC TCGCGAGTT TCGATATGTT TAAAGGCTAC GCGCACCGTT
251  CGGAAGTGTT tatCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 266; ORF 085.ng>:

g085.pep

```

1  MGKGQDFTPL RDALKDKAKG VFLIGVDAPO IRRDLGCGCL NLTDCVTLEE
51  AVQTAYAQAE AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 267>:

m085.seq

```

1  ATGGGTAAAG GGCAGGACTT CACGCCCTG CGCGATGCAC TGGTAGGCAA
51  GGCAAAAGGC GTGTTCTGA TTGGTGTCGA TCGCCCGCAA ATCCGCCGCG
101  ATTTGGACGG CTGCGGCTTG AATATGACCG ACTGCGCCAC TTTGGGAGAA
151  GCCGTTTCAGA CGGCATATGC CCAAGCCGAA GCAGGCGATA TTGTGTTGCT
201  CAGCCCCGCC TCGCGAGCT TTGATATGTT CAAAGGCTAC GCGCACCGTT
251  CGGAAGTGTT TATCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 268; ORF 085>:

m085.pep

```

1  MGKGQDFTPL RDALVGKAKG VFLIGVDAPO IRRDLGCGCL NMTDCATLGE
51  AVQTAYAQAE AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 085 shows 94.7% identity over a 94 aa overlap with a predicted ORF (ORF 085.ng) from *N. gonorrhoeae*:

m085/g085

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGCLNMTDCATLGEAVQTAYAQAE					
g085	MGKGQDFTPLRDALKDKAKGVFLIGVDAPOIRRDLGCGCLNLTDCVTLEEAVQTAYAQAE					
	10	20	30	40	50	60
	70	80	90			
m085.pep	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
g085	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 269>:

a085.seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCTG CGCGACGCGC TTGCCGGCAA
51  GGCAAAAGGC GTGTTCTGA TCGGTGTCGA TCGCCCGCAA ATCCGCCGCG
101  ATTTGGACGG CTGCGATCTG AATATGACCG ACTGCGCCAC TTTGGAAGAA
151  GCGGTTTCAGA AGGCATATGC CCAAGCCGAA GCGGGCGATA TCGTGCTGCT
201  CAGCCCCGCC TCGCGAGTT TCGATATGTT TAAAGGCTAC GCGCACCGTT
251  CGGAAGTGTT TATCGGGGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 270; ORF 085.a>:

a085.pep

```

1  MGKGQDFTPL RDALAGKAKG VFLIGVDAPO IRRDLGCDL NMTDCATLEE
51  AVQKAYAQAE AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

m085/a085 94.7% identity over a 94 aa overlap

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGCLNMTDCATLGEAVQTAYAQAE					

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```

|||||:|||||
a085  MGKGQDFTPLRDALAGKAKGVFLIGVDAFQIRRDLDGCDLNMTDCATLEEAVQKAYAE
      10      20      30      40      50      60
      70      80      90
m085.pep AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX
      |||||
a085  AGDIVLLSPACASFDMFKGYAHRSEVFIAFKALX
      70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 271>:

```

g086.seq
1  ATGGTGGTGC TGATGACGGC GTTCGGCCTG CTGATGATTT ATTCGGCTTC
51  TGTGTATTTG GCATCGAAGG AAGCGGCGA TCAGTTTTTC TATTTGACCA
101 GGCAGGCGGG GTTCGTCGTT GCCGGCCTTA TAGCGAGCGG TTTTATATGG
151 TTTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTCG
201 CTTATCCGGC CTGTTGCTGG TAGCCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTGGGTC CGTTGAATTT CCAGCCGACC
301 GAGCTGTTCA AGCTGGCAGT CATCCTTTAT TTGGCAAGCC TGTTACGCG
351 CCGTGAAGAA GTGTTGCGCA GCATGGAAG TTTGGGTTGG CAGTCGATTT
401 GGCGGGGGAC GGCCAACCTG ATTATGTCCG CCACCAATCC GCAGGCACGT
451 CGTGAACAT TAGAAATGTA CGgCCGTTTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTCTGAT AATGGTACAG CCGGATTTTCG
551 GTTCGTTTGT CGTCATTACC GTCATTACCG TTGGAATGCT GTTCTGGCA
601 GGATTGCCGT GGAAATATTT TTTTGTCTCG GTAGGCAGCG TCTTGGGTGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CGGGTAGTGG
701 CATTTTGGGA CCCGTGGAAG GACCCGAGG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGTTTCGGTA TGGGTTTGGG
801 TGCGAGTTTG AGCAAACGCG GCTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGGCCAT CATCGCTGAA GAATTCGGCT TCTTCGGGAT GTGCGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGCGG GCGTTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGtttgA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTTGGAT CGGTATCCAA AGTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA CCAAAGGTCT GACGctgCcg tTGATGTCTT ATGGcggTTC
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTTG CGTATCGATT
1151 ATGAAAACCG CCAGAAAATG CGCGTTACC GGGTGGAGTA AA

```

This corresponds to the amino acid sequence <SEQ ID 272; ORF 086.ng>:

```

g086.pep
1  MVVLMTAFGL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGFLW
51  FLCRMRTWRR LVPWIFALSG LLLVAVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTRREE VLRSMESLGW QSIWRGTANL IMSATNPQAR
151 RETLEMYGRF RAILPIMLV AFGLVLIMVQ PDFGSFVVIT VITVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFLDPWK DPQGAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
301 IFCYGWLVR AFSIGKQSRD LGLTFNAYIA SGIGIWIGIQ SFFNIGVNIG
351 ALPTKGLTLP LMSYGGSSVF FMLISMMLLL RIDYENRQKM RGYRVE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 273>:

```

m086.seq
1  ATGGTGGTGC TGATGACGGC GTTCAGCCTG CTGATGATTT ATTCGGCTTC
51  TGTGTATTTG GCATCAAAAG AAGCGGCGA TCAGTTTTTC TATTTGACCA
101 GACAGGCGGG GTTCGTCGTT GCCGGCTTGA TAGCGAGCGG TTTGTTATGG
151 TTTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTCG
201 CCTATCCGGC CTGTTGCTGG TAGTCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTGGGTC CGTTGAATTT CCAGCCGACC
301 GAGCTGTTCA AGCTGGCGGT CATCCTTTAT TTGGCAAGCC TGTTACGCG
351 CCGTGAAGAA GTGTTGcGCA GCATGGAAG TTTGGGTTGG CAGTCGATTT
401 GGCGGGGGAC GGCCAATCTG ATCATGTCCG CCACCAATCC GCAGrCACGT
451 CGTGAAACAT TAGAAATGTA CGGCCGTWTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTCTGAT AATGGTACAG CCGGATTTTCG

```

```

551  GTTCGTTTGT  CGTCATTACC  GTCATTGCCG  TTGGAATGCT  GTTTTGGCA
601  GGATTGCCGT  GGAAATATTT  TTTCGTCCTG  GTAGGCAGCG  TCTTGGGCGG
651  GATGGTGCTG  ATGATTACCG  CCGCTCCCTA  CCGTGTGCAG  CGGGTAGTGG
701  CATTTTGGGA  CCCGTGGAAA  GACCCGCAGG  GTGCCGGCTA  CCAGCTTACC
751  CACTCTCTGA  TGGCAATCGG  GCGCGGAGAG  TGGTTCGGTA  TGGGTTTGGG
801  TGCGAGTTTG  AGCAAACGCG  GCTTTCTGCC  GGAAGCGCAT  ACCGATTTTA
851  TTTTGGCCAT  CATCGCCGAA  GAATTCGGTT  TCTTCGGTAT  GTGCGTGCTG
901  ATATTCTGTT  ACGGCTGGCT  GGTGGTGCGG  GCGTTTCCCA  TCGGCAAGCA
951  GTCGCGCGAT  TTGGGTTTGA  CTTTCAACGC  CTATATCGCT  TCGGGTATCG
1001 GCATTTGGAT  CGGkrTCCAA  AGTTTCTTCA  ATATCGGTGT  GAACATCGGT
1051 GCTTTGCCGA  mCAAAGyCT  GACGCyGCCG  Tg.AtGTCCw  ATGGCGGTTT
1101 GTCAGTCTTT  TTCATGCTGA  TCAGCATGAT  GCTGCTGTkG  CGTATAGATT
1151 ATGAAAACCG  CCGGAAAATG  CGCGGTTATC  GGGTGGAGTA  A

```

This corresponds to the amino acid sequence <SEQ ID 274; ORF 086>:

```

m086.pep
1  MVVLMTAFSL  LMIYSASVYL  ASKEGGDQFF  YLTRQAGFVV  AGLIASGLLW
51  FLCRMRTWRR  LVPWIFALSG  LLLVVVLIAG  REINGATRWI  PLGPLNFQPT
101 ELFKLAVILY  LASLFTRREE  VLRSMESLGW  QSIWRGTANL  IMSATNPQXR
151 RETLEMYGRX  RAILPIMLV  AFGLVLIMVQ  PDFGSFVVIT  VIAVGMLFLA
201 GLPWKYFFVL  VGSVLGGMVL  MITAAPYRVQ  RVVAFLDPWK  DPQGAGYQLT
251 HSLMAIGRGE  WFGMGLGASL  SKRGFLPEAH  TDFIFAIIE  EFGFFGMCVL
301 IFCYGWLVR  AFSIGQSRD  LGLTFNAYIA  SGIGIWIGXQ  SFFNIGVNIG
351 ALPKXGLTXP  XMSXGGSSVF  FMLISMMLLX  RIDYENRRKM  RGYRVE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 086 shows 96.7% identity over a 396 aa overlap with a predicted ORF (ORF 086.ng) from *N. gonorrhoeae*:

m086/g086

	10	20	30	40	50	60
m086.pep	MVVLMTAFSLLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
	: : : : :					
g086	MVVLMTAFGLLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m086.pep	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLFLKLAVILYLASLFTRREE					
	: : : : :					
g086	LVPWIFALSGLLLVAVLIAGREINGATRWIPLGPLNFQPTLFLKLAVILYLASLFTRREE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m086.pep	VLRSMESLGWQSIWRGTANLIMSATNPQXRRETLEMYGRXRRAILPIMLVAFGLVLIMVQ					
	: : : : :					
g086	VLRSMESLGWQSIWRGTANLIMSATNPQARRETLEMYGRFRAILPIMLVAFGLVLIMVQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m086.pep	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
	: : : : :					
g086	PDFGSFVVITVITVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m086.pep	DPQGAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIEEFGFFGMCVL					
	: : : : :					
g086	DPQGAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIEEFGFFGMCVL					
	250	260	270	280	290	300
	310	320	330	340	350	360

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```

m086.pep  IF CYGWL VVRAFSIGKQSRDLGLTFNAYIASGIGIWIGXQSFFNIGVNIGALPXXGLTXP
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
g086       IF CYGWL VVRAFSIGKQSRDLGLTFNAYIASGIGIWIGIQSFFNIGVNIGALPTKGLTLP
          310      320      330      340      350      360

          370      380      390
m086.pep  XMSXGGSSVFFMLISMMLLXRIDYENRRKMRGYRVEX
          |||||||||||||||||||||||||:|||||||
g086       LMSYGGSSVFFMLISMMLLLRIDYENRQKMRGYRVEX
          370      380      390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 275>:

a086.seq

```

1  ATGGTGGTGC TGATGACGGC GTTCAGCCTG CTGATGATTT ATTCGGCTTC
51  TGTGTATTTG GCATCAAAAG AAGGCGGCGA TCAGTTTTTC TATTTGACCA
101 GACAGGCGGG GTTCGTCGTT GCCGGCTTGA TAGCGAGCGG TTTGTTATGG
151 TTTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTCG
201 CCTATCCGGC CTGTTGCTGG TAGTCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAATTT CCAGCCGACC
301 GAGCTGTTCA AGCTGGCGGT CATCCTTTAT TTGGCAAGCC TGTTCACGCG
351 CCGTGAAGAA GTGTTGCGCA GCATGGAAG TTTGGGTGG CAGTCGATTT
401 GCGGGGGGAC GGCCAATCTG ATCATGTCCG CCACCAATCC GCAGGCACGT
451 CGTGAACAT TAGAAATGTA CGGCCGTTTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTGCTGAT AATGGTACAG CCGGATTTCG
551 GTTCGTTTGT CGTCATTACC GTCATTGCCG TTGGAATGCT GTTTTGGCA
601 GGATTGCCGT GGAAATATTT TTTTCGTCCT GTAGGCAGCG TCTTGGGCGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CGGGTAGTGG
701 CATTTTTTGA CCCGTGGAAA GACCCGCAGG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGTA TGGGTTTGGG
801 TGCGAGTTTG AGCAAACGCG GCTTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGGCCAT CATCGCCGAA GAATTCGGTT TCTTCGGTAT GTGCGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGCGG GCGTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGTTTGA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTTGGAT CCGTATCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA CCAAAGGTCT GACGCTGCCG TTGATGTCTT ATGGCGGTTT
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTTG CGTATAGATT
1151 ATGAAAACCG CCGGAAAATG CGCGTTTACC GGGTGAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 276; ORF 086.a>:

a086.pep

```

1  MVVLMTAFSL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW
51  FLCRMRTWRR LVPWIFALSG LLLVVVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTRREE VLRSMESLGW QSIWRGTANL IMSATNPQAR
151 RETLEMYGRF RAILPIMLV AFGLVLIMVQ PDFGSFVVIT VIAVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK DPQAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFGMCVL
301 IF CYGWL VVR AFSIGKQSRD LGLTFNAYIA SGIGIWIGIQ SFFNIGVNIG
351 ALPTKGLTLP LMSYGGSSVF FMLISMMLL RIDYENRRKM RGYRVE*

```

m086/a086 98.0% identity over a 396 aa overlap

```

          10      20      30      40      50      60
m086.pep  MVVLMTAFSLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
a086       MVVLMTAFSLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR
          10      20      30      40      50      60

          70      80      90     100     110     120
m086.pep  LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLFLKAVILYLASLFTRREE
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
a086       LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLFLKAVILYLASLFTRREE

```

277

	70	80	90	100	110	120
m086.pep	130	140	150	160	170	180
a086	VLRSMESLQWQSIWRGTANLIMSATNPQXRRETLEMYGRXRRAILPIMLVAFGLVLIMVQ					
	130	140	150	160	170	180
m086.pep	190	200	210	220	230	240
a086	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
	190	200	210	220	230	240
m086.pep	250	260	270	280	290	300
a086	DPQGAGYQLTHSLMAIGRGWFGMGLGASLSKRGFLPEAHTDFIFAIIAEEFFGFGMCVL					
	250	260	270	280	290	300
m086.pep	310	320	330	340	350	360
a086	IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGXQSFFNIGVNIGALPKXGLTXP					
	310	320	330	340	350	360
m086.pep	370	380	390			
a086	XMSXGGSSVFFMLISMMLLXRIDYENRRKMRGYRVEX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 277>:

```

g087.seq
1  ATGGGCGGTA  AAACCTTTAT  GCTGATGGCG  GGC GGAACGG  GCGGACACAT
51  TTTCCAGCT  CTGGCTGTGG  CGGATTCATT  GCGCGTGC GC  GGT CATCATG
101 TAATTTGGCT  GGGCAGCAAG  GATTTCGATGG  AAGAGCGCAT  CGTGCCGCAA
151 TACGGCATA  GCTTGGAAC  GCTGGCGATT  AAAGGAATAC  GCGGCAACGG
201 CATCAAACGC  AAGCTGATGC  TTCCGTTTAC  TCTGTACAAA  ACCGTCCGCG
251 AAGCGCAGCG  GATTATCCGC  AAACACCGTG  TCGAGTCCGT  CATCGGCTTC
301 GCGGTTTTG  TTACCTTTCC  CGGCGGTCTG  GCGGCGAAAC  TCTTGGGCGT
351 GCCGATTGTG  ATTCACGAGC  AAAACGCCGT  GGCAGGCTTG  TCCAACCGCC
401 AccTGTGCGc  ctGGGCGAAA  CGGGTGTGT  ACGCTTTTCC  GAAAGCGTTC
451 AGCCACGAAG  GCGGTTTGGT  CGGCAACCCC  GTCCGCGCCG  ATATTAGCAA
501 CCTGCCCCGT  CCTGCCGAAC  GCTTCCAAGG  GCGCGAAGGC  CGTCTGAAAA
551 TTTTGGTGGT  CGGCGGCAGT  TTGGGTGCGG  ACGTTTGTAA  CAAAACCGTA
601 CCGCAGGCGT  TGGCACTGCT  GCCTGAAGAG  GTGCGCCCGC  AGATGTACCA
651 CCAGTCGGGG  CGTAACAAGC  TGGGCAATCT  TCAGGCGGAT  TATGACGCGT
701 TGGGCGTGAA  AGCGGAATGC  GTGGAATTTA  TTACCGACAT  GGTGTCCGCC
751 TACCGTGATG  CCGATTGGT  GATTTGCCGT  GCCGGCGCGC  TGACGATTGC
801 CGAGTTGACG  GCGGCGGGGC  TGGGCGCGTT  GTTAGTGCCG  TATCCTCAGC
851 CCGTTGATGA  CCATCAAACC  GCCAACGCGC  GTTTCATGGT  GCAGGCAGAA
901 GCGGGGCTGC  TGTGCGCGCA  AACCAGTTG  ACGGCGGAAA  AACTCGCCGA
951 AATCCTCGGC  AGCCTCAACC  GCGAAAAATG  CCTCAAATGG  GCGGAAAACG
1001 CCCGTACGTT  GGCATTGCCG  CACAGCGCGG  ATGACGTTGC  CGAAGCCGCG
1051 ATTGCGTGTG  CGGCGTAAA

```

This corresponds to the amino acid sequence <SEQ ID 278; ORF 087.ng>:

```

g087.pep
1  MGGKTFMLMA  GGTGGHIFPA  LAVADSLRVR  GHHVIWLGSK  DSMEERIVPQ
51  YGIRLET LAI  KGIRNGIKR  KLMLPFTLYK  TVREAQRIIR  KHRVECVIGF
101 GGFVTFPGGL  AAKLLGVPIV  IHEQNAVAGL  SNRHLSRWAK  RVLVYAFPKAF
151 SHEGGLVGNP  VRADISNLPV  PAERFQGREG  RLKILVVGGS  LGADVLNKTV

```

201 PQALALLPEE VRPQMYHQSG RNKLGNLQAD YDALGVKAEC VEFITDMVSA
 251 YRDADLVICR AGALTIAELT AAGLGALLVP YPHAVDDHQT ANARFMVQAE
 301 AGLLLPQTQL TAEKLAIEILG SLNREKCLKW AENARTLALP HSADDDVAEAA
 351 IACAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 279>:

m087.seq
 1 ATGGGCGGTA AAACCTTTAT GCTGawkkCG GCGGGAACGG GCGGACATAT
 51 TTTCCCCGCG CTGGCGGTGG CGGATTCATT GCGCGCGCGC GGCCATCATG
 101 TGATTTGGCT GGGCAGCAAG GATTCGATGG AAGAGCGTAT CGTGCCGCAA
 151 TACGGCATAC GCTTGGAAC GCTGGCGATT AAAGGCGTGC GCGGCAACGG
 201 CATCAAACGC AAACCTGATGC TGCCGGTTAC TTTGTATCAA ACCGTCCGCG
 251 AAGCGCAGCG GATTATCCGC AAACACCGTG TCGAGTGGCGT CATCGGCTTC
 301 GCGGCTTCG TTACCTTCCC CGGCGGTTTG GCGGCGAAGC TATTArCGGT
 351 GCCGATTGTG ATTCACGAGC AAAACGCCGT GGCAGGTTTG TCCAACCGCC
 401 ACCTGTCGCG CTGGGCGAAG CGGGTGTGTG ACGCTTTTCC GAAAGCGTTC
 451 AGCCACGAAG GCGGCTTGGT CGGCAACCCC GTCCGCGCCG ATATTAGCAA
 501 CCTGCCCCTG CCTGCCGAAC GCTTCCAAGG GCGTGAAGGC CGTCTGAAAA
 551 TTTTGGTGGT CGGCGGCAGT TTGGGCGCGG ACGTTTTGAA CAAAACCGTA
 601 CCGCATGCAT TGGCTTTGCT GCCCGACAAT GCGCGTCCGC ATATGTACCA
 651 CCAATCGGGA CGGGGCAAGC TGGGCATCTT GCAGGCGnnn nnnnnnnnnn
 701 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 751 nnnGCGGGAT TGGGTGCGTT GTTAGTGCCG TATCCTCACG CGGTGACGA
 801 TCACCAAACC GCCAACGCGC GTTTTATGGT GCAGGCGGAG GCGGGATTGC
 851 TGTTGCCGCA AACCCAGTTG ACGGCGGAAA AACTCGCCGA GATTCTCGGC
 901 GGCTTAAACC GCGAAAAATG CCTCAAATGG GCAGAAAACG CCCGTACGTT
 951 GGCAGTCCG CACAGTGGG ACGACGTGGC GGAAGCCGCG ATTGCGTGTG
 1001 CGGCGTAA

This corresponds to the amino acid sequence <SEQ ID 280; ORF 087>:

m087.pep
 1 MGGKTFMLXX GGTGGHIFPA LAVADSLRAR GHVVIWLGSK DSMEERIVPQ
 51 YGIRLETLAI KGVRGNGIKR KLMLPVTLYQ TVREAQRIIR KHRVECVIGF
 101 GGFVTFPGGL AAKLLXVPIV IHEQNAVAGL SNRHLSRWAK RVLVAFPKAF
 151 SHEGGLVGNP VRADISNLPV PAERFQREG RLKILVVGGS LGADVLNKTIV
 201 PHALALLPDN ARPHMYHQSG RGKLGILQAX XXXXXXXXXXX XXXXXXXXXXX
 251 XAGLGALLVP YPHAVDDHQT ANARFMVQAE AGLLLPQTQL TAEKLAIEILG
 301 GLNREKCLKW AENARTLALP HSADDDVAEAA IACAA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 087 shows 83.9% identity over a 355 aa overlap with a predicted ORF (ORF 087.ng) from *N. gonorrhoeae*:

m087/g087

	10	20	30	40	50	60
m087.pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVIWLGSKDSMEERIVPQY	YGIRLETLAI				
g087	MGGKTFMLMAGGTGGHIFPALAVADSLRVRGHHVIWLGSKDSMEERIVPQY	YGIRLETLAI				
	10	20	30	40	50	60
	70	80	90	100	110	120
m087.pep	KGVRGNGIKRKLMLPVTLYQTVREAQRIIRKHRVEC <u>VIGF</u> GGFVTFPGGLAAKLLXVPIV					
g087	KGIRGNGIKRKLMLPFTLYKTVREAQRIIRKHRVEC <u>VIGF</u> GGFVTFPGGLAAKLLGVPIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
g087	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
	130	140	150	160	170	180

279

	190	200	210	220	229	
m087.pep	RLKILVVGGSLGADVLNKTVP	HALALLPDNARPHMYHQSGR	KGILQA-----			
g087	RLKILVVGGSLGADVLNKTVP	QALALLPEEVRPQMYHQSGR	NKLGNLQADYDALGVKAEC			
	190	200	210	220	230	240
				230	240	250
m087.pep	-----			AGLGALLVPYPHAVDDHQTANARFMVQAE		
g087	VEFITDMVSAYRDADLVICRAGALTIAELTAAGLGALLVPYPHAVDDHQTANARFMVQAE					
	250	260	270	280	290	300
	260	270	280	290	300	310
m087.pep	AGLLLPQTQLTAEKLAELGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
g087	AGLLLPQTQLTAEKLAELGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 281>:

a087.seq

```

1  ATGGGCGGTA AAACCTTTAT GCTGATGGCG GCGGAACGG GCGGACATAT
51  TTTCCCGCG CTGGCGGTGG CGGATTCATT GCGCGCGCG GGCCATCATG
101 TAATTTGGCT GGGCAGCAAG GATTCGATGG AAGAGCGCAT CGTGCCGCAA
151 TACGACATCC TGCTCGAAAC GCTGGCGATT AAAGGCGTGC GCGGCAACGG
201 CATCAAACGC AAGCTGATGC TGCCGTTTAC TTGTATCAA ACTGTCCGCG
251 AAGCGCAGCA GATTATCCGC AAACACCGTG TCGAGTGCCT CATCGGCTTC
301 GCGGCTTCG TTACCTTTCC CGGCGGTTTG GCGGCGAAGT TATTAGCGCT
351 GCCGATTGTG ATTCACGAGC AAAACGCCGT GGCAGGTTTG TCCAACCGCC
401 ACCTGTGCG CTGGGCGAAG CGGGTGTTGT ACGCTTTTCC GAAAGCGTTC
451 AGCCACGAAG GCGGCTTGGT CGGCAACCCC GTCCGCGCCG ATATTAGCAA
501 CCTGCCCGTG CTGCCGAAC GCTTCCAAGG GCGTGAAGGC CGTCTGAAAA
551 TTTTGGTGGT CGGCGCAGT TTGGGCGCGG ACGTTTTGAA CAAAACCGTA
601 CCGCAGGCAT TGGCTTTGCT GCGCGACAAT GCGCGTCCGC AGATGTACCA
651 CCAATCGGGA CGGGGCAAGC TGGGCAGCTT GCAGGCGGAT TACGACGCGC
701 TGGGCGTGCA AGCGGAATGC GTGGAATTTA TTACCGATAT GGTGTCCGCC
751 TACCGCGATG CCGATTGGT GATTGCGCT GCCGGCGCGC TGACGATTGC
801 CGAGTTGACG GCGGCGGGAT TGGGTGCGTT GTTAGTGCCG TATCCTCACG
851 CCGTTGATGA CCATCAAACC GCCAACGCGC GTTTTATGGT GCAGGCGGAG
901 GCGGGATTGC TGTTGCCGCA AACCAGTTG ACGGCGGAAA AACTCGCCGA
951 GATTCTCGGC GGCTTAAACC GCGAAAAATG CCTCAAATGG GCAGAAAACG
1001 CCCGTACGTT GGCAGTCCG CACAGTGCGG ACGACGTTGC CGAAGCCGCG
1051 ATTGCGTGTG CGGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 282; ORF 087.a>:

a087.pep

```

1  MGGKTFMLMA GGTGGHIFPA LAVADSLRAR GHVHWLWLSK DSMEERIVPQ
51  YDILLETIAI KVRGNGIKR KLMLPFTLYQ TVREAQQIIR KHRVECVIGF
101 GGFVFEPGGL AAKLLGVPIV IHEQNAVAGL SNRHLRSWAK RVLVYAFPKAF
151 SHEGGLVGNP VRADISNLPV PAERFQREG RLKILVVGGS LGADVLNKTVP
201 PQALALLPDN ARPQMYHQSG RGKLGSLQAD YDALGVQAEC VEFITDMVSA
251 YRDADLVICR AGALTIAELT AAGLGALLVP YPHAVDDHQT ANARFMVQAE
301 AGLLLPQTQL TAEKLAELG GLNREKCLKW AENARTLALP HSADDVAEAA
351 IACAA*

```

m087/a087 85.4% identity over a 355 aa overlap

	10	20	30	40	50	60
m087.pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVHWLWLSKDSMEERIVPQY	GIRLETIAI				
a087	MGGKTFMLMAGGTGGHIFPALAVADSLRARGHHVHWLWLSKDSMEERIVPQY	DILLETIAI				
	10	20	30	40	50	60

280

	70	80	90	100	110	120
m087.pep	KGVVRNGIKRKLMLPVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLXVPIV					
a087	KGVVRNGIKRKLMLPFTLYQTVREAQQIIRKHRVECVIGFGGFVTFPGGLAAKLLGVPIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQGREG					
a087	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQGREG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m087.pep	RLKILVVGGSLGADVLNKTVPHALALLPDNARPHMYHQSGRGKLGILQAXXXXXXXXXXX					
a087	RLKILVVGGSLGADVLNKTVPQALALLPDNARPMYHQSGRGKLGSLQADYDALGVQAEC					
	190	200	210	220	230	240
	250	260	270	280		
m087.pep	XX-----XXXXXXXXXAGLGALLVPYPHAVDDHQTANARFMVQAE					
a087	VEFITDMVSAYRDADLVICRAGALTIAELTAAGLGALLVPYPHAVDDHQTANARFMVQAE					
	250	260	270	280	290	300
	290	300	310	320	330	
m087.pep	AGLLLPQTLTAEKLAELGGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
a087	AGLLLPQTLTAEKLAELGGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 283>:

g088.seq

```

1  ATGTTTTTAT GGCTCGCACA TTTCAGCAAC TGGTTAACCG GTCTGAATAT
51  TTTTCAATAC ACCACATTCC GCGCCGTTAT GCGGCGTTG ACCGCCTTGG
101 CGTTTTCCTT GATGTTCCGC CCGTGGACGA TACGCAGGCT GACCGCGCTC
151 AAATGCGGGC AGGCAGTGCG TACCGACGGC CCGCAAACCC ACCTCGTCAA
201 AAACGGCACG CCGACGATGG GCGGTTCGCT GATTCTGACC GCCATTACCG
251 TGTCACCCTT GTTGTTGGGC AACTGGGCGA ACCCGTATAT CTGGATTCTC
301 TTGGGCGTAT TGCTTGCCAC CGGTGCGCTC GGTTTTACG ACGACTGGCG
351 CAAAGTCGTT TATAAAGACC CCAACGGCGT GTCCGCCAAA TTCAAAATGG
401 TGTGGCAGTC AAGCGTTGCC GTTatcgCG GTttggcATT GTTTTACctt
451 gCcgCcaATT CCGCCAACAA TATTTTGATT GTCCCGtttT TCAAACAAAT
501 CGCCCTGCCG CTGGGCGTGG TCGGCTTttt gGtggttTCT TACCTGACCA
551 TCGTCGGCAC ATCCAACGCC GTCAACCTCA CcgaCGGCTT GGACGGCCTT
601 GCCGCcttcc cgttcgtcct cgttgccgcC GGGCTCGCCA ttttcgccTA
651 CGTCAGCGGA CACTACCAAT TTCCCAATA CCTCCAGCTT CCCTATGTCG
701 CCGGCGCGAA CGAAGTCGCT ATATTCTGCA CCGCCATGTG CCGGCGGTGC
751 CTCGGATTTT TGTGGTTCAA CGCCTATCCC GCGCAAGTCT TTATGGGCGA
801 TGTCGGCGCG CTGGCATTGG GTGCCGCGCT CGGTaccGtt gCCGTcaTcg
851 tCCGCCAAGA ATTTGTcctc gtcattatGG GCGGTCTGTT cgtcgtagaa
901 gccgtgTCCG TTATGCTTca tgtcggCTGG TACAAGAAAA Ccaaaaaacg
951 CATCTTcCTg acgGcaccga ttcacacca ttaCCaactt cgatgCTGGa
1001 aagaaaacgca agtcgctcgtc CGTTtCTGGA TTAAtAccat cgtcgtggtt
1051 tTgatagggt tGagtaccct caAAattcgc ggaaactatg ccgTCCGAAC
1101 ACCTTTCAGA CGGCATTGA ACGCGCAATA A

```

This corresponds to the amino acid sequence <SEQ ID 284; ORF 088.ng>:

g088.pep

```

1  MFLWLAHFSN WLTGLNIFQY TTFRAVMAAL TALAFSLMFG PWTIRRLTAL
51  KCGQAVRTDG PQTHLVKNGT PTMGGSLILT AITVSTLLWG NWANPYIWL
101 LGVLLATGAL GFYDDWRKVV YKDPNGVSAK FKMVWQSSVA VIAGLALFYL
151 AANSANNILI VPFFKQIALP LGVVGFLVLS YLTIVGTSNA VNLTDGLDGL

```

201 AAFPFVLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFCTAMCGAC
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGFLVVE
 301 AVSVMLHVGW YKKTKKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV
 351 LIGLSTLKIR GNYAVRTPFR RHLNAQ*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 285>:

m088.seq

```

1  ATGTTTTTAT GGCTCGCACA TTTCAGCAnC TGGTTAACCG GTCTGAATnn
51  nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
101 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
151 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
201 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
251 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
301 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
351 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
401 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
451 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
501 nnnnnnnnnn nnnGGCGTGG TCGGCTTTTT GGTGTTGTCT TACCTGACCA
551 TCGTCGGCAC ATCCAATGCC GTCAACCTCA CCGACGGCTT GGACGGCCTT
601 GCGACCTTCC CCGTCGTCCT CGTTGCCGCC GGCCTCGCCA TCTTCGCCTA
651 TGCCAGCGGC CACTCACAAT TTGCCCAATA CCTGCAATTA CCTTACGTTG
701 CCGGCGCAAA CGAAGTGGTG ATTTTCTGTA CCGCCATGTG CGGCGCGTGC
751 CTCGGTTTCT TGTGGTTTAA CGCCTATCCC GCGCAAGTCT TTATGGGCGA
801 TGTGGTGCA TTGGCATTGG GTGCCGCGCT CGGTACCGTC GCCGTTATCG
851 TCCGCCAAGA GTTTGTCCCTC GTCATTATGG GCGGATTATT TGTCGTAGAA
901 GCCGTATCCG TTATGCTTCA GGTGGGCTGG TATAAGAAAA CCAAAAAACG
951 CATCTTCCTG ATGGCGCCCA TCCATACCA CTACGAACAA AAAGGCTGGA
1001 AAGAAACCCA AGTCGTCGTC CGCTTTTGA TTATTACCAT CGTCTGGTG
1051 TTGATCGGTT TGAGTACCCT CAAAATCCGC TGAACCTATG CCGTCTGAAC
1101 ATCTTTCAGA CGGCATTGA ACGCGCAATA A

```

```

1  MFLWLAHFSN WLTGLNIFQY TTFRAVMAAL TALAFSLMFG PWTIRRLTAL
51  KCGQAVRTDG PQTHLVKNGT PTMGGSLILT AITVSTLLWG NWANPYIWIL
101 LGVLLATGAL GFYDDWRKVV YKDPNGVSAK FKMVWQSSVA VIAGLALFYL
151 AANSANNILI VPFFKQIALP LGVVGFLVLS YLTIVGTSNA VNLTDGLDGL
201 AAFPFVLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFCTAMCGAC
251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGFLVVE
301 AVSVMLHVGW YKKTKKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV
351 LIGLSTLKIR GNYAVRTPFR RHLNAQ*

```

This corresponds to the amino acid sequence <SEQ ID 286; ORF 088>:

m088.pep

```

1  MFLWLAHFSX WLTGLNXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
51  XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
101 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
151 XXXXXXXXXXX XXXXXXXXXXX XGVVGFLVLS YLTIVGTSNA VNLTDGLDGL
201 ATFPVVLVAA GLAIFAYASG HSQFAQYLQL PYVAGANEV IFCTAMCGAC
251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGFLVVE
301 AVSVMLQVGW YKKTKKRIFL MAPIHHHYEQ KGWKETQVVV RFWIITIVLV
351 LIGLSTLKIR XTYAVXTSFR RHLNAQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 088 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 088.ng) from *N. gonorrhoeae*:

m088/g088

```

m088.pep                                10      20      30
                                         GVVGFLVLSYLTIVGTSNAVNLTGDLGDLA
                                         |||
g088      IAGLALFYLAANSANNILIVPFFKQIALPLGVVGFLVLSYLTIVGTSNAVNLTGDLGDLA
              150      160      170      180      190      200

```

282

	40	50	60	70	80	90
m088.pep	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVIFCTAMCGACLGLWFNAYPA					
g088	AFPFVLVAAGLAIFAYVSGHYQFSQYLQLPYVAGANEVAIFCTAMCGACLGLWFNAYPA					
	210	220	230	240	250	260
	100	110	120	130	140	150
m088.pep	QVFMGVDVGALALGAALGTVAIVRQEFVLVIMGGLFVVEAVSVMLQVGWYKTKKRIFLM					
g088	QVFMGVDVGALALGAALGTVAIVRQEFVLVIMGGLFVVEAVSVMLHVGWYKTKKRIFLT					
	270	280	290	300	310	320
	160	170	180	190	200	
m088.pep	APIHHHHEQKGWKETQVVVRFWIITIVLVLIGLSTLKIRXTYAVXTSFRRLNAQX					
g088	APIHHHYQLRCWKETQVVVRFWIITIVVLIGLSTLKIRGNVAVRTPFRRLNAQX					
	330	340	350	360	370	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 287>:

a088.seq

```

1  ATGTTTTTAT  GGCTCGCACA  TTTCAGCAAC  TGGTTAACCG  GTCTGAATAT
51  TTTTCAATAC  ACCACATTCC  GCGCCGTCAT  GCGCGCGTTG  ACCGCCTTGG
101 CGTTTTCCCT  GATGTTCCGC  CCGTGGACGA  TACGCAGGCT  GACCGCGCTC
151 AAATGCGGGC  AGGCAGTGCG  TACCGACGGT  CCGCAAACCC  ACCTCGTCAA
201 AAACGGCACG  CCGACGATGG  GCGGTTGCGT  GATTCTGACC  GCCATTACCG
251 TGTCCACCC  GTTGTGGGGC  AACTGGGCAA  ACCCGTATAT  CTGGATTCTC
301 TTGGGCGTAT  TGCTCGCCAC  GGGCGCACTC  GGTTTTTACG  ACGACTGGCG
351 CAAAGTCGTC  TATAAGACC  CCAACGGCGT  GTCCGCCAAA  TTCAAATGG
401 TGTGGCAGTC  AAGCGTTGCC  ATTATCGCCG  GTTGTGCATT  GTTTTACCTT
451 GCCGCCAATT  CCGCCAACAA  TATTTTGATT  GTCCCGTTCT  TCAAACAAAT
501 CGCCCTGCCG  CTGGGCGTGG  TCGGCTTTT  GGTGTGTCT  TACCTGACCA
551 TCGTCGGCAC  ATCCAATGCC  GTCAACCTCA  CCGACGGCTT  GGACGGCCTT
601 GCGACCTTCC  CCGTCGTCCT  CGTTGCCGCC  GGCCTCGCCA  TCTTCGCCTA
651 TGCCAGCGGC  CACTCACAAT  TTGCCCAATA  CCTGCAATTA  CCTTACGTTG
701 CCGGCGCAA  CGAAGTGGTG  ATTTTCTGTA  CCGCATGTG  CGGCGCGTGC
751 CTCGGTTTCT  TGTGGTTTAA  CGCCTATCCC  GCGCAAGTCT  TTATGGGCGA
801 TGTCGGTGCA  TTGGCATTGG  GTGCCGCGCT  CGGTACCGTC  GCCGTCATCG
851 TCCGCCAAGA  GTTTGTCCTC  GTCATTATGG  GCGGATTATT  TGTCTAGAA
901 GCCGTATCCG  TTATGCTTCA  GGTCCGGCTG  TATAAGAAAA  CCAAAAAACG
951 CATCTTCCTG  ATGGCGCCCA  TCCATACCA  CTACGAACAA  AAAGGCTGGA
1001 AAGAAACCCA  AGTCGTCGTC  CGCTTTTGA  TTATTACCAT  CGTCTGGTG
1051 TTGATCGGTT  TGAGTACCCT  CAAAATCCGC  TGAACCTATG  CCGTCTGAAC
1101 ACCTTTCAGA  CGGCATTGTA  ACGCGCAATA  A

```

This corresponds to the amino acid sequence <SEQ ID 288; ORF 088.a>:

a088.pep

```

1  MFLWLAHFSN  WLTGLNIFYQ  TTFRAVMAAL  TALAFSLMFG  PWTIRRLTAL
51  KCGQAVRTDG  PQTHLVKNGT  PTMGGSILIT  AITVSTLLWG  NWANPYIWL
101 LGVLLATGAL  GFYDDWRKV  YKDPNGVS  AKFKMVWQSSVA  IAGLALFYL
151 AANSANNILI  VPFFKQIALP  LGVVGFVL  VLSYLTIVGTSNA  VNLTGDLGDL
201 ATFPVVLVAA  GLAIFAYASG  HSQFAQYL  QLQPYVAGANEVV  IFCTAMCGAC
251 LGFLWFNAYP  AQVFMGVDGA  LALGAALGT  VAVIVRQEFVL  VIMGGLFVVE
301 AVSVMLQVGW  YKKTKKRIFL  MAPIHHH  HEQKGWKETQVVV  RFWIITIVLV
351 LIGLSTLKIR  *TYAV*TPFR  RHLNAQ*

```

m088/a088 99.5% identity over a 205 aa overlap

	150	160	170	180	190	200
m088.pep	XXXXXXXXXXXXXXXXXXXXXXXXXGTVGFLVLSYLTIVGTSNAVNLTGDLGDL					
a088	IAGLALFYLAANSANNILIVPFFKQIALPLGVVGFVLVLSYLTIVGTSNAVNLTGDLGDL					

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	150	160	170	180	190	200
	210	220	230	240	250	260
m088.pep	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVIFCTAMCGACLGFLWFNAYPA					
a088	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVIFCTAMCGACLGFLWFNAYPA					
	210	220	230	240	250	260
	270	280	290	300	310	320
m088.pep	QVFMGDIVGALALGAALGTAVIVRQEFVLVIMGGLFVVEAVSVMLQVGWYKTKKRIFLM					
a088	QVFMGDIVGALALGAALGTAVIVRQEFVLVIMGGLFVVEAVSVMLQVGWYKTKKRIFLM					
	270	280	290	300	310	320
	330	340	350	360	370	
m088.pep	APIHHHYEQKGWKETQVVVRFWIITIVLVIGLSTLKIRXTYAVXTSFRRLNAQX					
a088	APIHHHYEQKGWKETQVVVRFWIITIVLVIGLSTLKIRXTYAVXTPFRRLNAQX					
	330	340	350	360	370	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 289>:

g089.seq

```

1  ATGCCGCCCA AAATCACGAA GAGCGGGTTT TGCAAACCGG CAATCGCGGC
51  GGCGGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATG AATACCACGC
101 CGTTTTTCTC GCCGATTTT TCCACACGGT GCGGCAAGCC TTGGAAGGTT
151 TTGACGTGTT CCAGCAATGC TTCGCGCGGC AAACCGACGG CCTCGCACAA
201 AGCCACGGCA GCCATAACGT TGGCGGCGTT GTGCAAACCT TGCAGCGGGA
251 TGTCTTGCGT AGAAATCAAA TCTTCATTGC CTTGTTTAA ACAGCCCGTC
301 CCGCGTTCCA ACCAAAAATC GGCTTCGTGT TCCAAGGAAA ACCGTTTCAC
351 TTCACGCCCT GCCCGTTTCA TGGCGCGGCA GAACACGTCG TCCGCATTCA
401 AAACCTGCAC TCCATCGCCA CGGAAAATCT CGGCTTTGGT ATGCGCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 290; ORF 089.ng>:

g089.pep

```

1  MPPKITKSGF CKPAIAAAVA PTFVPLLSSM NTPFFSPIF STRCGKPWKV
51  LTCSSNASRG KPTASHKATA AITLAALCKP CSGMSCVEIK SSLPCFKQPV
101 PRSNQKSASC SKENRFTSRP ARFMARQNTS SAFKTCTPSP RKISALVCA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 291>:

m089.seq

```

1  ATGCCGCCCA AAATCackAw GAGCGGATTT TGCAAACCGG CAATCGCGGC
51  GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATA AACACCACGC
101 CGTTTTTCTC GCCGATTTT TCCACGCGGT GCGGCAGGCC TTGGAAGGTT
151 TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG CCTCACACAA
201 AGCCACKGCA GCCATGACGT TAGCGGCGTT GTGCAKACCT TGCAACGGwA
251 TGTCTTGCGT GACAAATCAAA TCTTCATTGC CTTGTTTCAG GCGGCCTGTC
301 TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA ACCATTTTAC
351 CTCGCGCCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG TCCGCATTCA
401 AAACCTGCAC GCCGTCGCCA CGGAAAATCT TGGCTTTGGT ATGCGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 292; ORF 089>:

m089.pep

```

1  MPPKITXSGF CKPAIAAAVA PTFVPLLSSI NTPFFSPIF STRCGRPWKV
51  LTCSSNASRD KPMASHKATA AMTLAALCXP CNGMSCVTIK SSLPCFRRPV
101 SRSNQKSASC SNENHFTSRP ARFIARQNAS SAFKTCTPSP RKILALVCA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 089 shows 88.6% identity over a 149 aa overlap with a predicted ORF (ORF 089.ng)

from *N. gonorrhoeae*:

m089/g089

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	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPT FVPLLSSINTTPFFSPIFSTRCGRPWKVLTCSNASRD					
	: : : : :					
g089	MPPKITXSGFCKPAIAAAVAPT FVPLLSSMNTTPFFSPIFSTRCGRPWKVLTCSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPCNGMSCVTIKSSLPCFRRPVSRNQKSASCSNENHFTSRP					
	: : : : : :					
g089	KPTASHKATAAITLAALCKPCSGMSCVEIKSSLPCFKQPVPRSNQKSASCSKENRFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	: : : :					
g089	ARFMARQNTISSAFKTCTPSPRKISALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 293>:

a089.seq

1	ATGCCGCTA	AAATCACGAA	GAGCGGATTT	TGCAAACCGG	CAATCGCGGC
51	GGCGGTCGCA	CCGACGTTTCG	TGCCTTTGCT	GTCGTCGATG	AACACCACGC
101	CATTTTCTC	GCCGATTTT	TCCACGCGGT	GCGGCAGGCC	TTGAAAGGTT
151	TTGACGTGTT	CGAGCAATGC	TTGCGCGGCG	AAACCGACGG	CTTCGCACAA
201	GGCAACGGCA	GCCATCACGT	TAGTGGCGTT	GTGCAAGCCT	TGCAGCGGAA
251	TATCTTGCCT	GGCAATCAAA	TCTTCATTGC	CTTGTTTCAG	GCGACCTGTC
301	TCACGTTCCA	ACCAAAAATC	GGCTTCGTAT	TCCAACGAAA	ACCATTTCAC
351	CTCGCGCCCG	GCGCGCTTCA	TCGCACGACA	GAACGCATCG	TCCGCATTCA
401	AAACCTGCAC	ACCGTCGCCA	CGGAAAATCT	TGGCTTTGGT	ATGCGCGTAG

This corresponds to the amino acid sequence <SEQ ID 294; ORF 089.a>:

a089.pep

1	MPPKITKSGF	CKPAIAAAVA	PTFVPLLSSM	NTTPFFSPIF	STRCGRP*KV
51	LTCSSNASRG	KPTASHKATA	AITLVALCKP	CSGISCVAIK	SSLPCFRRPV
101	SRSNQKSASY	SNENHFTSRP	ARFIARQNAS	SAFKTCTPSP	RKILALVCA*

m089/a089 91.9% identity over a 149 aa overlap

	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPT FVPLLSSINTTPFFSPIFSTRCGRPWKVLTCSNASRD					
	: : : : :					
a089	MPPKITXSGFCKPAIAAAVAPT FVPLLSSMNTTPFFSPIFSTRCGRPXKVLTCSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPCNGMSCVTIKSSLPCFRRPVSRNQKSASCSNENHFTSRP					
	: : : : : :					
a089	KPTASHKATAAITLVALCKPCSGISCVAIKSSLPCFRRPVSRNQKSASYSNENHFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	: : : :					
a089	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 295>:

g090.seq

1	ATGCGCGTAG	TCGAGCAAAT	CGTCGTAGCG	GTCGAGATGG	TCTTCGGAAT
---	------------	------------	------------	------------	------------

51	TGTTTCATCAC	CGTCGCCGCA	GTCGGGCGCA	GGCTTTCGGT	GTTTTCAGT
101	TGGAAGCTGG	AAAGCTCcca	CACCCACAG	TCCGCCTTT	TGCCTTCgcg
151	ctgCAATct	gcctccaaga	cgggcgtagc	gaATTGCC	GCAATGAcgg
201	tatccagccc	gcacttgatg	CAGAGatagc	ggaccaggct	ggttaccgTG
251	GTTttgcggt	tgctgCcggt	aatcgCaatc	accttgctgc	CGCGCGGgt
301	cAcaatTGTc	gccagCAATt	ggATGTCGCC	TAgCACGCGC	.ccgcccTTT
351	TGCTtgat				

This corresponds to the amino acid sequence <SEQ ID 296; ORF 090.ng>:

q090.pgp

1 MRVVEQIVVA VEMVFGNVHH RRRSRAQAFG VFQLEAGKLP HPHVRLFAFA
51 LQFCLQDGRT DIARNDDGIQP ALDAEADQA GYRGFAVAAG NRNHLVAAAV
101 HNVROOLDVA XHAXRRFA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 297>:

m090.seq

1	ATGCGCATAG	TCGAGCAAGT	CGTCGTAGCG	GTCGAGATGG	TCTTCGGA
51	TGTTCAACAC	CGTCGCCGCA	GTCGGACGCA	GGCTTTCGGT	GTTTTCAGT
101	TGGAAGCTGG	AAAGCTCCAA	CACCACACG	TCCGCTTTT	TGCTTCGCG
151	CTGCCATTCC	GCCTCCAAAA	CCGGCGTGCC	GATATTGCC	GCGATAACGG
201	TATCCAGCCC	GCACTTGATA	CAGAGATAGC	CGACCAGGCT	CGTTACCGTG
251	GTTTTCGCCGT	TGCTGCCGGT	AATCGCAATT	ACCTTGTCGT	CCCGGCGGTT
301	CACAATGTCC	GCCAGCAATT	CGATGTCGCC	CAACACGCGT	.CCGCCGTTT
351	TGCTTGA				

This corresponds to the amino acid sequence <SEQ ID 298; ORF 090>:

m090.ppp

1 MRIVEQVVVA VEMVFGNVQH RRRSRTQAFG VFQLEAGKLQ HPHVRLFAFA
51 LPFRLQNRRA DIARDNGIQP ALDTEIADQA RYRGFAVAAG NRNYLVVPAV
101 HNVROQFDVA QHAXRRFA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 090 shows 83.9% identity over a 118 aa overlap with a predicted ORF (ORF 090.ng) from *N. gonorrhoeae*:

m090/q090

	10	20	30	40	50	60
m090.pep	MRIVEQVVVAVEMVFGNVQHRRRSRTQA	FGVFQLEAGKLQHPHVLFAFALPFLQN	RRA			
	: : :	:			:	:
g090	MRVVEQIVVAVEMVFGNVHHRRRSRA	QAFGVFQLEAGKLPHPHVRLFAFAL	QFCLQDGR			
	10	20	30	40	50	60

	70	80	90	100	110	119
m090.pep	DIARDNGIQPALDTEIADQARYRGFAVA	AAGNRNYLVVPVHNVRQQFDVAQHAXR	RFAX			
	: :					
g090	DIARNDGIQPALDAEIIDQAGYRGFAVA	AAGNRNHLVAAAVHNVRQQQLDVAXHAX	RFAX			
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 299>:

a090.seq

1	ATGCGCGTAG	TCGAGCAAGT	CGTCGTAGCG	GTCGAGATGG	TCTTCGGA
51	TGTTTCAGCAC	TGTCGCCGCA	GTCGGGCGCA	GGCTTTCGGT	GTTTTCAGT
101	TGGAAACTGG	AAAGCTCCAA	CACCCACACG	TCCGCCTTT	TGCCATTCGCG
151	CTGCAATTCC	GCCTCCAAA	CCGGCGCGCC	GATATTGCC	GCGATAACGG
201	TATCCAGCCC	ACACTTGATG	CAGAGATAGC	CGACCAGGCT	CGTTACCGTG
251	GTTTTCGCCGT	TGCTGCCGGT	AATCGCAATC	ACCTTGTCGC	CGCGGCGGTT
301	CACAATGTCC	GCCAGCAATT	CGATGTCGCC	CAACACGCGT	C. CGCCGTTT
351	CGCTTAA				

This corresponds to the amino acid sequence <SEQ ID 300; ORF 090.a>:

a090.pep
 1 MRVVEQVVVA VEMVFGNVQH CRRSRAQAFG VFQLETGKLQ HPHVRLFAFA
 51 LQFRLQNRRA DIARDNGIQP TLDAEIQDA RYRGFAVAAG NRNLVAAAV
 101 HNVRRQFDVA QHAXRRFA*

m09/a090 91.5% identity over a 117 aa overlap

	10	20	30	40	50	60
m090.pep	MRIVEQVVVA	VEMVFGNVQH	RRRSRTQAF	GVFQLEAGKLQ	HPHVRLFAF	ALPFRLQNRRA
a090	MRVVEQVVVA	VEMVFGNVQH	CRRSRAQAF	GVFQLETGKLQ	HPHVRLFAF	ALQFRLQNRRA
	10	20	30	40	50	60

	70	80	90	100	110	119
m090.pep	DIARDNGIQP	ALDTEIADQ	ARYRGFAVA	AGNRNLYLV	VPVHNVRRQ	FDVAQHAXRRFAX
a090	DIARDNGIQP	TLDAEIQDA	RYRGFAVA	AGNRNLVAA	AVHNVRRQ	FDVAQHAXRRFAX
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae*

g090-1.seq This sequence contains multiple stop codons (not shown)

This corresponds to the amino acid sequence < ORF 090-1.ng>:

g090-1.pep (not shown)

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2>:

m090-1.seq

```

1  ATGACGGCGT  TTGCATTTC  GACGGCATCA  CAAAGCCTTA  AACGCTTCGA
51  TAAACACTTC  CGAACGGTGC  GCGTAGCCTT  TGAACATATC  AAAGCTCGCG
101 CAGGCGGGGC  TGAGCAACAC  AATATCGCCT  GCTTCGGCTT  GGGCATATGC
151 CGTCTGAACG  GCTTCTCCCA  AAGTGGCGCA  GTCGGTCATA  TTCAAGCCGC
201 AGCCGTCCAA  ATCGCGGCGG  ATTTGCGGCG  CATCGACACC  AATCAAGAAC
251 ACGCCTTTTG  CCTTGCCTAC  CAGTGCATCG  CGCAGGGGCG  TGAAGTCCTG
301 CCCTTTACCC  ATGCCGCCCA  AAATCACGAA  GAGCGGATT  TGCAAACCGG
351 CAATCGCGGC  GGCAGTCGCG  CCGACATTCG  TGCCTTTGCT  GTCGTCGATA
401 AACACCACGC  CGTTTTTCTC  GCCGATTTT  TCCACGCGGT  GCGGCAGGCC
451 TTGGAAGGTT  TTGACGTGTT  CGAGCAATGC  TTCGCGCGAC  AAACCGATGG
501 CCTCACACAA  AGCCACGGCA  GCCATGACGT  TAGCGGCGT  GTGCAGACCT
551 TGCAACGGAA  TGTCTTGCGT  GACAATCAAA  TCTTCATTGC  CTTGTTTCAG
601 GCGGCCTGTC  TCGCGTTCCA  ACCAGAAATC  AGCTTCGTGT  TCCAACGAAA
651 ACCATTTTAC  CTCGCGCCCG  GCACGCTTCA  TCGCGCGGCA  GAACGCATCG
701 TCCGCATTCA  AAACCTGCAC  GCCGTGCGCA  CGGAAAATCT  TGGCTTTGGT
751 ATGCGCATAG  TCGAGCAAGT  CGTCGTAGCG  GTCGAGATGG  TCTTCGAAAA
801 TGTTCAGCAC  CGTCGCCGCA  GTCGGACGCA  GGCTTTCGTT  GTTTCCAGT
851 TGGAAGCTGG  AAAGCTCCAA  CACCCACACG  TCCGCTTTT  TGCTTCGCG
901 CTGCCATTCC  GCCTCCAAA  CCGGCGTGCC  GATATTGCC  GCGATAACGG
951 TATCCAGCCC  GCATTGATA  CAGAGATAGC  CGACCAGGCT  CGTTACCGTG
1001 GTTTTGCCGT  TGCTGCCGTT  AATCGCAATT  ACCTTGTCGT  CCGGCGGTT
1051 CACAATGTC  GCCAGCAATT  CGATGTCGCC  CAACACGCGT  CCGCCGTTT
1101 GCTTGAACGC  CTCAATATCC  GGCTGCCGCT  CGCTGATGCC  GGGACTGAGA
1151 GCCAGAATAT  CGAAACCGTT  GTCCAGCGCA  TCTTTCAGAC  GGCCCGTGTA
1201 AAACACCAAC  CCGTCAAACA  TCTTACCGAT  TTGCGACACG  CGTTCCGGCT
1251 TCAGCTCCGC  ATCATACGCA  GCAACCTCCG  CGCCGTTTT  GCGCAGGTAG
1301 GCAATCATGG  AAATACCCGT  ACCGCCGAGT  CCGCGACGA  GGATTTTTTT
1351 GTTTTGAAAA  GTCATTTTGG  TTTGTCCTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 3; ORF 090-1>:

m090-1.pep

```

1  MTAFAFQTAS  QSLKRFDKHF  RTVRVAFEH  KARAGGAEQH  NIACFGLGIC
51  RLNGFSQSGA  VGHIAAAVQ  IAADLRRI  DTD NQEHAFCLAY  QCIAQGREVL
101 PFTHAAQNHE  ERILQTGNRG  GSRADIRAF  VVDKHHAVFL  ADFFHAVRQA
151 LEGFDVFEQC  FARQTDGLTQ  SHGSHDVSGV  VQTLQRNVLR  DNQIFIALFO
201 AACLAFQPEI  SFVFQRKPFY  LAPGTLHRAA  ERIVRIQNLH  AVATENLGFG
251 MRIVEQVVVA  VEMVFGNVQH  RRRSRTQAF  GVFQLEAGKLQ  HPHVRLFAFA
301 LPFRLQNRRA  DIARDNGIQP  ALDTEIADQ  RYRGFAVAAG  NRNLYLVPAV
351 HNVRRQFDVA  QHASAVLLER  LNIRLPLADA  GTESQNIETV  VQRIQFQARV
401 KHQPVKHLTD  LRHAFRLQLR  IIRSNLRAV  AQVGNHGNTR  TAESGDEDF
451 VLKSHFGLS*
  
```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 303>:

```
g091.seq
  1  ATGGAAATAC CCGTGCCGCC AAGTCCGGCG ACGAGGATTT TTTTGTTTGA
 51  AAGTCATTTT GGTTTTGTCC TAAAACAAAT CATATTGGGC AGGAGACGTC
101  CGCCCTTGCC CAAGCCGCTT TCAGACGGCA TCGCGAGCCG ATTAATAACC
151  CGCCTTCAGG CGTTGGTCAT TGTCGCAGCT GTTTTGGTCT CCGTTTGTAC
201  AAGCCTTGCC AAGCCATTGT TGAGCGAGCG CAAGGTCTTG GCGCACGCCG
251  CGTCCATCGT AATACATCAA GCCCAAATTG TATTGGGCTT GGGCATCCCC
301  TTGTTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 304; ORF 091.ng>:

```
g091.pep
  1  MEIPVPPSPA TRIFLFESHF GFVLKQIILG RRRPPLPKPL SDGIASRLIT
 51  RLQALVIVAA VLVSVLTSLA KPILLSERKVL AHAASIVIHQ AQIVLGLGIP
101  LF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 305>:

```
m091.seq
  1  ATGGAAATAC CCGTACCGCC GAGTCCGGCG ACGAGGATTT TTTTGTTTGA
 51  AAAGTCATTT TGGTTTGTCC TAAAACAAAT CATATTGAGC AGGAGATGTC
101  CGCCCTTGCC CAAGCCGCTT TCAGACGGCA TCGCGAGCTG TTCAATAACC
151  CGCCTTCAGG CGTTGGTCAT TGTCGCAGCC GTCTTGGTCT CCGTTTGTAC
201  AAGCCTTGCC AAACCATTCT TGTGCAAGGG CGCGGTCTTG GCGCACGCCG
251  CGTCTTTCGG CATAATCAC GCCCAAATTG TTTTGGGCTT GGGCTACCCC
301  CTGCGC...
```

This corresponds to the amino acid sequence <SEQ ID 306; ORF 091>:

```
m091.pep
  1  MEIPVPPSPA TRIFLFEKSF WFVLKQIILS RRCPPPLPKPL SDGIASCSIT
 51  RLQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLGLGYP
101  LR.
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 091 shows 84.2% identity over a 101 aa overlap with a predicted ORF (ORF 091.ng) from *N. gonorrhoeae*:

m091/g091

	10	20	30	40	50	60
m091.pep	MEIPVPPSPATRIFLFEKSFVFWVLKQIILSRRCPPLPKPLSDGIASCSITRLQALVIVAA					
	: :					
g091	MEIPVPPSPATRIFLFESHFGFVLKQIILGRRRPPLPKPLSDGIASRLITRLQALVIVAA					
	10	20	30	40	50	60
	70	80	90	100		
m091.pep	VLVSVLTSLAKPFLCKGAVLAHAASFGIHHAAQIVLGLGYPLR					
	: : : :					
g091	VLVSVLTSLAKPILLSERKVLAAHAASIVIHQAQIVLGLGIPLFX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 307>:

```
a091.seq
  1  ATGGAAATAC CCGTGCCGCC AAGTCCGGCG ACGAGGATTT TTTTGTTTTG
 51  GAAATCATTT TGGTTTGTCC TAAAACAAAT CATATTGAGC AGGGGATGTC
101  TGATCCTGCT CAAGCCGCTT TCAGACGGCA TCGCGAGCTG TTCAATAACC
151  CGCTTTCAGG CGTTGGTCAT TGTCGCAGCT GTCTTGGTAT CCGTTTGTAC
201  AAGCCTTGCC AAGCCATTCT TGTGCAAGGG CGCGGTCTTG GCGCACGCCG
251  CGTCTTTCGG CATAATCAC GCCCAAATTG TTTTGGGC
```

This corresponds to the amino acid sequence <SEQ ID 308; ORF 091.a>:

a091.pep

```

1  MEIPVPPSPA TRIFLFWKSF WFLVKQIILS RGCLILLKPL SDGIASCSIT
51 RFQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLG

```

m091/a091 93.8% identity over a 96 aa overlap

```

              10      20      30      40      50      60
m091.pep    MEIPVPPSPATRIFLFEKSFVFLVKQIILSRRCPLPKPLSDGIASCSITRLQALVIVAA
              |||||
a091         MEIPVPPSPATRIFLFEKSFVFLVKQIILSRGCLILLKPLSDGIASCSITRFQALVIVAA
              10      20      30      40      50      60

              70      80      90      100
m091.pep    VLVSVLTSLAKPFLCKGAVLAHAASFGIHHAQIVLGLGYPLR
              |||||
a091         VLVSVLTSLAKPFLCKGAVLAHAASFGIHHAQIVLG
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 309>:

g092.seq

```

1  ATGTTTTTTA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGTGCGC
51  AAACGGTCAG ACCTTTAAAA TAACGCCTTT ACGCACTAAA AACCAACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTAA GCAACATCCA TTTGTGCGGT
151 ATCGGCGGCG TCGGCATGAG CGGTATCGCC GAAGTCTTGC ACAATTGGG
201 CTTTAAAGTT TCCGGTTCGG ATCAGGCGCG .AAATGCCGCT ACCGAGCATT
251 TGAGCAGCCT GGGCATTCAA GTTTATCCCG GCCATACCGC AGAACACGTT
301 AACGGTgcgg ATGTCGTCGT TGCCTTACC GCCGTCAAGA AAGAAaatcC
351 CGAAGTgtgc gctGCGTTGG AGCGGCAAAT TCCCGTTATT CCGCGCGCCT
401 TGATGCTGGC AGAGCTGATG CGCTTCCGTG ACGgcatcgc cattgccggT
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTC GACCCCACTT TCGTTATCGG CGGCAAACTC AACGCCGCAG
551 GCACCAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAATCCGATG CCTCTTTCCT ACATCTGACC CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCAGAGC GTCGAAAAAC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTGTG GTGTTGACAG CGAACACGTC CGCGCGATTT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GGCGCGCAAA TGAAATTAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTGCTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTTGG AGCCATCGGc gtggcGCTgg
1001 aagtcGgCGC ATcggttgAA GCGAtcCAAA AaggCTTGCT CGGCTTTGAA
1051 GGCGTCGGCC GCCGCTTCCA AAAATAcggc gacatCAagt tgccaaacgg
1101 cggGaccgCT TTgctGGTGG ACGATTAcgg ACACCACCCC GTCGAAATGG
1151 CGGcaaccct tgccgcTGCA CGCGGCGCGT ATCCGAAAAA acgtTTGGTG
1201 CtcgCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTACTCAATA CCGTTGatgC GCTGGTACTG ACCGAAGTTT
1301 AtgccgccgG CGAAGAGCCG GTTGCCGCCG CGgactcCCG CGCCTTGGCG
1351 CGTGCTATCC GCGTATTGGG CAAACTTGAG CCGATTACT GCGAAAatgt
1401 cgccgACCTG CCGCAAATGC TGATGAATGT TTTACAGGAT Ggcgatgttg
1451 tgttgAATAT GggTgcggga agcatcaacc gcgttccttc cgcgctgttg
1501 gaattgtcga AACAGAtttg A

```

This corresponds to the amino acid sequence <SEQ ID 310; ORF 092.ng>:

g092.pep

```

1  MFFISIRYIF VRKLWCANGQ TFKITPLRTK NQPERNIMMK NRVSNIHFVG
51  IGGVMSGIA EVLHNLGFKV SGSDQARNAA TEHLSSLGIQ VYPGHTAEHV
101 NGADVFAST AVKKNPEVV AALERQIPVI PRALMLAELM RFRDGLAIAAG
151 THGKTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK

```

```

251 AFLCVDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEVGASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP VAAADSRALA
451 RAIRVLGKLE PIYCENVADL PQMLMNVLQD GDVVLNMGAG SINRVPSALL
501 ELSKQI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 311>:

```

m092.seq
1 ATGTTTTTTA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGCGCGC
51 AAACGTCAG CCCTTTAAAA TAACGCCTTT ACGCATCGAA AATCCACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTTA CCAACATCCA TTTTGTCTGGT
151 ATCGGCGGCG TCGGCATGAG CGGCATCGCC GAAGTCTTGC ACAATTTGGG
201 CTTTAAAGTT TCCGGTTCGG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGGGCAGCCT GGGCATTCAA GTTTATCCCG GCCATACCGC CGAACACGTT
301 AACGGTGC GG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTCCGTG ACGGCATCGC CATGCGCGGC
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAACTC AACGCCGCGC
551 GCACTAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTGT GTATTGACAG CGAACACGTC CGCGCGATT TGCCTCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCAAAA TGAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GCGCTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 CGGGACCGCG CTCTTGTTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CGGCGACCCT TGCCGCCGCA CGCGGCGCGT ATCTGGA AAA ACGTTTGGTA
1201 CTCGCCCTTC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTGTAAGA
1251 CTTTACCAAA GTCCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCCGCCCG TGAAGAGCCG ATTGCCGCCG CCGATTCCCG CGCTCTTGCC
1351 CGCGCCATCC GCGTGTTGGG CAAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTGTAACGT TTTGCAGGAC GCGGACATCG
1451 TGTGTAATAT GGGCGCGGGA AGCATCAACC GCGTCCCCGC CGCGCTGCTG
1501 GCATTGTCGA AACAGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 312; ORF 092>:

```

m092.pep
1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVNTNIHFVG
51 IGGVGMSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKENPEVV AALEQQIPVI PRALMLAELM RFRDGLAIAAG
151 THGKTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEVGASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYLEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLLNVLQD GDIVLNMAG SINRVPAALL
501 ALSKQI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 092 shows 96.6% identity over a 506 aa overlap with a predicted ORF (ORF 092.ng) from *N. gonorrhoeae*:

```

m092/g092
10      20      30      40      50      60
m092.pep MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFVGIGGVGMSGIA

```

	10	20	30	40	50	60
g092	MFFISIRYIFVRKLWCANGQTFKITPLRTKNQPERNIMMKNRVSNIH FVGIGGVGMSGIA					
	70	80	90	100	110	120
m092.pep	EVLHNLGFKVSGSDQARNAATEHLGSLGIQVYPGHTAEHVN GADVVTSTAVKKENPEVV					
g092	EVLHNLGFKVSGSDQARNAATEHLSSLGIQVYPGHTAEHVN GADV VVAVSTAVKKENPEVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m092.pep	AALEQQIPIV IPRALMLAELMRFRDGI A IAGTHGKT TTTSLTASILGAAGLDPTFVIGGKL					
g092	AALERQIPIV IPRALMLAELMRFRDGI A IAGTHGKT TTTSLTASILGAAGLDPTFVIGGKL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m092.pep	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTN IDEDHMDTYGHSVEK LHQAFID					
g092	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTN IDEDHMDTYGHSVEK LHQAFID					
	190	200	210	220	230	240
	250	260	270	280	290	300
m092.pep	FIHRMPFYGKAFLCIDS EHVRAILPKVSKPYATYGLDDTADIYATDIEN VGAQM KFTVHV					
g092	FIHRMPFYGKAFLCVDSEHVRAILPKVSKPYATYGLDDTADIYATDIEN VGAQM KFTVHV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m092.pep	QMGKGHEQGSFEVVLNMPGRHNVLNALAAIGVALEVGASVEAIQKGLLGFEVGRRFQKYG					
g092	QMGKGHEQGSFEVVLNMPGRHNVLNALAAIGVALEVGASVEAIQKGLLGFEVGRRFQKYG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m092.pep	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYLEKRLVLAFQPHRYTRTRDLFEDFTK					
g092	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYPEKRLVLAFQPHRYTRTRDLFEDFTK					
	370	380	390	400	410	420
	430	440	450	460	470	480
m092.pep	VLNTVDALVLTEVYAAGEEPIAAADSRALARAIRVLGKLEPIYCENVADLP EMLLNVLQD					
g092	VLNTVDALVLTEVYAAGEEPVAAADSRALARAIRVLGKLEPIYCENVADLP QMLMNVLQD					
	430	440	450	460	470	480
	490	500				
m092.pep	GDIVLNMGAGSINRVPAALLALSKQIX					
g092	GDVV LNMGAGSINRVPSALLELSKQIX					
	490	500				

a092.seq

1	ATGTTT	TTTCAATCCG	CTATATATT	GTCAGAAAAC	TATGGCGCGC
51	AAACGGTCAG	CCCTTTAAAA	TAACGCCTTT	ACGCATCGAA	AATCCACCGG
101	AACGCACAT	TATGATGAAA	AATCGAGTGA	CCAACATCCA	TTTGTCTGGT
151	ATCGGCGGCG	TCGGCATGAG	CGGTATCGCG	GAAGTCTTGC	ACAAATTGGG
201	TTTTAAAGTT	TCCGGTTCGG	ATCAGGCGCG	AAATCGCGCT	ACGAGCATTT
251	TGGGCGAGCCT	GGGCATTCAA	GTTTATCCCG	GCCATACCGC	AGAACACGTT

```

301 AACGGTGC GG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATTGCCGGC
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAATC AACGCCGCAG
551 GCACCAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGT GTTGAGAAGC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTATTGACAG CGAACACGTC CGCGCGATTT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGG CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GGCGCGCAAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GGTGTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 TGGAACCGCG CTCTTGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CGGCGACCCT TTCCGCGCGA CGCGGCGCGT ATCCGGA AAA ACGTTTGTA
1201 CTCGCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTCCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCCGCCGG TGAAGAGCCG ATTGCCGCGC CTGATTCCCG CGCTCTTGCC
1351 CGCGCCATCC GCGTGTTGGG CAAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTTGAACGT TTTGCAGGAC GGCGACATCG
1451 TGTTGAATAT GGGTGCGGGA AGCATCAACC GCGTCCCGC CGCGCTGCTG
1501 GAATTGTCGA AACAGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 314; ORF 092.a>:

a092.pep

```

1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVTNIHFVG
51 IGGVGMMSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKENPEVV AALEQQIPVI PRALMLAELM RFRDGIATAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEVGASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNNGTA LLVDDYGHHP VEMAATLSAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLLNVLQD GDIVLNMGAG SINRVPAALL
501 ELSKQI*

```

m092/a092 99.4% identity over a 506 aa overlap

	10	20	30	40	50	60
m092.pep	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFVGIGGVGMMSGIA					
a092	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFVGIGGVGMMSGIA					
	10	20	30	40	50	60
m092.pep	EVLHNLGFKVSGSDQARNAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
a092	EVLHNLGFKVSGSDQARNAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
	70	80	90	100	110	120
m092.pep	EVLHNLGFKVSGSDQARNAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
a092	EVLHNLGFKVSGSDQARNAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
	130	140	150	160	170	180
m092.pep	AALEQQIPVIPRALMLAELMRFRDGIATAGTHGKTTTTSLTASILGAAGLDPTFVIGGKL					
a092	AALEQQIPVIPRALMLAELMRFRDGIATAGTHGKTTTTSLTASILGAAGLDPTFVIGGKL					
	130	140	150	160	170	180
m092.pep	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
a092	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
	190	200	210	220	230	240
m092.pep	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
a092	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					

292

	190	200	210	220	230	240
	250	260	270	280	290	300
m092.pep	FIHRMPFYGKAFLCIDSEHVRMAILPKVSKPYATYGLDDTADIYATDIENVGAQMKFTVHV					
a092	FIHRMPFYGKAFLCIDSEHVRMAILPKVSKPYATYGLDDTADIYATDIENVGAQMKFTVHV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m092.pep	QMKGHEQGSFEVVLNMPGRHNVNALAAIGVALEVGASVEAIQKGLLGFEVGRFRFQKYG					
a092	QMKGHEQGSFEVVLNMPGRHNVNALAAIGVALEVGASVEAIQKGLLGFEVGRFRFQKYG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m092.pep	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYLEKRLVLAQPHRYTRTRDLFEDFTK					
a092	DIKLPNGGTALLVDDYGHHPVEMAATLSAARGAYPEKRLVLAQPHRYTRTRDLFEDFTK					
	370	380	390	400	410	420
	430	440	450	460	470	480
m092.pep	VLNTVDALVLTEVYAAGEEPIAAADSRLARAIRVLGKLEPIYCENVADLPEMLLNVLQD					
a092	VLNTVDALVLTEVYAAGEEPIAAADSRLARAIRVLGKLEPIYCENVADLPEMLLNVLQD					
	430	440	450	460	470	480
	490	500				
m092.pep	GDIVLNMGAGSINRVPAALLLSKQIX					
a092	GDIVLNMGAGSINRVPAALLELSKQIX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 315>:

g093.seq

```

1  aTGCAGAATt ttgGCAAAGT ggccgtATTG ATGGGtggtT TTTCCAGCGA
51  ACGAGAAatc tcgcTGGACA GCgGTACCGC CATTTTGAAC GCCTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGACC CTAAGGAAAC GCCGTTATCC
151 GAACTGAAGG AGCGGGGCTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCGAA GACGGGGCTG TTCAGGGTGC ATTGGAAGTGT TTGGGCATTC
251 CCTATACCGG CAGCGGTGTC GCCGCCTCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGCGCA GGCATTGGGA TTACCCGTTT CCGAGTTCGC
351 CGTACTGTAC GATGATACCG ATTTTCGATG CGTCGAAGAA AAATTGGGTC
401 TGCCGATGTT TGTGAAGCCG GCGGCCGAAG GCAGCAGCgt cggcgtggta
451 aAAGTCAAAG AAAaaggccg TCTGAAAAGC GTTtacgaag aatTGAAaCA
501 CCTTcagggg cgaAAatcatt gccgAacgTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATA ACATCATCCC
601 CGCAACCGAG TTTTACGAct acgaagccaa GtacaacCGA GACGAcacca
651 tttatCAATG TCCTTCGGAA GATTTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTTCGCG CGCACAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 316; ORF 093.ng>:

g093.pep

```

1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKERGFQTA FNILHGTYGE DGAQVGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLY DDTDFDAVEE KLGLPMFVKP AAEGSSVGVV
151 KVKEKGRLKS VYEELKHLQG RNHCRTFYRR RRIFLPRPER QRAARHTHHP
201 RNRVLRRLRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGSRTGNRCGRLLR
251 ARRFQRYRR QTLVGNQHP ARYDRP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 317>:

m093.seq

```

1  ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CTAAAGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCrAA GACGGGGCGG TTCAGGGTGC ATTGGAAGTGT TTGGGCATTTC
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGGCA GGCATTGGGA TTGCCCCTTC CCGAGTTCGC
351 CGTCTGCAC GACGACACTG ATTTTCGATGC CGTCGAAGAA AAATTGGGCC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTACGAAG AATTGAAACA
501 CCTTCAGGG. CGAAATCATT GCCGAACGTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATA ACATCATTCC
601 CGCAACCGAG TTTTACGACT ACGAAGCCAA GTACAACCGC GACGACACCA
651 TTTATCAATG TCCTTCGAA GATTTGACCG AAGCCGAAGA AAGCCTGATG.
701 CGCGAACTGG CGGTCGCGG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCTT GCCCGGTATG ACGAGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 318; ORF 093>:

```

m093.pep
1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGX DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AAEGSSVGVV
151 KVKGKGR LKS VYEELKHLQX RNHCRTFYRR RRIFLPRPER QRAARHTHS
201 RNRVLR LRSQ VQPRRHLSM SFGRFDRSR KPDARTGGS RAGNRCGR LR
251 ARRF PQRYR QTL SVGNQHP ARYDEP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 093 shows 96.7% identity over a 276 aa overlap with a predicted ORF (ORF 093.ng) from *N. gonorrhoeae*:

m093/g093

	10	20	30	40	50	60
m093.pep	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPL SELKAQGFQTA					
g093	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPL SELKERGFQTA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m093.pep	FNILHGTYGX DGAVQGALELLG IPYTGSGVAASAIGMDKYRCKLIWQALGLPVPEFAVLH					
g093	FNILHGTYGEDGAVQGALELLG IPYTGSGVAASAIGMDKYRCKLIWQALGLPVPEFAVLY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m093.pep	DDTDFDAVEEKLGLPMFVKPAAEGSSVGVV KVKGKGR LKS VYEELKHLQXRNHCRTFYRR					
g093	DDTDFDAVEEKLGLPMFVKPAAEGSSVGVV KVEKGR LKS VYEELKHLQGRNHCRTFYRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m093.pep	RRIFLPRPERQRAARHTHSRNRVLR LRSQVQPRRHLSMSFGRFDRSR RKPARTGGSR					
g093	RRIFLPRPERQRAARHTHSRNRVLR LRSQVQPRRHLSMSFGRFDRSR RKPARTGGSR					
	190	200	210	220	230	240
	250	260	270			
m093.pep	RAGNRCGR LRARRFPQRYRQ T LSVGNQHPARYDEPX					
g093	RTGNRCGR LRARRFPQRYRQ T LSVGNQHPARYDRPX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 319>:

a093.seq

```

1   ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CCAAGGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCGAA GACGGGGCTG TTCAGGGTGC ATTGGAAGT TTGGGCATTC
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTTGGCA GGCATTGGGA TTGCCCGTTC CCGAGTTCGC
351 CGTCCTGCAC GACGACACTG ATTTTCGATGC CGTCGAAGAA AAATTGGGCC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTTACGAAG AATTGAAACA
501 CTTTCAGGG. CGAAATCATT GCCGAACGGT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCTG TGTGAAACCG CAAAGGCCTG CCCGGCATA ACATCATCCC
601 CGCGACCGAG TTTTATGACT ACGAAGCCAA GTACAACCGC AACGACACCA
651 TTTATCAATG TCCTTCGGAA GATCTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTGCGGG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 320; ORF 093.a>:

a093.pep

```

1   MQNFGKQAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGE DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AAEGSSVGVV
151 KVKGKGR LKS VYEELKHFX RNHCRTVYRR RRIFLPCVER QRPARTHHHP
201 RDRVL* LRSQ VQPQRHHLMS SFGSRSDRSRR KPDARTGGSR RAGNRCGR LR
251 ARRFPPQRYRR QTLVGNQHP ARYDRP*

```

m093/a093 95.7% identity over a 276 aa overlap

	10	20	30	40	50	60
m093.pep	MQNFGKQAVLMGGFSSEREISLDSGTAILNALKSKGIDAYAFDPKETPLSELKAQGFQTA					
a093	MQNFGKQAVLMGGFSSEREISLDSGTAILNALKSKGIDAYAFDPKETPLSELKAQGFQTA					
	10	20	30	40	50	60
m093.pep	70	80	90	100	110	120
	FNILHGTYXGDGAVQGALELLGIPYTGSGVAASAIGMDKYRCKLIWQALGPLVPEFAVLH					
a093	FNILHGTYGEDGAVQGALELLGIPYTGSGVAASAIGMDKYRCKLIWQALGPLVPEFAVLH					
	70	80	90	100	110	120
m093.pep	130	140	150	160	170	180
	DDTDFDAVEEKLGLPMFVKPAAEGSSVGVVVKVGKGR LKSVYEELKHLQXRNHCRTFYRR					
a093	DDTDFDAVEEKLGLPMFVKPAAEGSSVGVVVKVGKGR LKSVYEELKHFXRNHCRTVYRR					
	130	140	150	160	170	180
m093.pep	190	200	210	220	230	240
	RRIFLPRPERQRAARHTHHSRNRVLR LRSQVQPRRHLSMSFGRFDRSR RKP DARTGGSR					
a093	RRIFLPCVERQRPARTHHPRDRVLX LRSQVQPRRHLSMSFGRSDRSRR RKP DARTGGSR					
	190	200	210	220	230	240
m093.pep	250	260	270			
	RAGNRCGR LRARRFPQRYRRQTLVGNQHPARYDEPX					
a093	RAGNRCGR LRARRFPQRYRRQTLVGNQHPARYDRPX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 321>:

```
g094.seq
  1  ATGTATTTCGC  CTTTGCCCAA  GCGGGCGTTG  GTGCCTGCGG  CGTTGAGTTT
51  GCCGCCGATA  ACGAAAGTGG  GGTCGAGTCC  TGCCCGCGCG  AGGATGGAGG
101 CGGTCAAGGCT  GGTGGTCGTG  GTTTTGCCGT  GCGTAaccgpc  aatggcgatg
151 cCGTCAACGGA  AGCGCATCAG  CTCTGCCAGC  ATCAAGGCGC  GCGBAATAAC
201 GGGAAATTTGC  CGCTCCAACG  CAgcgacaAC  TTCGGgattt  TCTTTCTTGA
251 CGGCGGTAGA  GGCAACGACG  ACATccgcAC  CGTTAACGTG  TTCTGCGGTA
301 TGGCCGGGAT  AA
```

This corresponds to the amino acid sequence <SEQ ID 322; ORF 094.ng>:

g094.pep
1 MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
51 PSRKRISSAS IKARGITGIC RSNAATTSGF SFLTAVEATT TSAPLTCSAV
101 WPG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 323>:

```
m094.seq
  1  ATGTATTTCG  CTTTGCCCAA  GCGGGCGTTA  GTGCCTGCGG  CGTTGAGTTT
 51  GCCGCCGATA  ACGAAAGTCG  GGTCAAGTCC  TGCCGCGCCG  AGGATGGAGG
101  CGGTCAGGCT  GGTGGTCGTG  GTTTTGCCGT  GCGTGCCGGC  AATGGCGATG
151  CCGTCACGGA  AGCGCATCAA  CTCCGCCAAC  ATCAGGGCGC  GCGBAATAAC
201  GGGCAATTTG  TGCTCCAACG  CAGCGACAAC  TTCGGGATTT  TC'TTTTTGA
251  CGGCGGTAGA  GGTAAACGAC  ACATCCGCAC  CGTTAACGTG  TTCGCGCGTA
301  TGGCCGGGAT  AA
```

This corresponds to the amino acid sequence <SEQ ID 324; ORF 094>:

m094.pep

1	MYSPLPKRAL	VPAALSLPPI	TKVGSSPAAP	RMEAVRLVVV	VLPCVPAMAM
51	PSRKRINSAN	IRARGITGIC	CSNAATTSGF	SFLTAVEVTT	TSAPLTCSAV
101	WPG*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

a094.pep

```

1  MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
51  PSRKRINSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCSAV
101 WPG*

```

m094/a094 100.0% identity over a 103 aa overlap

```

              10      20      30      40      50      60
m094.pep      MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKRINSAN
|||||
a094           MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKRINSAN
              10      20      30      40      50      60

              70      80      90     100
m094.pep      IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX
|||||
a094           IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX
              70      80      90     100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 327>:

g095.seq

```

1  ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTGC GCGCCGACGT
51  TTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
101 GCATAAGGTT TGCTCACTTT GGGCAAATC GCGCGGACGT GTTCGCTGTC
151 AACACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
201 TAAACGCCTG ATGCAGTTTT TCGACGCTGT GCCCGTAGGT ATCCATATGG
251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGGGTCA GTGTAGGAAA
301 GAGGCATCGG ATCGTCGGCT TCGGCAACGA TGTATTCGCC TTTGCCCAAG
351 CGGGCGTTGG TGCCTGCGGC GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 328; ORF 095.ng>:

g095.pep

```

1  MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF QONRADVFAV
51  NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRGQCRK
101 EASDRRLRQR CIRLCPSGRW CLRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 329>:

m095.seq

```

1  ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTGC GCGCCGACGT
51  TTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
101 GCATAAGGTT TGCTCACTTT GGGCAAATC GCGCGGACGT GTTCGCTGTC
151 AATACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
201 TAAACGCCTG ATGCAGTTTT TCGACGCTGT GCCCGTAGGT ATCCATATGG
251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG
301 GATGCATCCG ACCGTCGGCT TCGGCAACGA TGTATTCGCC TTTGCCCAAG
351 CGGGCGTTAG TGCCTGCGGC GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 330; ORF 095>:

m095.pep

```

1  MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF QONRADVFAV
51  NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRGQCRK
101 DASDRRLRQR CIRLCPSGRX CLRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 095 shows 97.6% identity over a 124 aa overlap with a predicted ORF (ORF 095.ng) from *N. gonorrhoeae*:

m095/g095

```

              10      20      30      40      50      60
m095.pep      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQONRADVFAVNTQKGFAVEG
|||||

```

297

```

g095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
              10      20      30      40      50      60
              70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
          |||||
g095      HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKEASDRRLRQRCIRLCPSGRW
              70      80      90      100     110     120

m095.pep  CLRRX
          ||||
g095      CLRRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 331>:

```

a095.seq
1  ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTGC GCGCCGACGT
51 TTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC
151 AATACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
201 TAAACGCCTG ATGCAGCTTC TCAACACTGT GCCCGTAGGT ATCCATATGG
251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG
301 GATGCATCCG ACCGTCGGCT TCGGCAACGA TGTATTGCC TTTGCCCAAG
351 CGGGCGTTGG TGCCTGCGGC GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 332; ORF 095.a>:

```

a095.pep
1  MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
51 NTQKGFAVEG HTVDEIDKRL MQLLNTVPVG IHMFVDIGN DGHNRCQCRK
101 DASDRRLRQR CIRLCPSGRW CLRR*

m095/a095  96.0% identity in 124 aa overlap

              10      20      30      40      50      60
m095.pep  MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
          |||||
a095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
              10      20      30      40      50      60
              70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
          |||||
a095      HTVDEIDKRLMQLLNTVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRW
              70      80      90      100     110     120

m095.pep  CLRRX
          ||||
a095      CLRRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 333>:

```

g096.seq
1  ATGGCCGGTC ATACCGGGCA GGGTGTGAT TTCCAACAGA TAGAGTTTGC
51 CGTCGGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCGATT
101 GCCTGTGCGC CGCGAACCGC CAGTTCGCGC ATCAGGCTTT CTTGCGCTTC
151 GGTCAAATCT TCCGAAGGAC ATTGAtaaat ggtgTCGTCT CGGttgtAct

```

1 MAGHTQGVD FQIEFAVGI FEEIDAAAF RTDCLCAANR QFAHQAFFGF
51 GQIFRRTLIN GVSVVLGEV VVKLGCDDV YAGQPFVQD GAGIFAAADK
101 TFGNDFAPEG VSILRKRFSD GLFL*

1	ATGGCTCGTC	ATACCGGGCA	GGGTGTTGAT	TTCCAACAGA	TAGAGTTTGC
51	CGTCGGTATC	TTTGAGGAAA	TCGACGCGCA	CGCAGCCTTC	CGCACCGATT
101	GCCTGCGCGC	CGCGAACCGC	CAGTTCGCGC	ATCAGGCTTT	CTTCGGCTTC
151	GGTCAAATCT	TCCGAAGGAC	ATTGATAAA	GGTGTCTGTC	CGGTTGTA
201	TGGCTTCGTA	GTCTGAAAC	TCGGTTCGGG	GAATGATGTG	TATGCCGGGC
251	AGCCCTTTGC	CGTTACAGAC	GGGCGAGGAA	TATTCGCCGC	CGCCGATAAA
301	ACGTTCCGCA	ATGATTTCGC	CC.TGAAGGT	GTTTCAATTC	TTCGTAAACG
351	CTTTTCAGAC	GGCCTTTTCC	TTTGA		

1 MARHTGQGVDFQQIEFAVGI FEEIDAAHAF RTDCLRAANR QFAHQAFFGF
51 GQIFRRTLIN GVVAVVLGFV VVKLGCGNDV YAGQPFAVQD GAGIFAADK
101 TFGNDFAXEG VSILRKRFSD GLFL*

		10	20	30	40	50	60
m096.pep		MARHTGQGVDFQQIEFAVGIFEEIDAHA	AFR	TDCLRAANRQFAHQ	AF	FGGQIFRRTLIN	
g096		MAGHTGQGVDFQQIEFAVGIFEEIDAHA	AFR	TDCLCAANRQFAHQ	AF	FGGQIFRRTLIN	
		10	20	30	40	50	60
		70	80	90	100	110	120
m096.pep		GVVAVVLGFVVVKLGCGNDVYAGQPF	AVQDGAGIFAAADKTF	GNDFAXEGVSILRKR	FSD		
		:					
g096		GVVSVVLGFVVVKLGCGDDVYAGQPF	AVQDGAGIFAAADKTF	GNDFAPEGV	SILRKR	FSD	
		70	80	90	100	110	120
m096.pep	GLFLX						
g096	GLFLX						

1	ATGGCCGGTC	ATACCGGGCA	GGGTGTTGAT	TTCCAACAGA	TAGAGTTTGC
51	CGTCGGTATC	TTTGAGGAAA	TCGACGCGCA	CGCAGCCTTC	CGCACCATT
101	GCCTGCGCGC	CGCGAACC GC	CAGTTCGCGC	ATCAGGCTTT	CTTCGGCTTC
151	GGTCAGATCT	TCCGAAGGAC	ATTGATAAAT	GGTGTCGTTG	CGGTGTACT
201	TGGCTTCGTA	GTCAATAAAC	TCGGTCGCGG	GGATGATGTG	TATGCCGGGC
251	AGGCCCTTGC	CGTTCAACAC	AGGACAGGAA	TATTCGCCGC	CGCCGATAAA
301	CCGTTTCGCA	ATGATTTCGC	CCT. GAAAG	GTTTCAATTC	TTCTAAACG
351	CTTTTCAGAC	GGCCTTTTCC	TTTGA		

1 MAGHTGQGVDFQQIEFAVGI FEEIDAHAAR RTDCLRAANR QFAHQAFFGF

299

51 GQIFRRTLIN GVVAVVLGFV VIKLGRGDDV YAGQAFVQH RAGIFAAADK
 101 PFGNDFAXES VSILRKRFSD GLFL*

m096/a096 92.7% identity in 124 aa overlap

	10	20	30	40	50	60
m096.pep	MARHTGQGVD	FQQIEFAVGIFEE	IDAHA	AFRTDCLRA	ANRQFAHQ	AFFGQIFRRTLIN
a096	MAGHTGQGVD	FQQIEFAVGIFEE	IDAHA	AFRTDCLRA	ANRQFAHQ	AFFGQIFRRTLIN
	10	20	30	40	50	60
	70	80	90	100	110	120
m096.pep	GVVAVVLGFV	VVKLGCGNDV	YAGQPF	AVQDGAGI	FAAADKTF	GNDFAXEGVSILRKRFSD
a096	GVVAVVLGFV	VIKLRGDDV	YAGQAF	VQHRAGI	FAAADKPF	GNDFAXESVSILRKRFSD
	70	80	90	100	110	120
m096.pep	GLFLX					
a096	GLFLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 339>:

g097.seq

1	ATGGATATTT	CAAAACAAAC	ATTGCTGGAT	AGGGTTTTTA	ACCTGAAGGC
51	AAACGGTACG	ACGGTACGTA	CCGAGTTGAT	GGCGGGTTTG	ACGACCTTTT
101	TGACGATGTG	CTACATCGTT	ATCGTCAATC	CCCTGATTTT	GGGCGAGACC
151	GGAAATGGATA	TGGGGGCGGT	ATTCGTGCT	ACCTGTATCG	CATCCGCCAT
201	CGGCTGTTTT	GTCATGGGTT	TTATCGGCAA	CTATCCGATT	GCGCTTGCCC
251	CGGGGATGGG	GCTGAATGCC	TATTTACCT	TTGCCGTCGT	TAAGGGTATG
301	GGCGTGCCCT	GGCAGGTGGC	GTTGGGTGCG	GTGTTCAATT	CCGGTCTGAT
351	TTTCATCCTG	TTCAGCTTTT	TTAAAGTCAG	GGAAATGCTG	GTCAACGCAC
401	TGCCTATGGG	TTTGAAAATG	TCGATTGCCG	CCGGTATCGG	TTTGTTTTTG
451	GCACTGATTT	CCCTGAAAGG	CGCAGGCATT	ATCGTTGCCA	ATCCGGCAAC
501	CTTGGTCGGC	TTGGGCGATA	TTCATCAGCC	CAGCGCACTG	TTGGCATTGT
551	TCGGTTTTGT	CATGGTGGTC	GTATTGGGGT	ATTTCCGCGT	TCAAGGCGCA
601	ATCATCATCA	CCATTCTGAC	GATTACCGTC	ATTGCCAGCC	TGATGGGTTT
651	GAACGAGTTT	CACGGCGTGG	TCGGCGAAGT	ACCGGGCATT	GCGCCGACCT
701	TTATGCAGAT	GGATTTTAAA	GGTCTGTTA	CCGTCAGCAT	GGTCAGCGTG
751	ATTTTCGTCT	TCTTCTTGGT	CGATTTGTTC	GACAGTACCG	GAACGCTGGT
801	CGGCGTATCC	CACCGTGCCG	GAATGCTGGT	GGACGGTAAG	CTGCCCCGCC
851	TGAAACGCGC	ACTGCTTGCA	GACTCTACCG	CCATTGTGGC	AGGTGCGGCT
901	TTGGGTACTT	CTTCAACCAC	GCCTTATGTG	GAAAGCGCGG	CGGGCGTATC
951	GGCAGGCGGA	CGGACCGGCC	TGACGGCGGT	TACCGTCGGC	GTATTGATGC
1001	TGGCGTGTCT	GATGTTCTCC	CCATTGGCGA	AAAGTGTTCC	GGTATTTGCC
1051	ACCGCGCCCG	CACTGCTTTA	TGTCGGCACG	CAGATGCTCC	GCAGTGCGAG
1101	GGACATTGAT	TGGGACGATA	TGACTGAAGC	CGCGCCCGCG	TTCTGACCA
1151	TTGTCTTCAT	GCCGTTTACC	TATTCGATTG	CAGACGGCAT	CGCCTTCGGC
1201	TTTCATCAGCT	ATGCCGTGGT	CAAACTTTTG	TGTCGCCGGA	CTGGGGACGT
1251	GCCGCCTATG	GTATGGGTTG	TTGCCGTATT	GTGGGCATTG	AAATTCTGGT
1301	ATTTGGGCTG	A			

This corresponds to the amino acid sequence <SEQ ID 340; ORF 097.ng>:

g097.pep

1	MDISKQTLDD	RVFNLKANGT	TVRTELMAGL	TTFLTMCYIV	IVNPLILGET
51	GMDMGAVFVA	TCIASAIGCF	VMGFIGNYPI	ALAPGMGLNA	YFTFAVVKGM
101	GVPWQVALGA	VFISGLIFIL	FSFFKVREML	VNALPMGLKM	SIAAGIGLFL
151	ALISLKGAGI	IVANPATLVG	LGDIHQPSAL	LALFGFVMVV	VLGYFRVQGA
201	IIITILTITV	IASLMGLNEF	HGVVGEVPGI	APTFMQMDFK	GLFTVSMVSV
251	IFVFFLVDLF	DSTGTLVGVS	HRAGLLVDGK	LPRLKRALLA	DSTAIIVAGAA
301	LGTSSSTPYV	ESAAGVSAGG	RTGLTAVTVG	VLMLACLMFS	PLAKSVPVFA
351	TAPALLYVGT	QMLRSARDID	WDDMTEAAPA	FLTIVFMPFT	YSIADGIAFG

401 FISYAVVKLL CRRTGDVPPM VWVAVLWAL KFWYLG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 341>:

```
m097.seq
1  ATGGACACTT CAAAACAAAC ACTGTTGGAC GGGATTTTTA AGCTGAAGGC
51  AAACGGTACK ACGGTGCGTA CCGAGTTGAT GGCGGGTTTG ACAACTTTTT
101 TGACGATGTG CTACATCGTT ATCGTCAACC CTCyGATTTT GGGCGAGACC
151 GGCATGGATA TGGGGGCGGT ATTCGTCGCT ACCTGTATCG CGTCTGCCAT
201 CGGCTGTTTT GTTATGGGTT TTGTCGGCAA CTATCCGATT GCACTCGCAC
251 CGGGGATGGG GCTGAATGCC TATTTACCTT TTGCCGTCGT TAAGGGTATG
301 GGCGTGCCTT GGCAGGTTGC GTTGGGTGCG GTGTTCATCT CCGGTCTGAT
351 TTTTATCCTG TTCAGCTTTT TTAAAGTCAG GGAAATGCTG GTCAACGCAC
401 TGCCTATGGG TTGAAAATG TCGATTGCTG CCGGTATCGG TTTGTTTTTG
451 GCACTGATTT CCTGAAAGG CGCAGGCATT ATCGTTGCCA ATCCGGCAAC
501 CTTGGTCGGT TTGGGCGATA TTCATCAGCC GTCCGCGTTG TTGGCATTGT
551 TCGGTTTTGC TATGGTGGTC GTATTGGGAC ATTTCCGCGT TCAAGGCGCA
601 ATCATCATCA CCATCTTGAC CATTACCGTC ATTGCCAGCC TGATGGGTTT
651 GAATGAATTT CACGGCATCA TCGGCGAAGT ACCGAGCATT GCGCCGACTT
701 TTATGCAGAT GGATTTTGAA GGCCTGTTTA CCGTCAGCAT GGTCAGTGTG
751 ATTTTCGTCT TCTTCTTGGT CGATCTATTT GACAGTACCG GAACGCTGGT
801 CGGCATATCC CACCGTGCCG GGCTGCTGGT GGACGGTAAG CTGCCCCGCC
851 TGAAACGCGC ACTGCTTGCA GACTCTACCG CCATTGTGGC AGGTGCGGCT
901 TTGGGTACTT CTCCACCAC GCCTTATGTG GAAAGCGCGG CGGGCGTATC
951 GGCAGGCGGA CGGACCGGCC TGACGGCGGT TACCGTCGGC GTATTGATGC
1001 TCGCCTGCCT GATGTTTTCA CCTTTGGCGA AAAGTGTTCC CGCTTTTGCC
1051 ACCGCGCCCG CCCTGCTTTA TGTCGGCACG CAGATGCTCC GCAGTGCGAG
1101 GGATATTGAT TGGGACGATA TGACGGAAGC CGCACCTGCG TTCCTGACCA
1151 TTGTTTTTCAT GCCGTTTACT TATTTCGATT GAGACGGCAT CGCTTTTCGC
1201 TTCATCAGTT ATGCCGTGGT TAAACTTTTA TGCCGCCGCA CCAAAGACGT
1251 TCCGCCTATG GTATGGATTG TTGCCGTATT GTGGGCACTG AAATTCCTGGT
1301 ATTTGGGCTG A
```

This corresponds to the amino acid sequence <SEQ ID 342; ORF 097>:

```
m097.pep
1  MDTSKQTLDD GIFKLKANGT TVRTELMAGL TTFLTMCIYIV IVNPXILGET
51  GMDMGAVFVA TCIASAIGCF VMGFVGNYP I ALAPGMGLNA YFTFAVVKGM
101 GVPWQVALGA VFISGLIFIL FSFFKVREML VNALPMGLKM SIAAGIGLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFAMVV VLGHFRVQGA
201 IIITILTITV IASLMGLNEF HGIIGEVP SI APTFMQMDFE GLFTVSMVSV
251 IFVFFLVDLF DSTGTLVGIS HRAGLLVDGK LPRLKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VLMLACLMFS PLAKSVPAFA
351 TAPALLYVGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG
401 FISYAVVKLL CRRTKDVP PM VWIVAVLWAL KFWYLG*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 097 shows 96.3% identity over a 436 aa overlap with a predicted ORF (ORF 097.ng) from *N. gonorrhoeae*:

```
m097/g097

      10      20      30      40      50      60
m097.pep  MDTSKQTLDDGIFKLKANGTTVRTELMAGLTTFLTMCIYIVIVNPXILGETGMDMGAVFVA
          || ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g097      MDISKQTLDDRVLNFKANGTTVRTELMAGLTTFLTMCIYIVIVNPLILGETGMDMGAVFVA
          10      20      30      40      50      60

      70      80      90     100     110     120
m097.pep  TCIASAIGCFVMGFVGNYP IALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL
          ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g097      TCIASAIGCFVMGFIGNYP IALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL
          70      80      90     100     110     120

      130     140     150     160     170     180
```

301

m097.pep	FSFFKVVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL
g097	FSFFKVVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL
	130 140 150 160 170 180
m097.pep	LALFGFAMVVVLGHFRVQGAIITILTITVIASLMGLNEFHGIIGEVPSIAPTTFMQMDFE
g097	LALFGFAMVVVLGHFRVQGAIITILTITVIASLMGLNEFHGVVGEVPGIAPTTFMQMDFK
	190 200 210 220 230 240
m097.pep	GLFTVSMVSIVFVFFLVLDLFDSTGTLVGISHRAGLLVDGKLPRLKRALLADSTAIVAGAA
g097	GLFTVSMVSIVFVFFLVLDLFDSTGTLVGIVSHRAGLLVDGKLPRLKRALLADSTAIVAGAA
	250 260 270 280 290 300
m097.pep	LGTSSSTPYVESAAAGVSAGGRTGLTAVTVGVMLACLMSPLAKSVPAFATAPALLYVGT
g097	LGTSSSTPYVESAAAGVSAGGRTGLTAVTVGVMLACLMSPLAKSVPAFATAPALLYVGT
	310 320 330 340 350 360
m097.pep	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVPPM
g097	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTGDVPPM
	370 380 390 400 410 420
m097.pep	VWIVAVLWALKFWYLGX
g097	VWVAVLWALKFWYLGX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 343>

a097.seq

1	ATGGACACTT	CAAAACAAAC	ACTGTTGGAC	GGGATTTTTA	AGCTGAAGGC
51	AAACGGTACG	ACGGTGCGTA	CCGAGTTGAT	GGCGGGTTTG	ACAACTTTTT
101	TGACGATGTG	CTACATCGTT	ATCGTCAACC	CTCTGATTTT	GGGCGAGACC
151	GGCATGGATA	TGGGGCGGT	ATTCGTCGCT	ACCTGTATCG	CGTCTGCCAT
201	CGGCTGTTT	GTTATGGGT	TTGTCGGCAA	CTATCCGATT	GCACTCGCAC
251	CGGGGATGGG	GCTGAATGCC	TATTTACCT	TTGCCGTCGT	TAAGGGTATG
301	GGCGTGCTT	GGCAGGTTGC	GTTGGGTGCG	GTGTTTATCT	CCGGTCTGAT
351	TTTCATCCTG	TTCAGCTTT	TTAAAGTCAG	GGAAATGCTG	GTCAACGCAC
401	TGCCTATGGG	TTTGAAAATG	TCGATTGCTG	CCGGTATCGG	TTTGTTTTTG
451	GCACTGATTT	CCCTGAAAGG	CGCAGGCATT	ATCGTTGCCA	ATCCGGCAAC
501	CTTGGTCGGC	TTGGGCGATA	TTCATCAGCC	GTCCGCGTTG	TTGGCACTGT
551	TCGGTTTTGC	CATGGTGGTC	GTATTGGGAC	ATTTCCGCGT	TCAAGGCGCA
601	ATCATCATCA	CCATTTTGAC	GATTACCGTC	ATTGCCAGCC	TGATGGGTTT
651	GAACGAATTT	CACGGCATCA	TCGGCGAAGT	GCCGAGCATT	GCGCCGACTT
701	TTATGCAGAT	GGATTTTAAA	GGGTTGTTTA	CCGTCAGCAT	GGTCAGCGTG
751	ATTTTCGTCT	TTTTCTAGT	CGATCTGTTC	GACAGTACCG	GAACACTGGT
801	CGGTGTATCG	CATCGTGCCG	GACTGCTGGT	GGACGGTAAG	CTGCCCCGCC
851	TGAAACGCGC	ACTGCTTGCA	GACTCTACCG	CTATTGTGGC	AGGTGCGGCT
901	TTGGGTACTT	CTTCAACCAC	GCCTTATGTG	GAAAGTGGCG	CGGGCGTATC
951	GGCAGGCGGG	CGGACAGGTC	TGACGGCGGT	TACCGTCCGC	GTATTGATGC
1001	TCGCCTGCCT	GATGTTTTCA	CCTTTGGCGA	AAAGTGTTC	CGCTTTTGCC
1051	ACCGCGCCCG	CCCTGCTTTA	TGTCGGCAGC	CAGATGCTCC	GCAGTGCGAG
1101	GGACATCGAT	TGGGACGATA	TGACGGAAGC	CGCACCAGCA	TTCTTGACCA
1151	TTGTCTTCAT	GCCGTTTACC	TATTCGATTG	CAGACGGCAT	CGCTTTCGGC
1201	TTCATCAGTT	ATGCCGTGGT	TAAACTTTTA	TGCCGCCGCA	CCAAAGACGT
1251	TCCGCCTATG	GTATGGATTG	TTGCCGTATT	GTGGGCACTG	AAATTCTGGT

1301 ATTTGGGCTG A

This corresponds to the amino acid sequence <SEQ ID 344; ORF 097.a>:

a097.pep

```

1  MDTSKQTLDD GIFKLKANGT TVRTELMAGL TTFLTMCIYIV IVNPLILGET
51  GMDMGAVFVA TCIASAIGCF VMGFVGNYPY ALAPGMGLNA YFTFAVVKGM
101 GVPWQVALGA VFISGLIFIL FSFFKVRML VNALPMGLKM SIAAGIGLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFAMVV VLGHFRVQGA
201 IITILTITV IASLMGLNEF HGIIGEVPSI APTFMQMDFK GLFTVSMVSV
251 IFVFFLVDLF DSTGTLVGVS HRAGLLVDGK LPRLKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VLMLACLMFS PLAKSVPAFA
351 TAPALLYVGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG
401 FISYAVVKLL CRRTKDVPPM VWIVAVLWAL KFWYLG*

```

m097/a097 99.3% identity in 436 aa overlap

	10	20	30	40	50	60
m097.pep	MDTSKQTLDDGIFKLKANGTTVRTELMAGLTTFLTMCIYIVIVNPIXILGETGMDMGAVFVA					
a097	MDTSKQTLDDGIFKLKANGTTVRTELMAGLTTFLTMCIYIVIVNPLILGETGMDMGAVFVA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m097.pep	TCIASAIGCFVMGFVGNYPYALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
a097	TCIASAIGCFVMGFVGNYPYALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m097.pep	FSFFKVRMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL					
a097	FSFFKVRMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m097.pep	LALFGFAMVVVLGHFRVQGAIIITILTITVIASLMGLNEFHGIIGEVPSIAPTFMQMDFE					
a097	LALFGFAMVVVLGHFRVQGAIIITILTITVIASLMGLNEFHGIIGEVPSIAPTFMQMDFK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m097.pep	GLFTVSMVSVIFVFFLVDLFDSTGTLVGISHRAGLLVDGKLPRLKRALLADSTAIVAGAA					
a097	GLFTVSMVSVIFVFFLVDLFDSTGTLVGVS HRAGLLVDGKLPRLKRALLADSTAIVAGAA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m097.pep	LGTSSSTTPYVESAGVSAGGRTGLTAVTVGVMLACLMFSPLAKSVPAFATAPALLYVGT					
a097	LGTSSSTTPYVESAGVSAGGRTGLTAVTVGVMLACLMFSPLAKSVPAFATAPALLYVGT					
	310	320	330	340	350	360
	370	380	390	400	410	420
m097.pep	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVPPM					
a097	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVPPM					
	370	380	390	400	410	420
	430					
m097.pep	VWIVAVLWALKFWYLGX					
a097	VWIVAVLWALKFWYLGX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 345>:

```
g098.seq
1  ATGACCGCCG ACGGTCTCTT CGTCGCTTTC AACTTCAATA CGTTTGCCGT
51  TGTGCGAATA TTGATACCAG TACAGCAGGA TGCTGCCGAG GCTGGCGATC
101 AGTTTGTCCG CGATGTCGCG CGCTTCGCTG TCGGGATGGC TTTTCGCTTC
151 GGGATGAACG CAGCCGAGCA TGGACACGCC GGTACGCATC ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTTGAG CTTGGTTTTA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAAGTG TGCGACTTCT TCAAACTCGC
351 ATTTTGTGC CAAATTAGAA TGTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 346; ORF 098.ng>:

```
g098.pep
1  MTADGLFVAF NFNTFAVVRI LIPVQDAAQ AGDQFVGDDVA RFVGMFAFAF
51  GMNAAEHGHA GTHHVHRMGM CRQAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV CDFFKLAFLC QIRMS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 347>:

```
m098.seq
1  ATGACCGCCG ATGGTCTCTT CGTCGCTTTC AACCTCAATG CGTTTGCCGT
51  TGTGCGAATA TTGATACCAG TACAAGAGGA TGCTGCCGAG GCTGGCGATC
101 AGTTTGTCCG CGATGTCGCG CGCTTCACTT TCCGGATGGC TTTCACGTTT
151 AGGATGAACG CAGCCCAGCA TGGATACGCC GGTACGCATT ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTTGAG CTTGGTTTTA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAGGTG GGCGACTTCT TCAAACTCGC
351 ATTTTGTGC CAAATCAGAA TGTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 348; ORF 098>:

```
m098.pep
1  MTADGLFVAF NLNAFAVVRI LIPVQEDAAE AGDQFVGDDVA RFTFRMAFTF
51  RMNAAQHGYA GTHYVHRMGM CRQAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV GDFFKLAFLC QIRMS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 098 shows 89.6% identity over a 125 aa overlap with a predicted ORF (ORF 098.ng) from *N. gonorrhoeae*:

```
m098/g098

      10      20      30      40      50      60
m098.pep MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAAQHGYA
|||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g098      MTADGLFVAFNFNTFAVVRI LIPVQDAAQAGDQFVGDDVARFAVGMFAFAFGMNAAEHGHA
      10      20      30      40      50      60

      70      80      90     100     110     120
m098.pep GTHYVHRMGMC RQAFQNFNHTDRQAAHGFE LGFISGQLEFVGQMAVNQQV GDFFKLAFLC
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g098      GTHHVHRMGMC RQAFQNFNHTDRQAAHGFE LGFISGQLEFVGQMAVNQQV CDFFKLAFLC
      70      80      90     100     110     120

m098.pep QIRMSX
|||
g098      QIRMSX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 349>:

```
a098.seq
1  ATGACCGCCG ATGGTCTCTT CGTCGCTTTC AACCTCAATG CGTTTGCCGT
51  TGTGCGAATA TTGATACCAG TACAAGAGGA TGCTGCCGAG GCTGGCGATC
```

```

101 AGTTTGTCTCGG CGATGTCGCG CGCTTCACTT TCCGGATGGC TTTCACGTTT
151 AGGATGAACG CAGCCCAGCA TGGATACGCC GGTACGCATT ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTTGAG CTTGGTTTTA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAGGTG GCGACTTCT TCAAACCTCG
351 ATTTTGTGTC CAAATCAGAA TGTCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 350; ORF 098.a>:

a098.pep

```

1 MTADGLFVAF NLNAFAVVRI LIPVQEDAAE AGDQFVGDDVA RFTFRMAFTF
51 RMNAAQHGYA GTHYVHRMG CROAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV GDFFKLAFLC QIRMS*

```

m098/a098 100.0% identity in 125 aa overlap

	10	20	30	40	50	60
m098.pep	MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAAQHGYA					
a098	MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAAQHGYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m098.pep	GTHYVHRMGMCROAFQNFNHTDRQAAHGFE LGFISGQLEFVGQMAVNQQVGDFFKLAFLC					
a098	GTHYVHRMGMCROAFQNFNHTDRQAAHGFE LGFISGQLEFVGQMAVNQQVGDFFKLAFLC					
	70	80	90	100	110	120
m098.pep	QIRMSX					
a098	QIRMSX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 351>:

g099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTGGA
51 GCTGACGGGC AAACGGCAGG CGGGCATTAC TGCCACAGAC ATCGTGTGTTG
101 CACTGACCGA ATTCTTGCCT AAAGAGCGCG TGGTCGGGGC GTTTGTCTGAA
151 TTTTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGAGT TCGGCGCGAC TGCCGCCATG TCGCCATCG
251 ACGCGCAAAC TATTGATTAT TTGAAACTGA CCGGACGTGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAAACC GCAGGCTTAT GGGCAGGTGG
351 CTTGAAAACC GCCGTTTATC CGCGCGTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCGAGCAACC CGCACGCGCG TTTTGCCACC
451 GCCGATTGTT CGGCGAAAGG GCTGGCGAAG CTTTACGAAG AGCCTTCAGA
501 CGGCCAAATG CCTGACGGTG CAGTGATTAT TGCCCGGATT ACTTCGTGTA
551 CCAATACTTC CAACCCGCGC AACGTTGTCT CCGCCGCACT GTTGGCACGC
601 AATGCCAACC GCCTCGGCTT GAAACGCAAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGGAATCTA TTTGAAAGAA GCAGGCTTGT
701 TGCCCGAAAT GGAAAACTC GGCTTCGGTA TCGTCGCCTT CGCATGTACC
751 ACCTGTAACG GCATGAgcgG CGCGCTcgaC CCGAAAATCC AACAAGAAAT
801 CATCGACCGC GAtttgtacg cCACC GCCGT ATTGT CAGGC AACC GCAACT
851 TCGACGGCCG TATCCATCCG TATGCGAAAC AGGCTTTCCT CGCTTCGCCT
901 CCTTTGGTCG TTGCCTACGC ATTGGCAGGT AGCATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGGCCG CGAAATCCGC CTGAAAGATA
1001 TCTGGCCGAC AGACGAAGAA ATCGATGCCA TCGTTGCCGA ATATGTGAAA
1051 CCGCAACAAT TCCGCGACAT TTATATCCCG ATGTCCGACA CCGGCACAGC
1101 GCAAAAAGCA CCAAGCCCGC TGTACGACTG GCGACCGATG TCCACCTACA
1151 TCCGCCGTCC GCCCTATTGG GAAGGCGCAC TGGCAGGGGA ACGTACATTA
1201 AGAGGTATGC GTCCGCCGGC GATTTTGCCC GACAACATCA CCACCGACCA
1251 CATCTCgcca tCCAATGCGA TTTTGCCCGG cagTGCgca ggtgaATATT

```

```

1301  TGGCGAAAAAT GGGTTTGCCT GAAGAagaCT TCAACTCTTA CGCAACCCAC
1351  CGCGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401  GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTtcgt
1451  tggcacgcgT tgaacCAGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501  GAAACCTATA TGAACGCAA ACAGCCGCTT ATCATCATTG CCGGTGCGGA
1551  CTATGGTCAA GGCTCAAGCC GCGACTGGGC GGCGAAGGGC GTGCGGCTGG
1601  CGGGTGTGGA AGCCATCGCC GCCGAAGGTT TCGAGCGCAT CCACCGCACC
1651  AACCTCATCG GCATGGGCGT CTTGCCGCTG CAATTCAAAC CCGGCACCAA
1701  CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTCGGCG
1751  AACGCACACC GCGTGCGGC CTGACCCTCG TGATTCACCG TAAAAACGGA
1801  GAAACCGTCG AAGTTCCGGT TACCTGCCGC CCGGATACCG CAGAAGAAGC
1851  ATTGGTATAT GAAGCCGGCG GCGTATTGCA ACGGTTTGCA CAGGACTTTT
1901  TGGAAGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 352; ORF 099.ng>:

g099.pep

```

1  MLGRASMMRL PDIVGVELTG KRQAGITATD IVLALTEFLR KERVVGAFVE
51  FFGEGARSLs IGDRATISNM TPEFGATAAM FAIDAQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWAGGLKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAAKGLAK PYEESDQGM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLKRK PWVKSSFAPG SKVAGIYLKE AGLLPEMEKL GFGIVAFAC
251 TCNGMSGALD PKIQEIIIDR DLYATAVLSG NRNFDGRIHP YAKQAFSLAP
301 PLVVAYALAG SIRFDIENDV LGVADGREIR LKDIWPTDEE IDAIVAIEYVK
351 PQQFRDIYIP MSDTGTAKA PSPLYDWRPM STYIRPPYW EGALAGERTL
401 RGMRPAILP DNITTDHISP SNAILAGSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMNKQPL IIIAGADYGO GSSRDWAAG VRLAGVEAIA AEGFERIHRT
551 NLIGMGVLP QFKPGTNRHT LQLDGTETYD VVGERTPRCG LTLVIHRKNG
601 ETVEVPVTCR PDTAEEALVY EAGGVLRFA QDFLEGNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 353>:

m099.seq

```

1  ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTTGA
51  GCTGAACGGC AAACGGCAGG CGGGCATTAC GGCGACGGAT ATTGTGTTGG
101 CACTGACCGA GTTCTGCGC AAAGAACGCG TGGTCGGGGC GTTTGTGCGAA
151 TTCTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCGATG TTCGCTATTG
251 ATGAGCAAAC CATTGATTAT TTGAAACTGA CCGGACGCGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAAACC GCAGGCTTGT GGGCAGATGC
351 CTTGAAAACC GCCGTTTATC CTCGCGTTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCAAGTAACC CGCATGCCCG TTTTGCAGAC
451 GCCGATTTGG CGGCGAAAGG GCTGGCGAAG CCTTACGAAG AGCCTTCGGA
501 CGGCCAAATG CCCGACGGCT CGGTCATCAT CGCCGCGATT ACCAGTTGCA
551 CCAACACTTC CAACCCGCGC AACGTTGTTG CCGCCGCGCT CTTGGCACGC
601 AATGCCAACC GTCTCGGCTT GAAACGCAAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGAAATCTA TTTGAAAGAA GCGGGCCTGT
701 TGCCCCGAAAT GGAAAAACTC GGCTTCGGTA TCGTCGCCTT CGCCTGCACC
751 ACCTGCAACG GCATGAGTGG CGCGCTGGAT CCGAAAATCC AGAAAGAAAT
801 CATCGACCGC GATTTGTACG CCACCGCCGT ATTATCAGGC AACCGCAACT
851 TCGACGGCCG TATCCACCCG TATGCGAAAC AGGCTTTCCT CGCTTCGCCT
901 CCGTTGGTCG TTGCCTACGC GCTGGCAGGC AGTATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGGCAA GGAAATCCGC CTGAAAGACA
1001 TTTGGCCTGC CGATGAAGAA ATCGATGCCG TCGTTGCCGA ATATGTGAAA
1051 CCGCAGCAGT TCCGCGATGT GTATGTACCG ATGTTGACA CCGGCACAGC
1101 GCAAAAAGCA CCCAGTCCGC TGTACGATTG GCGTCCGATG TCCACCTACA
1151 TCCGCCGTCC GCCTTACTGG GAAGGCGCGC TGGCAGGGGA ACGCACATTA
1201 AGAGGTATGC GTCCGCTGGC GATTTTGCCC GACAACATCA CCACCGACCA
1251 CCTCTCGCCG TCCAATGCGA TTTTGGCCGT CAGTGCCGCA GGCGAGTATT
1301 TGGCGAAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGCGCGGACC ACTTGACCGC CCAACGCGCT ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAAAA ACGAAGACGG CAGCGTGCGC CAAGGCTCGT
1451 TCGCCCGCGT CGAACCCGAA GGCGAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACGCAA ACAGCCGCTC ATCATCATTG CCGGTGCGGA

```

```

1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTAGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACCTTATCG GCATGGGCGT GTTGCCGCTG CAGTTCAAAC CCGACACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTGGTCGGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTCG TGATTACCG TAAAAACGGC
1801 GAAACCGTTG AAGTTCCCGT TACCTGCTGC CTCGATACTG CAGAAGAAGT
1851 ATTGGTATAT GAAGCCGCGC GCGTGTGCA ACGGTTTGCA CAGGATTTTT
1901 TGAAGGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 354; ORF 099>:

```

m099.pep
  1 MLGRASMMRL PDIVGVELNG KRQAGITATD IVLALTEFLR KERVVGAFVE
  51 FFGEGARSLS IGDRATISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
 101 VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
 151 ADLAAKGLAK PYEESPQDGM PDGSVIIAAI TSCTNTSNPR NVVAAALLAR
 201 NANRLGLKRK PWKSSFAPG SKVAEIYLKE AGLLPEMEKL GFGIVAFAC
 251 TCNGMSGALD PKIQKEIIDR DLYATAVLSG NRNFDGRIHP YAKQAFVLA
 301 PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPADEE IDAVVAEYVK
 351 PQQFRDVYVP MFDTGTAQKA PSPLYDWRPM STYIRRPYVW EGALAGERTL
 401 RGMRLAILP DNITTDHLSP SNAILAVSAA GEYLAKMGLP EEDFNSYATH
 451 RGDHLTAQRA TFANPKLFNE MVKNEDGSRV QGSFARVEPE GETMRMWEAI
 501 ETYMNKQPL IIIAGADYGO GSSRDWAAKG VRLAGVEAIV AEGFERIHR
 551 NLIGMGVLP LQFKPDNRHT LQLDGTETYD VVGERTPRCD LTLVIHRNG
 601 ETVEVPVTC LDTAEEVLVY EAGGVLRFA QDFLEGNA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 099 shows 96.2% identity over a 639 aa overlap with a predicted ORF (ORF 099.ng) from *N. gonorrhoeae*:

m099/g099

	10	20	30	40	50	60
m099.pep	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
	:					
g099	MLGRASMMRLPDIVGVELTGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m099.pep	IGDRATISNMTPEFGATAAMFAIDEQTIDYLKLTGRDDAQVKLVETYAKTAGLWADALKT					
	:					
g099	IGDRATISNMTPEFGATAAMFAIDAQTIDYLKLTGRDDAQVKLVETYAKTAGLWAGGLKT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m099.pep	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEESPQDGM PDGSVIIAAI					
	:					
g099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEESPQDGM PDGAVIIAAI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m099.pep	TSCTNTSNPRNVVAAALLARNANRLGLKRPWKSSFAPGSKVAEIYLKEAGLLPEMEKL					
	:					
g099	TSCTNTSNPRNVVAAALLARNANRLGLKRPWKSSFAPGSKVAGIYLKEAGLLPEMEKL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m099.pep	GFGIVAFACCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFVLA					
	:					
g099	GFGIVAFACCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFVLA					
	250	260	270	280	290	300
	310	320	330	340	350	360

307

m099.pep	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIWPADEEIDAVVAEYVKPQQFRDVFYVP
g099	PLVVAYALAGSIRFDIENDVLGVADGREIRLKDIWPTDEEIDAIVA EYVKPQQFRDIYIP
	310 320 330 340 350 360
m099.pep	MFDTGTAQKAPSPLYDWRPMSTYIRRPYWE GALAGERTLRGMRPLAILPDNITTDHLS P
g099	MSDTGTAQKAPSPLYDWRPMSTYIRRPYWE GALAGERTLRGMRPPAILPDNITTDHISP
	370 380 390 400 410 420
m099.pep	SNAILAVSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVKNE DGSVR
g099	SNAILAGSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVRNE DGSVR
	430 440 450 460 470 480
m099.pep	QGSFARVEPEGETMRMWEAIE TYMNRKQPLII IAGADYGQGS SRDWA AKGVRLAGVEAIV
g099	QGSLARVEPEGQ TMRMWEAIE TYMNRKQPLII IAGADYGQGS SRDWA AKGVRLAGVEAIA
	490 500 510 520 530 540
m099.pep	AEGFERIHR TNLIGMGVLP LQFKPDTNRHTLQLDGTET YDVVGERTPRCDLTLVIHRKNG
g099	AEGFERIHR TNLIGMGVLP LQFKPGTNRHTLQLDGTET YDVVGERTPRCGLTLVIHRKNG
	550 560 570 580 590 600
m099.pep	ETVEVPVTCCLDTAE EVLVYEAGGV LQRFAQDFLEGNAAX
g099	ETVEVPVTCRPDTAE EALVYEAGGV LQRFAQDFLEGNAAX
	610 620 630 640

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 355>:

a099.seq

```

1  ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTTGA
51  GCTGAACGGC AACCGGAAGG CGGGCATTAC GGCGACGGAT ATTGTGTTGG
101 CACTGACCGA GTTCTGCGC AAAGAACGCG TGGTCGGGGC GTTGTGCGAA
151 TTCTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGAGT TCGGCGCGAC TGCCGCGATG TTCGCTATTG
251 ATGAGCAAAC CATTGATTAT TTGAACTGA CCGGACGCGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAAACC GCAGGCTTGT GGGCAGATGC
351 CTTGAAAACC GCCGTTTATC CGCGCGTTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCGAGCAACC CGCACGCGCG TTTTGCAGCC
451 GCCGATTTGG CCGGCAAAGG CTGGCTAAA CCTTACGAAG AGCCTTCAGA
501 CGGCCAAATG CCTGACGGTG CAGTGATTAT TGCCGCGATT ACTTCCTGTA
551 CCAATACTTC CAATCCGCGC AACGTTGTCG CCGCCGCGCT GTTGGCACGC
601 AATGCCAACC GCCTCGGCTT GCAACGCAAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAGTAG CCGAAATCTA TTTGAAAGAA GCAGATCTGC
701 TGCCCGAAAT GGA AAAACTC GGCTTCGGTA TCGTTGCCTT CGCATGTACC
751 ACCTGTAACG GCATGAGCGG CGCGCTGGAT CCGAAAATCC AGAAAGAAAT
801 CATCGACCGC GATTGTACG CCACCGCCGT ATTGTCAGGC AACC GCAACT
851 TTGACGGCCG TATCCATCCG TATGCGAAAC AGGCTTTCCT CGCTTCGCTT
901 CCGTTGGTCG TTGCCTACGC GCTGGCAGGC AGCATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGGCAA AGAAATCCGC CTGAAAGACA
1001 TTTGGCCTAC CGATGAAGAA ATCGATGCCA TCGTTGCCGA ATATGTGAAA
1051 CCGCAGCAAT TTCGCGACGT TTATATCCCG ATGTTGACGA CCGGCACAGC
1101 GCAAAAAGCA CCAAGCCCGC TGTACGACTG GCGTCCAATG TCTACCTATA
1151 TCCGCCGCCC ACCTTACTGG GAAGGCGCAC TGGCAGGGGA ACGCACATTA
1201 AGCGGTATGC GTCGCTGGC GATTTTGCCC GACAACATCA CCACCGACCA

```

```

1251 TCTCTCGCCA TCCAATGCGA TTTTGGCAAG CAGTGCCGCA GGCGAATATT
1301 TGGCAAAAT GGGTTTGCTT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGTGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCGA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTTTCGC
1451 TGGCACGCGT TGAACCCGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGCGCGGA
1551 CTACGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTGGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACTTGATCG GTATGGGCGT GTTGCCGCTG CAGTTCAAAC CGGGTACCAA
1701 CCGCCACACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTGCGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTTG TGATTCACCG TAAAACGGC
1801 GAGACCGTCG AAGTCCCCAT TACGTGCCGC CTCGATACCG CAGAAGAAGT
1851 GTTGGTATAT GAAGCCGGTG GCGTATTGCA ACGGTTTGCA CAGGATTTTT
1901 TGAAGGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 356; ORF 099.a>:

a099.pep

```

1 MLGRASMMRL PDIVGVELNG KRKAGITATD IVLALTEFLR KERVVGAFVE
51 FFGEGARSLS IGDRATISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAGKGLAK PYEESDQGM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLQRK PWVKSSFAPG SKVAEIYLKE ADLLPEMEKL GFGIVAFAC
251 TCNGMSGALD PKIQKEIIDR DLYATAVLSG NRNFDGRIHP YAKQAFFLASP
301 PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPTDEE IDAIVAEYVK
351 PQQFRDVYIP MFDTGTAQKA PSPLYDWRPM STYIRPPYVW EGALAGERTL
401 SGMRLAILP DNITTDHLSP SNAILASSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMNRRQPL IIIAGADYQG GSSRDWAAKG VRLAGVEAIV AEGFERIHRT
551 NLIGMGVLPL QFKPGTNRHT LQLDGTETYD VVGERTPRCD LTLVIHRKNG
601 ETVEVPITCR LDTAEVLVY EAGGVLQRFA QDFLEGNA*

```

m099/a099 97.5% identity in 639 aa overlap

	10	20	30	40	50	60
m099.pep	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFFGEGARSLS					
a099	MLGRASMMRLPDIVGVELNGKRKAGITATDIVLALTEFLRKERVVGAFVEFFFGEGARSLS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m099.pep	IGDRATISNMTPEFGATAAMFAIDEQTIDY LKLTGRDDAQVKLVETYAKTAGLWADALKT					
a099	IGDRATISNMTPEFGATAAMFAIDEQTIDY LKLTGRDDAQVKLVETYAKTAGLWADALKT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m099.pep	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEESDQMPDGSVIIAAI					
a099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAGKGLAKPYEESDQMPDGAVIIAAI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m099.pep	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWKSSFAPGSKVAEIYLKEAGLLPEMEKL					
a099	TSCTNTSNPRNVVAAALLARNANRLGLQRKPWKSSFAPGSKVAEIYLKEADLLPEMEKL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m099.pep	GFGIVAFAC TT CNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAF FLASP					
a099	GFGIVAFAC TT CNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAF FLASP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m099.pep	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIWPADEEIDAIVAEYVKPQQFRDVYVP					

q102.seq

g102.pep

```

1  MSAKTPSLFG  GAMIIAGKVI  GAGMFPNPTA  NLGDGLIGSL  IVLLYTWFPF
51  SSGALMILEV  NTHNPRGASF  DTMVKDLLGR  GWNIINGIAV  ALVLYGSTYA
101 YILVGGDLTA  KGIGSAVGGK  ISLTVGQLVF  FGILAFVCWA  SARLVDREFTG
151 VLIIGMVLTF  IWATGGLVAD  AKPSVLFDTQ  APVGTGYWIY  AATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWAGT  LVALVIYVLW  QTAIQSNLPR
251 NEFAPVIAAE  RQLSVLNETL  SKFAQTGDM  KILSLFPYMA  IATSLGLVTL
301 GLFDNIADIF  KWNDMSMGRG  TKTVALNFLP  PLISWLLLP  GFFTAIGASG
351 LAATVWDQGI  IPAMLLYVSP  QKIGAGKTYK  VYGGWLWMLV  FLFGIANIAA
401 QVLSQMEVLP  VFKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 359>:

```

m102.seq
1  ATGCCCAACA  AAACCCCTTC  ACTGTTCCGGC  GCGCGCATGA  TTATCGCCGG
51  CACGGTCATC  GCGCGAGGCA  TGCTCGCCAA  CCCGACCGCC  ACATCCGGCG
101 TATGGTTTAC  CGGCTCGCTG  GCCGTGTTGC  TGTACACCTG  GTTTTCTATG
151 CTTTCAGCG  GCCTGATGAT  TTTGGAAGTC  AACACCCATT  ATCCGCACGG
201 CGCAAGTTTC  GACACGATGG  TCAAAGACCT  GCTCGGACGC  GGCTGGAACA
251 TCATCAACGG  CATCGCCGTC  GCCTTCGTTT  TATACCTGCT  TACTTACGCT
301 TATATCTTCG  TCGGCGGCGA  CCTGACCGCC  AAAGGCTTAG  GCAGCGCGGC
351 AGGCGGCGAC  GTTTCACCTA  CCGTCGGACA  ACTCGTCTTC  TTCGGCATCC
401 TCGCCTTTTG  CGTATGGGCA  TCCGCACGCT  TGGTCGACCG  CTTACCCGGC
451 GTCCTTATCG  GCGGCATGGT  ATTGACCTTT  ATTTGGGCGG  CCGCGCGGCT
501 GATTGCCGAT  GCCAAGCCGT  CCGTCTCTCT  CGATACCCAA  GCCCCCGCCG
551 GCACAACTA  CTGGATTTC  GCGGCCACCG  CCCTGCCCGT  CTGCCTCGCT
601 TCCTTCGGCT  TCCACGGCAA  CGTCTCCAGC  CTGCTCAAAT  ACTTTAAAGG
651 CGACGCGCCC  AAGTGGCTA  AATCCATCTG  GACGGGCACA  CTGATTGCGC
701 TGGTAATTTA  CGTCTCTGG  CAAACCGCCA  TCCAAGGCAA  CCTGCCGCGC
751 AACGAGTTCG  CCCCCTCAT  CGCCGCCGAA  GGGCAAGTCT  CCGTCTCAT
801 CGAAACCTG  TCCAAATTC  CCCAAACCGG  CAATATGGAC  AAAATATGT
851 CCCTGTTTC  CTATATGGCG  ATCGCCACCT  CGTTTTTAGG  CGTAACGCTC
901 GGACTCTTCG  ACTACATCGC  CGACATCTTC  AAATGGAACG  ACAGCATCTC
951 CGGCCGCACC  AAAACCGCCG  CGCTGACCTT  CCTGCCGCCC  CTGATTTCCT
1001 GCCTGCTCTT  CCCCACCGGC  TTCGTTACCG  CCATCGGCTA  CGTCGGCCTG
1051 GCGGCAACCG  TCTGGACAGG  CATCATCCCC  GCCATGCTGC  TCTACCGTTC
1101 GCGCAAAAAA  TTCGGCGCAG  GCAAAACCTA  TAAAGTTTAC  GGCGGCTTGT
1151 GGCTGATGGT  TTGGGTCTTC  CTTTTCGGCA  TCGTCAACAT  CGCCGCACAG
1201 GTATTGAGCC  AAATGGAAC  CGTCCCCGTA  TTAAAGGAT  AA

```

This corresponds to the amino acid sequence <SEQ ID 360; ORF 102>:

```

m102.pep..
1  MPNKTPSLFG  GAMIIAGTVI  GAGMLANPTA  TSGVWFTGSL  AVLLYTWFSM
51  LSSGLMILEV  NTHYPHGASF  DTMVKDLLGR  GWNIINGIAV  AFVLYLLTYA
101 YIFVGGDLTA  KGLGSAAGGD  VSLTVGQLVF  FGILAFVCWA  SARLVDREFTG
151 VLIIGMVLTF  IWAAGGLIAD  AKPSVLFDTQ  APAGTNYWIY  AATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWGT  LIALVIYVLW  QTAIQGNLPR
251 NEFAPVIAAE  GQVSVLIETL  SKFAQTGNMD  KILSLFSYMA  IATSLGLVTL
301 GLFDYIADIF  KWNDISISRT  KTAALTFLPP  LISCLLFPTG  FVTAIGYVGL
351 AATVWTGIIP  AMLLYRSRKK  FGAGKTYKVY  GGLWLMVWVF  LFGIVNIAAQ
401 VLSQMEVLPV  FKG*

```

m102/g102 86.0% identity in 415 aa overlap

	10	20	30	40	50	60
m102.pep	MPNKTPSLFGGAMIIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
g102	MSAKTPSLFGGAMIIAGKVIAGMFPNPTANLGDGLIGSLIVLLYTWFPFSSGALMILEV					
	10	20	30	40	50	60
m102.pep	NTHYPHGASFDTMVKDLLGRGWNIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGD					
g102	NTHNPRGASFDTMVKDLLGRGWNIINGIAVALVLYGSTYAYILVGGDLTAKGIGSAVGGK					
	70	80	90	100	110	120
m102.pep	NTHYPHGASFDTMVKDLLGRGWNIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGD					
g102	NTHNPRGASFDTMVKDLLGRGWNIINGIAVALVLYGSTYAYILVGGDLTAKGIGSAVGGK					
	130	140	150	160	170	180
m102.pep	VSLTVGQLVFFGILAFVCWASARLVDREFTGVLIGGMVLTFIWAAGGLIADAKPSVLFDTQ					
g102	ISLTVGQLVFFGILAFVCWASARLVDREFTGVLIGGMVLTFIATGGLVADAKPSVLFDTQ					
	130	140	150	160	170	180
m102.pep	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWGTGLIALVIYVLW					

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	10	20	30	40	50	60
m102.pep	MPNKTPSLFGGAMIIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSSGLMILEV					
a102	MPTKTPSLFGGAMIIAGTXIGAGMLANPTATSGVWFTGSLAVLLYTWFSSGLMILEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m102.pep	NTHYPHGASFDTMVKDLLGRGWNIIINGIAVAFVLYLLTYAIFVGGDLTAKGLGSAAGGD					
a102	NTHYPHGAXFDTMVKDLLGRSWNIINGIAVAFVLYLLTYAIFVGGDLTAKGLGSAAGGN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m102.pep	VSLTVGQLVFFGILAFCVWASARLVDRFTGVLIGGMVLTFIWAAGGLIADAKPSVLFDTQ					
a102	VSLTVGQLVFFGILAFCVWASARLVDRFTSVLIGGMVLTFIWATGGLIADAKLPVLFDTQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m102.pep	APAGTNYWIIYAATALPVCCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
a102	APTGTNYWIIYVATALPVCCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
	190	200	210	220	230	240
	250	260	270	280	290	300
m102.pep	QTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL					
a102	QTAIQXNLPRNEFAPVIAAEGQVSVXIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m102.pep	GLFDYIADIFKWNDSISGRKTAAFLPPLISCLLFPTGFVTAIGYVGLAATVWTGIIP					
a102	GLFDYIADIFKWNDSVSGRKTAAFLPPXISCLLFPTGFVTAIGYVGLAATVWTGIIP					
	310	320	330	340	350	360
	370	380	390	400	410	
m102.pep	AMLLYRSRKKFGAGKTYKVYGGWLWMVWVFLFGIVNIAAQVLSQMELVPVFKGX					
a102	AMLLYRSRKKFGAGKTYKVYGGWLWMVWVFLFGIXNIAAXVLSQMELVPVFKGX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 363>:

```

g105.seq
1   Atgtccgcag aaaCATACAc acAAAtcggc tGGgtaggct taggGcaaat
51  gGgtctgcct atgGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCCAC AAAACTGCCC CCATCTCgc CAAAGGAGCA
151 AAAGTTTACG GCagcACCGC CGAACTCGTC CGCGCCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG ACCCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAAACCTTC CATTTTCGGC ATGTCGGCAA
501 AGGCTCGGGC GCGAAACTCG TCTTGAATC GCTCTTAGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGA CTGCCTATGTT
651 TCAACAAAA AAATCACTAT GGGCAAACCG TGAGTTCCCC CTGCCTTTG
701 CACTCAAACA CGCTTCCAAA GAcctTAACC TCGccgtcAA AGAGCTTGAA
751 CAGGCAGGCA ACACCCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTT GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAATTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 364; ORF 105.ng>:

```
g105.pep
  1  MSAETTYTQIG WVGLGQMGLP MVTRLLDGGI EVGVYNRSPD KTAPISAKGA
  51  KVGYSTAELV RACPVIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
101  TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLILFGG SEAVLNPLQK
151  IFSLVGKKTFF HFGDVGKGSF AKLVNLNLLG IFGEAYSEAM LMARQFGIDT
201  DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
251  QAGNTLPAVE TVAASyrKAV EAGYGEQDVS GYVLKLAEH
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 365>:

```
m105.seq
  1  ATGTCCGCAA ACGAATACGC ACAAATCGGC TGGaTAGGCT TAGGGCAAAT
  51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101  TATACAACCG CTCGCCCACG AAAACTGCCC CCATCTCCGC CAAAGGCGCA
151  AAAGTTTACG GCAACACCGC CGAACTCGTC CGCGACTATC CCGTCATTTT
201  CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251  GCGACGGATT GGCCGCAAm ATCATCGTCA ACATGAGCAC CATCTCCCCG
301  ACCGAAaAGC TCGCCGTCAA AGCACTTGTC GAAGCGCAGm GaCAGTTTGC
351  CGAAGCACCC GTTTCGGGAT CGGTCGGGCC CGCCACCAAC GGCACGCTGC
401  TGATTCTGTT CGGCGGCAGC GAACCGtTTT AAACCCGCTG CAAAAAATAT
451  TTTCCCTCGT CGGCAAAAAA ACCTTCCATT TCGGCGATGT CGGCAAGGT
501  TCGGGCGCGA AACTCGTCTT GAACTCGCTC TTGGGCATTT TCGGCGAaCG
551  TAcAGCGAAs GmTgCTGATG GCGCGGCAGT TCGGCATCGA TACCGACACC
601  ATCGTCGAAG CCATCGGsGA CTCGGCAATG GACTCGCCCA TGTTCAAAC
651  CAAAAAATCC CTGTGGGCAA ACCGCGAATT CCCGmCCGmC TTCGCCCTCA
701  AACACGCCTC CAAAGACCTC AACCTCGCCG TCAAAGAGCT TGAACAGGCA
751  GGCAACACCC TGCCCGCCGT CGAAACCGTT GCTGCCAGCT ACCGCAAAGC
801  AGTCGAAGCC GGCTACGGGA CACAGGACGT TTCCGGCGTT TACCTGAAAC
851  TGGCAGAACA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 366; ORF 105>:

```
m105.pep
  1  MSANEYAQIG WIGLGQMGLP MVTRLLDGGI EVGVYNRSPD KTAPISAKGA
  51  KVGYNTAELV RDYPVIFLMV SDYAAVCDIL NGVRDGLAGX IIVNMSTISP
101  TEKLAVKALV EAQRQFAEAP VSGSVGPATN GTLLILFGGS EPFXTRCKKY
151  FPSSAKKPSI SAMSAKVRAR NSSXTRSWAF SANVQRXXLM ARQFGIDTDT
201  IVEAIGDSAM DSPMFQTKKS LWANREFPPX FALKHASKDL NLAVKELEQA
251  GNTLPAVETV AASyrKAVEA GYGTQDVSGV YLKLAEH
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 105 shows 79.9% identity over a 289 aa overlap with a predicted ORF (ORF 105.ng) from *N. gonorrhoeae*:

```
m105/g105

      10      20      30      40      50      60
g105.pep  MSAETTYTQIGWVGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGSTAELV
          |||: |:| |||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m105      MSANEYAQIGWIGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV
          10      20      30      40      50      60

      70      80      90     100     110     120
g105.pep  RACPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPTENLAVKALVEAAGGQFAEA
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m105      RDYPVIFLMVSDYAAVCDILNGVRDGLAGXIIIVNMSTISPTEKLAVKALVEAQR-QFAEA
          70      80      90     100     110

      130     140     150     160     170     180
g105.pep  PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGSAKLVNLSLLG
          ||||| ||||| ||||| ||||| : :| :| :| :| :| :| :| :| :| :|
m105      PVSGSVGPATNGTLLILFGGSEPFXTRCKKYFPSSAKKP-SISAMSAKVRARNSSXTRSW
          120     130     140     150     160     170
```

314

	190	200	210	220	230	240
g105.pep	IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK					
	:	::				
m105	AFSANVQRXXLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPXXFALKHASK					
	180	190	200	210	220	230
	250	260	270	280	289	
g105.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEH					
m105	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGTQDVSGVYLKLAEH					
	240	250	260	270	280	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 367>:

a105.seq

```

1  ATGTCCGCAA  ACGAATACAC  ACAAATCGGC  TGGATAGGCT  TAGGGCAAAT
51  GGGTCTGCCT  ATGGTAACGC  GGCTCTTGGA  CGGCGGCATC  GAAGTCGGCG
101 TATACAACCG  CTCGCCCGAC  AAAACTGCCC  CCATCTCCGC  CAAAGGCGCA
151 AAAGTTTACG  GCAACACCGC  CGAACTCGTC  CGCGACTATC  CCGTCATTTT
201 CCTGATGGTT  TCCGACTATG  CCGCCGTGTG  CGACATCCTG  AACGGAGTCC
251 GCGACGGATT  GGCCGGCAAA  ATCATCGTCA  ACATGAGCAC  CATCTCCCCG
301 ACCGAAAACC  TCGCCGTCAA  AGCACTTGTC  GAAGCCGCAG  GCGGACAGTT
351 TGCCGAAGCA  CCCGTTTCCG  GATCGGTCGG  GCCCGCCACC  AACGGCACGC
401 TGCTGATTCT  GTTCGGCGGC  AGCGAAGCCG  TTTTAAACCC  GCTGCAAAAA
451 ATATTTTCCC  TCGTCGGCAA  AAAAACCTTC  CATTTTCGGC  ATGTCGGCAA
501 AGGTTTCGGG  GCGAAACTCG  TCTTGAATC  GCTCTTGGGC  ATTTTCGGCG
551 AAGCGTACAG  CGAAGCGATG  CTGATGGCGC  GGCAGTTCGG  CATCGATACC
601 GACACCATCG  TCGAAGCCAT  CGCGGGCTCG  GCAATGGACT  CGCCCATGTT
651 CCAAACCAAA  AAATCCCTGT  GGGCAAACCG  CGAATTCCCA  CCCGCCTTCG
701 CCCTCAAACA  CGCCTCCAAA  GACCTCAACC  TCGCCGTCAA  AGAGCTTGAA
751 CAGGCAGGCA  ACACCCTGCC  CGCCGTCGAA  ACCGTTGCTG  CCAGCTACCG
801 CAAAGCAGTC  GAAGCCGGCT  ACGGCGAACA  GGACGTTTCC  GGCCTTTACC
851 TGAATTGGC  AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 368; ORF 105.a>:

a105.pep

```

1  MSANEYTQIG  WIGLGQMGLP  MVTRLDDGGI  EVGVYNRSPD  KTAPISAKGA
51  KVGYNIAELV  RDYPVIFLMV  SDYAAVCDIL  NGVRDGLAGK  IIVNMSTISP
101 TENLAVKALV  EAAGGQFAEA  PVSGSVGPAT  NGTLLILFGG  SEAVLNPLQK
151 IFSLVGKKTFF  HFGDVGKGS  AKLVNLSLLG  IFGEAYSEAM  LMARQFGIDT
201 DTIVEAIGGS  AMDSPMFQTK  KSLWANREFP  PAFALKHASK  DLNLAVKELE
251 QAGNTLPAVE  TVAASYRKAV  EAGYGEQDVS  GVYLKLAEH*

```

m105/a105 96.5% identity in 289 aa overlap

	10	20	30	40	50	60
m105.pep	MSANEYQAIGWIGLGQMGLPMVTRLDDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
a105	MSANEYTQIGWIGLGQMGLPMVTRLDDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m105.pep	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPENLAVKALVEAAG-QFAEA					
a105	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPENLAVKALVEAAGGQFAEA					
	70	80	90	100	110	120
	120	130	140	150	160	179
m105.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGSAGKLVNLSLLG					
a105	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGSAGKLVNLSLLG					
	130	140	150	160	170	180
	180	190	200	210	220	230

315

```

m105.pep    IFGDV-QRXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPXAFALKHASK
|||:: :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a105        IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
              190      200      210      220      230      240

m105.pep    240      250      260      270      280
DLNLAVKELEQAGNTLPAVETVAASYRKA VEAGYGEQDVSGVYLKLA EHX
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a105        DLNLAVKELEQAGNTLPAVETVAASYRKA VEAGYGEQDVSGVYLKLA EHX
              250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 369>:

g105-1.seq

```

1   ATGTCGCGAG AAACATACAC ACAAATCGGC TGGGTAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCCGC CAAAGGAGCA
151 AAAGTTTACG GCAGCACCGC CGAACTCGTC CGCGCCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCGG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG ACCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAACCTTC CATTCGGCG ATGTCGGCAA
501 AGGCTCGGGC GCGAAACTCG TCTTGAATC GCTCTTAGG ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCG GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCTATGTT
651 TCAAACAAAA AAATCACTAT GGGCAAACCG TGAGTTCCCC CCTGCCTTTG
701 CACTCAAACA CGCTCCAAA GACCTTAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTT GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAATTGGC AGAACA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 370; ORF 105-1.ng>:

g105-1.pep

```

1   MSAETTYQIG WVGLGQMGLP MVRLLDGGI EVGVYNRSPD KTAPISAKGA
51  KVIYGSTAELV RACPVI FLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
101 TENLAVKALV EAAGQFAEA PVSGSVGPAT NGTLLILFPG SEAVLNPLQK
151 IFSLVGKKTFF HFGDVGKGS AKLVNLSLG IFGEAYSEAM LMARQFGIDT
201 DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 371>:

m105-1.seq

```

1   ATGTCGCGCAA ACGAATACGC ACAAATCGGC TGGATAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCCGC CAAAGGCGCA
151 AAAGTTTACG GCAACACCGC CGAACTCGTC CGCGACTATC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCGG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG GCCGCCACC AACGGCACGC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TCGTCGGCAA AAAACCTTC CATTCGGCG ATGTCGGCAA
501 AGGTTCGGGC GCGAAACTCG TCTTGAATC GCTCTTGGG ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCG GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGACTCG GCAATGGACT CGCCCATGTT
651 CCAAACAAAA AAATCCCTGT GGGCAAACCG CGAATCCCC CCCGCTTCG
701 CCCTCAAACA CGCCTCCAAA GACCTCAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTC GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAACTGGC AGAACA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 372; ORF 105-1>:

m105-1.pep

```

1   MSANEYAQIG WIGLGQMGLP MVRLLDGGI EVGVYNRSPD KTAPISAKGA
51  KVIYNTAELV RDYPVIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP

```

101	TENLAVKALV	EAAGGQFAEA	PVSGSVGPAT	NGTLLILFGG	SEAVLNPLQK
151	IFSLVGKKT	HFGDVGKSG	AKLVLSLLG	IFGAYSEXM	LMARQFGIDT
201	DTIVEAIGDS	AMDSPMFQTK	KSLWANREFP	PAFALKHASK	DLNLAVKELE
251	QAGNTLPAVE	TVAASYRKAV	EAGYGEQDVS	GVYKLAEH*	

m105-1/g105-1 96.9% identity in 289 aa overlap

	10	20	30	40	50	60
m105-1.pep	MSANEYAQIGWIGLGMGLPMVTRLRLDGGIEVGVYNRSPDKTAPISAKGAKVYGN	TAE	LV			
g105-1	MSAETYYTQIGWVGLGMGLPMVTRLRLDGGIEVGVYNRSPDKTAPISAKGAKVYG	STAE	LV			
	10	20	30	40	50	60
m105-1.pep	RDYPVIFLVM	SDYAAVCDILNGVRDGLAGKII	VNMSTISPTENLAVKALVEAAGGQFAEA			
g105-1	RACPVIIFLVM	SDYAAVCDILNGVRDGLAGKII	VNMSTISPTENLAVKALVEAAGGQFAEA			
	70	80	90	100	110	120
m105-1.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVLN	SLLG				
g105-1	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVLN	SLLG				
	130	140	150	160	170	180
m105-1.pep	IFGEAYSEXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKH	ASK				
g105-1	IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKH	ASK				
	190	200	210	220	230	240
m105-1.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVS	GVYLKLA	EHX			
g105-1	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVS	GVYLKLA	EHX			
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 373>:

a105-1.seq

1	ATGTCGCGAA	ACGAATACAC	ACAAATCGGC	TGGATAGGCT	TAGGGCAAA
51	GGGTCTGCCT	ATGGTAACGC	GGCTCTTGGA	CGCGGCATC	GAAGTCGGCG
101	TATACAACCG	CTGCGCCGAC	AAACTGCCC	CCATCTCCGC	CAAAGCGCTA
151	AAAGTTTACG	GCAACACCGC	CGAAGTCGT	CGCGACTATC	CGGTCATTTT
201	CCTGATGGTT	TCCGACTATG	CCGCGGTGT	CGACATCCTG	AACGGAGTCC
251	GCGACGGATT	GGCCGGCAAA	ATCATCGTCA	ACATGAGCAC	CATCTCCCCG
301	ACCGAAAAAC	TCGCGCTCAA	AGCACTGTG	GAAGCCGAG	CGGACAGGTT
351	TGCCGAAGCA	CCCGTTTCCG	GATCGGTCGG	GCCCCCACC	AACGGCACGC
401	TGCTGATTCT	GTTTCGGCGC	AGCGAAGCCG	TTTTAAACCC	GCTGCAAAAA
451	ATATTTTCCC	TCGTCCGGCA	AAAGAACTTC	CATTTCGGCG	ATGTCGGCAA
501	AGGTCGGGCG	GCGAAACTCG	TCTTGAACTC	GCCTTGGGCG	ATTTTCGGCG
551	AAGCGTACAG	CGAAGCGATG	CTGATGGCGC	GGCAGTTCGG	CATCGATACC
601	GACACCATCG	TCGAAGCCAT	CGCGGCGCTC	CGAATGGACT	CGCCCATGTT
651	CCAAACCAAA	AAATCCCTGT	GGGCAAAACG	GCAATTCCCA	CCGCGCTTCG
701	CCCTCAAACA	CGCCTCCAAA	GACCTCAACC	TCGCCGTCAA	AGAGCTTGAA
751	CAGGACGGCA	ACACCTTGCC	CGCGTGCAG	ACGTTGTGTG	CCAGCTACCG
801	CAAAGCAGCT	GAAGCCGGTG	ACGGCGAACA	GGACGTTTCC	GGCGTTTACC
851	TGAAATTGGC	AGAACACTGA			

This corresponds to the amino acid sequence <SEQ ID 374; ORF 105-1.a>:

a105-1.pep

1	MSANEYTOIG	WIGLGQMGLP	MVTRLDDGGI	EVGVYNRSPD	KTAPISAKGA
51	KVYQNGTAEV	RDYPIVIFLM	SDYAACV CDIL	NGVRDGLAGK	IVNMSTSP
101	TENLAVAKAL	EAAAGGQFAE	SVSGVSGPAT	NGTLILIFGG	SEAVLNPLQK
151	IFSLVGKKT	HFGDVGKGS	AKLVLSLLG	IFGEAYSEAM	LMARQFGIDT
201	DTIVEAIGS	AMDSPMFQTK	KSLWANREFP	PAFALKHAK	DLNLAVKELE
251	OAGNTLPAVE	TVAASYRKAV	EAGYGEODVS	GVYLKAE*	

a105-1/m105-1 99.0% identity in 289 aa overlap

10 20 30 40 50 60
 a105-1.pep MSANEYTQIGWIGLGQMGLPMVTRLLDGGIEVG VYNRSPDKTAPISAKGAKVYGNTAELV
 |||||:|||||

```

m105-1      MSANEYAQIGWIGLGQMGLPMVTRLDDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV
              10          20          30          40          50          60

a105-1.pep   70          80          90          100         110         120
RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA
|||||
m105-1      RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA
              70          80          90          100         110         120

a105-1.pep   130         140         150         160         170         180
PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVLSLLG
|||||
m105-1      PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVLSLLG
              130         140         150         160         170         180

a105-1.pep   190         200         210         220         230         240
IFGEAYSEAMLMARQFGIDTDITVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
|||||
m105-1      IFGEAYSEXMLMARQFGIDTDITVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK
              190         200         210         220         230         240

a105-1.pep   250         260         270         280         290
DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
|||||
m105-1      DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
              250         260         270         280         290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 375>:

```

g107.seq
1   ATGGTATTAA CCTTTATTTG GGCAACCGGC GGCCTGGTTG CCGATGCCAA
51  ACCGTCCGTC CTCTTCGACA CCCAAGCCCC CGTCGGCACC GGCTACTGGA
101 TTTACGCCGC CACCGCCCTG CCCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTTT CCAGCCTGCT CAAATACTTT AAAGGCGACG cgcCcaaagt
201 GgCGAaATCc atctggGcag gtacattggT TGCCttggta atttacgtcc
251 TCTggcaaac cgccatCcaa agcaacctGC cgcgcaacga gttcgcCCCC
301 gtgattgccg ccgagaggca actCTCCGTC CTgaatgaaa cccTGtccaa
351 attcgcccaa accggcgata tggataAaat attgtcccta tttccctaca
401 tggcaatcgc cacctccttt ttaggcgTAA Ccttaggcct gtttgacaac
451 atcgccggac atcttcaaat ggaacgacag tatgtccggg cggcaccaaa
501 accgtcgcg c tga

```

This corresponds to the amino acid sequence <SEQ ID 376; ORF 107.ng>:

```

g107.pep
1   MVLTFIWATG GLVADAKPSV LFDTQAPVGT GYWIYAATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWAGTLVALV IYVLWQTAIQ SNLPRNEFAP
101 VIAAERQLSV LNETLSKFAQ TGDMDKILSL FPYMAIATSF LGVTGLGLFDN
151 IAGHLQMERQ YVRAAPKPSR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 377>:

```

m107.seq
1   ATGGTATTGA CCTTTATTTG GCGGCCCGGC GGGCTGATTG CCGATGCCAA
51  GCCGTCCGTC CTCTTCGATA CCCAAGCCCC CGCCGGCACA AACTACTGGA
101 TTTACGCCGs CACCGCCCTG CCCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCGCTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCCC
301 GTCATCGCCG CCGAAGGGCA AGTCTCCGTC CTCATCGAAA CCCTGTCCAA
351 ATTCGCCCAA ACCGGCAATA TGGACAAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTTCGACTAC
451 ATCGCCCATC TTCAAATGGA ACGACAGCAT CTCCGGgCCG CACCAAACC
501 GCCGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 378; ORF 107>:

```

m107.pep..
1   MVLTFIWAAG GLIADAKPSV LFDTQAPAGT NYWIYAXTAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTAIQ GNLPRNEFAP

```

101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTLGLFDY
151 IAHLMQMERQH LRAAPKPPR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 107 shows 89.4% identity over a 170 aa overlap with a predicted ORF (ORF 107.ng) from *N. gonorrhoeae*:

m107/g107

	10	20	30	40	50	60
m107.pep	MVLTFIWAAGGLIADAKPSVLFDLTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	: : : : :					
g107	MVLTFIWATGGLVADAKPSVLFDLTQAPVGTGYWIYAATALPVCLASFGFHGNVSSLLKYF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m107.pep	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
	: : : : :					
g107	KGDAPKVAKSIWAGTLVALVIYVLWQTAIQSNLPRNEFAPVIAAERQLSVLNETLSKFAQ					
	70	80	90	100	110	120
	130	140	150	160	170	
m107.pep	TGNMDKILSLFSYMAIATSF LGVTLGLFDYIA-HLMQMERQH LRAAPKPPR					
	: : : : : :					
g107	TGDMDKILSLFPYMAIATSF LGVTLGLFDNIAGHLQMERQYVRAAPKPSR					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 379>:

a107.seq

```

1  ATGGTATTAA CCTTTATTTG GGCAACCGGC GGCTGATTG CCGATGCCAA
51  ACTGCCCGTC CTCTTCGACA CCAAGCCCC TACCGGCACC AACTACTGGA
101 TTTATGTCGC CACCGCCCTG CCCGTCTGCC TTGCGTCATT CGGTTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TCGCGTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTGATTGCCG CCGAAGGGCA AGTCTCCGTC CTGATTGAAA CCCTGTCCAA
351 ATTCGCCCAA ACCGCAATA TGACAAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTTCGACTAC
451 ATCGCCGACA TCTTCAAATG GAACGACAGC GTGTCCGGCC GCACCAAAC
501 CGCCGCGCTG ACCTCCTGTC CGCCTCTAAT TTCCTGCCTG CTCTTCCCCA
551 CCGGCTTTGT TACCGCCATC GGCTACGTCG GCCTGGCGGC AACCCTCTGG
601 ACAGGCATCA TCCCCGCCAT GCTGCTCTAC CGTTCGCGCA AAAAATTCGG
651 CGCAGGCAA ACCTATAAAG TTTACGGCGG CTTGTGGCTG ATGGTTTGGG
701 TCTTCCTTTT CGGCATCGTC AACATCGCCG CACAGGTATT GAGCCAAATG
751 GAACTCGTCC CCGTATTTAA AGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 380; ORF 107.a>:

a107.pep

```

1  MVLTFIWATG GLIADAKLPV LFDLTQAPTGT NYWIYVATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTAIQ GNLPRNEFAP
101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTLGLFDY
151 IADIFKWNDS VSGRTKTAAL TFLPPLISCL LFPTGFVTAI GYVGLAATVW
201 TGIIPAMLLY RSRKKFGAGK TYKVYGGWL MVWVFLFGIV NIAAQVLSQM
251 ELVPVFKG*

```

m107/a107 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m107.pep	MVLTFIWAAGGLIADAKPSVLFDLTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	: : : : :					
a107	MVLTFIWATGGLIADAKLPVLDLTQAPTGTNYWIYVATALPVCLASFGFHGNVSSLLKYF					
	10	20	30	40	50	60

319

	70	80	90	100	110	120
m107.pep	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
a107	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
	70	80	90	100	110	120
	130	140	150	160	170	
m107.pep	TGNMDKILSLFSYMAIATSFLGVTGLGFDYIAHLQMERQHLRAAPKPPRX					
a107	TGNMDKILSLFSYMAIATSFLGVTGLGFDYIADIFKWNDSVSGRTKTAALTFLPPLISCL					
	130	140	150	160	170	180
a107	LFPTGFVTAIGYVGLAATVWTGIIPAMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGIV					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 381>:

```

g108.seq
1  ATGttgccgg gCTTCAACCG GATATTCAaa cggTTTGCTC CAACACTCGG
51  AACggCGCAT AAAACGCCgc ccTTCCGCGT ATCCCGAACG GGGCGGCTAA
101 TCAGATCCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTTGTCTAT TTTGCCGGCG GCAATCTTAC TCGGCGGGTG
201 CGCCGCCGGC GGCAACACAT TCGGCAGCTT AGACGGCGGC ACGGGTATGG
251 GTGGCAGCAT CGTCAAAATG ACGGTAGAAA gccAATGCCG TCGGGAATTG
301 GACAGGCGCA GCGAATGGCG TTTGACCGCG CTGGCGATGA GTGCCGAAAA
351 ACAGGCGGAA TGGGAAAAACA AGATTTCGGG CTGCGCTACC GAAGAAGCAC
401 CTAACCAGCT GACCGGCAAC GATGTGATGC AGATGCTGAa ccagtccacG
451 CGCaatcagg cacTtgccgc CctgaccgTC AAAacggtTT CcgccctgCT
501 CAaacgcctg tACCGCTAa

```

This corresponds to the amino acid sequence <SEQ ID 382; ORF 108.ng>:

```

g108.pep
1  MLPGFNRIFK RFAPTLGTAH KTPPFALSRT GRLIRSYRHK RRGFNRKGIE
51  MNKTLSILPA AILLGGCAAG GNTFGSLDGG TGMGGSIVKM TVESQCRAEL
101 DRRSEWRLTA LAMSAEKQAE WENKICGCAT EEAPNQLTGN DVMQMLNQST
151 RNQALAAALT TVSACFKRL YR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 383>:

```

m108.seq
1  ATGTTGCCGG GCTTCAACCG GATATTCAAA CGGTTTGTTT CAACACTCGG
51  AACGGCGCAT AAAACGCCGC CCTTCGCGTT ATCCCGAACG GGGCGGCTAA
101 TCAGATTCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTTGTCTAT TTTGCCGGTG GCAATCTTAC TCGGCGGCTG
201 CGCCGCCGGA GGCGGTAACA CATTCGGCAG CTTAGACGGT GGCACAGGCA
251 TGGGCGGCAG CATCGTCAAA ATGGCGGTTG GGAGCCAATG CCGTGCGGAA
301 TTGGACAAAC GCAGCGAATG GCGTTTGACC GCGCTGGCGA TGAGTGCCGA
351 AAAACAGGCG GAGTGGGAAA ACAAGATTTG CGCTTGCGTC GCCAAGAAG
401 CACCCGAACG GATGACCGGC AACGATGTGA TGCAGATGCT GGCTCCGTCC
451 ACGCGCAATC AGGCACTTGC CGCCCTGACC GCCAAACCGG TTCCCGCCTG
501 CTTCAAACAC CTGTACCGCT AA

```

This corresponds to the amino acid sequence <SEQ ID 384; ORF 108>:

```

m108.pep
1  MLPGFNRIFK RFVPTLGTAH KTPPFALSRT GRLIRFYRHK RRGFNRKGIE
51  MNKTLSILPV AILLGGCAAG GGNTFGSLDG GTGMGGSIVK MAVGSQCRAE
101 LDKRSEWRLT ALAMSAEKQA EWENKICACV AQEAPERMTG NDVMQMLAPS
151 TRNQALAAALT AKTVSACFKH LYR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 108 shows 89.6% identity over a 173 aa overlap with a predicted ORF (ORF 108.ng) from *N. gonorrhoeae*:

m108/g108

320

	10	20	30	40	50	60
m108.pep	MLPGFNRIFKRFVPTLGTAKHTPPFALSRTGRLIRFYRHKRRGFNRKGIEMNKLSILPV					
g108	MLPGFNRIFKRFAPTLGTAKHTPPFALSRTGRLIRSYRHKRRGFNRKGIEMNKLSILPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m108.pep	AILLGGCAAGGNTFGSLDGGTGMGGSIVKMAVGSQCRAELDKRSEWRLTALAMSAEKQA					
g108	AILLGGCAAGG-NTFGSLDGGTGMGGSIVKMTVESQCRAELDRRSEWRLTALAMSAEKQA					
	70	80	90	100	110	
	130	140	150	160	170	
m108.pep	EWENKICACVAQEAPERMTGNDVMQMLAPSTRNQALAAALTAKTVSACFKHLYRX					
g108	EWENKICGCATEEAPNQLTGNDVMQMLNQSTRNQALAAALTAKTVSACFKRLYRX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 385>:

a108.seq

```

1  ATGTTGCCGG GCTTCAACCG GATATTCAAA CGGTTTGTTT CAACACTCGG
51 AACGGCGCAT AAAACGCCGC CCTTCGCGTT ATCCCGAACG GGGCGGCTAA
101 TCAGATTCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTGTCTAT TTTGCCGGTG GCAATCTTAC TCGGCGGCTG
201 CGCCGCCGGG GCGGGTAACA CATTCGGCAG CTTAGACGGC GGCACAGGTA
251 TGGCGCGCAG CATCGTCAAA ATGGCGGTAG AAAGCCAATG CCGTGCGGAA
301 TTGAACAAAC GCAGCGAATG GCGTTTGACC GCGCTGGCGA TGAGTGCCGA
351 AAAACAGGCG GAATGGGAAA ACAAGATTG CGCTTGCGTC GCCCAAGAAG
401 CACCCAACCA GCTGACCGGC AACGATGTGA TGCAGATGCT GGATCCGTCC
451 ACGCGCAATC AGGCACTTGC CGCCCTGACC GCCAAAACGG TTTCCGCCTG
501 CTTCAAACAC CTGTACCGCT AA

```

This corresponds to the amino acid sequence <SEQ ID 386; ORF 108.a>:

a108.pep

```

1  MLPGFNRIFK RFVPTLGTAK KTPPFALSRT GRLIRFYRHK RRGFNKRGIE
51 MNKTLNILPV AILLGGCAAG GGNTFGSLDG GTGMGGSIVK MAVESQCRAE
101 LNKRSEWRLT ALAMSAEKQA EWENKICACV AQEAPNQLTG NDVMQMLDPS
151 TRNQALAAALT AKTVSACFKH LYR*

```

m108/a108 96.5% identity in 173 aa overlap

	10	20	30	40	50	60
m108.pep	MLPGFNRIFKRFVPTLGTAKHTPPFALSRTGRLIRFYRHKRRGFNRKGIEMNKLSILPV					
a108	MLPGFNRIFKRFVPTLGTAKHTPPFALSRTGRLIRFYRHKRRGFNRKGIEMNKLSILPV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m108.pep	AILLGGCAAGGNTFGSLDGGTGMGGSIVKMAVGSQCRAELDKRSEWRLTALAMSAEKQA					
a108	AILLGGCAAGGNTFGSLDGGTGMGGSIVKMAVESQCRAELNKRSEWRLTALAMSAEKQA					
	70	80	90	100	110	120
	130	140	150	160	170	
m108.pep	EWENKICACVAQEAPERMTGNDVMQMLAPSTRNQALAAALTAKTVSACFKHLYRX					
a108	EWENKICACVAQEAPNQLTGNDVMQMLDPSTRNQALAAALTAKTVSACFKHLYRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 387>:

g109.seq

```

1 ATGTATTATC GCCGGGTTGT GGGGCTATCC GATGGACTTG GCGATTGGC
51 AGCCGGTATT GATCGTAGGC GTATGCTTAC CGCTTTTGA AGCGGGCATG
101 GAAATGACGC GCAAAGGCAA AACCACCCAA TCCGCCGCCA TCGTGGTGTT
151 CTCTTCCGTC TGGTCAATCC GGTTCGCGC TGGGCGTTGA CGATGCTGTT
201 GGATAATTTG GGCTTAATCG GCTGCAAAGA ACGCAGCGCG CAATTAGGTT
251 TTGTCGGACG AGTATTGATA CCCGCAGTAG GTTCTTAAT CTGTGTGTG
301 GCGATGGGTG CCGTCGGGAT GCTGCCCGGT ATCCCTCCGT TTTTGGAGCA
351 GTCAAATCT TTGGGCTAG

```

This corresponds to the amino acid sequence <SEQ ID 388; ORF 109.ng>:

g109.pep

```

1 MYYRRVGLS DGLGDLAAGI DRRRLTAFG SHHGNDQRQ NHPIRRHRGV
51 LFRVLNPFVG WALTMLLDNL GLIGCKERSA QLGFVGRVLI PAVGFLILCV
101 AMGAVGMLPG IPPFLEQFKS LG

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 389>:

m109.seq

```

1 ATGTATTATC GCCGGGTTAT GGGGCTATCC GATGGACTTG GCGATTGGC
51 AGCCGGTATT GAGCGTAGCC TTGGTCGTAG GCGTATACTT ACCGCTTTTG
101 GAAGCGGGCA TGGAAATGAC GCGCAAAGGC AAAACCACCC AATCCGCCGC
151 CATCGTGGTG TTCTCTCCG CTTGTCAAT CCGGTTTTCG GCTGGGCGTT
201 GACGATGCTG TTGGATAATT TGGGCTTAAT CCGCTGCAAA GAGCGCAGTG
251 CGCAATTAGG TTTCGCCGGA CGCGTGTGA TACCCGCACT AGGTTTCTTG
301 ATCTTGTGTG TGGCGATGGG TGCGGTCGGG ATGCTGCCCG GTATCCCGCC
351 GTTTTGGGAA CACTTCAAAT CTTTGGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 4; ORF 109>:

m109.pep

```

1 MYYRRVMGLS DGLGDLAAGI ERSLGRRRIL TAFSGHGND AQRQNHPIRR
51 HRGVLFRLVN PVFGWALTML LDNLGLIGCK ERSAQLGFAG RVLIPAVGFL
101 ILCVAMGAVG MLPGIPPFLE HFKSLG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 109 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 109.ng) from *N. gonorrhoeae*:

m109/g109

	10	20	30	40	50	60
m109.pep	MYYRRVMGLSDGLGDLAAGIERSLGRRLTAFGSGHGNDQRQNHPIRRHRGVLFRLVN					
	: : :					
g109	MYYRRVGLSDGLGDLAAGIDR----RRMLTAFSGHGNDQRQNHPIRRHRGVLFRLVN					
	10	20	30	40	50	

	70	80	90	100	110	120
m109.pep	PVFGWALTMLLDNLGLIGCKERSAQLGFAGRVLIPAVGFLILCVAMGAVGMLPGIPPFLE					
	:					
g109	PVFGWALTMLLDNLGLIGCKERSAQLGFVGRVLIPAVGFLILCVAMGAVGMLPGIPPFLE					
	60	70	80	90	100	110

m109.pep	HFKSLGX
	:
g109	QFKSLGX
	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 391>:

a109.seq

```

1 ATGTATTATC GCCGGGTTGT GGGGCTATCC GATGGACTTG GCGATTGGC
51 AGCCGGTATT GAGCGTAGCC TTGGTCGTAG GCGTATACTT ACCGCTTTTG
101 GAAGCGGGCA TGGAAATGAC GCGCAAAGGC AAAACCACCC AATCCGCCGC
151 CACCGTGGTG TTCTCTCCG CTTGGTCAAT CCGGTTTTCG GCTGGGCGTT

```

322

```

201 GACGATGCTG TTGGATAATT TGGGCTTAAT CGGCTGCAAA GAGCGCAGCG
251 CGCAATTAGG TTTCACCGGA CGCGTATTGA TACCCGTAGT AGGTTTCTTG
301 ATCTTGTGTG TGGCGATGGG TCGGGTCGGG ATGCTGCCCC GTATCCCGCC
351 GTTTTGGAG CACTTCAAT CTTGGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 392; ORF 109>:

a109.pep

```

1  MYRRRVVGLS DGLGDLAAGI ERSLGRRRIL TAFSGHGNDA AQRQNHPIRR
51  HRGVLFRLVN PVFGWALTML LDNLGLIGCK ERSAQLGFTG RVLIPVVGFL
101 ILCVAMGAVG MLPGIPPFLE HFKSLG*

```

m109/a109 97.6% identity in 126 aa overlap

	10	20	30	40	50	60
m109.pep	MYRRVMGLSDGLGDLAAGIERSLGRRRILTAFGSGHGNDAQRQNHPIRRHRGVLFRLVN					
a109	MYRRRVVGLSDGLGDLAAGIERSLGRRRILTAFGSGHGNDAQRQNHPIRRHRGVLFRLVN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m109.pep	PVFGWALTMLLDNLGLIGCKERSAQLGFAGRVLIPAVGFLILCVAMGAVGMLPGIPPFLE					
a109	PVFGWALTMLLDNLGLIGCKERSAQLGFTGRVLIPVVGFLILCVAMGAVGMLPGIPPFLE					
	70	80	90	100	110	120
m109.pep	HFKSLGX					
a109	HFKSLGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 393>:

g111.seq

```

1  ATGCCGTCTG AAACACGCCT GCCGAACCTT ATCCGCGCCT TGATATTTGC
51  CCTGGGTTC ATCTTCCTGA ACGCCTGTTC GGAaacaacC GCGCAaaccg
101 TTACCTGCA AGGCGAAACG ATGGGTACGA CcTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCCCCT GCCAAAATAC AAAAGCGCAT
201 TGATGATGCG CTAAAGAAG TCAACCGGCA GATGtccaCC TACCAGACCG
251 ATTCGAAAT CAGCCGTTt atacagacan atgctggaga gctcttcgcg
301 tntcatgcag nttctataac tgattccgcc gaagactgtc tgcctaatac
351 gcctatctca tcggcgctct ga

```

This corresponds to the amino acid sequence <SEQ ID 394; ORF 111.ng>:

g111.pep

```

1  MPSETRLPNL IRALIFALGF IFLNACSEQT AQTVTLQGET MGTTYTVKYL
51  SNNRDKLPSP AKIQKRIDDA LKEVNRQMSY YQTDSEISRF IQTAGELFAH
101 ASITDSAEDC LPNTPISSAL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 395>:

m111.seq

```

1  ATGCCGTCTG AAACACGCCT GCCGAACCTT ATCCGCGTCT TGATATTTGC
51  CCTGGGTTC ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCTGCA AGGCGAAACG ATGGGCACGA CCTATAYCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AWAACGCAT
201 CGATGACGCG CTAAAGAAk TCAACCGGyA GATGTCCACC TATCAGCCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC GCCTGAACCG
351 CTTGACACAC GGCGCGCTGG ACGTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTTCG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTTGAAACA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TGCGGGCGAA

```

```

601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCGTGGCGC ATCGGTATCG
701 AGCAGCCCAA TATCGTCCAA GGCGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAACCGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAAACGGC AAACGCCTCT CCCATATCAT CAACCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCATG
901 ACGGCGGACG GCTTGTCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAATCTCG TGTTTTCTCT ATTGTCAGGG
1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTTGA AAAACTGcTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 396; ORF 111>:

```

m111.pep
  1 MPSETRLPNF IRVLIFALGF IFLNACSEQT AQTVTLOGET MGTTYXVKYL
  51 SMNRDKLPSP AEIXKRIDDA LKEXNRXMST YQPDSEISRF NQHTAGKPLR
 101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFGPDK SVTREPSPEQ
 151 IKQAASYTGI DKIIILKQGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
 201 LEKYGIQNYL VEIGGELHGK GKNARGEPRW IGIEQPNIVQ GGNTQIIVPL
 251 NNRSLATSGD YRIFHVDKNG KRLSHIINPN NKRPISHNLA SISVVADSAM
 301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
 351 R*

```

ORF 111 shows 88.7% identity over a 97 aa overlap with a predicted ORF (ORF 111.ng) from *N. gonorrhoeae*:

```

m111.pep/g111.pep

      10      20      30      40      50      60
m111.pep MPSETRLPNFIRVLIFALGFIFLNACSEQTAQVTLOGETMGTTYXVKYLSMNRDKLPSP
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g111      MPSETRLPNLIRALIFALGFIFLNACSEQTAQVTLOGETMGTTYTVKYLSMNRDKLPSP
      10      20      30      40      50      60

      70      80      90     100     110     120
m111.pep AEIXKRIDDALKEXNRXMSTYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVRLNRLTH
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g111      AKIQKRIDDALKEVNRMSTYQTDSEISRFIQTXAGELFAXHAXSITDSAEDCLPNTPI
      70      80      90     100     110     120

      130     140     150     160     170     180
m111.pep GALDVTVGPLVNLWGFGPDKSVTREPSPEQIKQAASYTGIDKIIILKQGDYASLSKTHPK
g111      SALX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 397>:

a111.seq

```

  1 ATGCCGCTCG AAACACGCCT GCCGAACCTT ATCCGCACCT TGATATTTGC
 51 CCTGAGTTTT ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCTTGCA AGGTGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAGCGCAT
201 CGATGACGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC ACCTGAACCG
351 CCTGACACAC GCGCGCTGG ACGTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTCGG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAACAAG CAGCATCTTA TACGGGCATA GACAAAATCA TTTTGAAACA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TGCGGGCGAA
601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCTTGCGCG ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GGCGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAACCGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA

```

```

801 TAAAGCGGC AACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCGATG
901 ACGGCGGACG GCTTGTCCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAAGCTCG TGTTCCTCTG ATTGTCAGGG
1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTTGA AAAAGTCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 398; ORF 111.a>:

a111.pep

```

1  MPSETRLPNF IRTLIFALSF IFLNACSEQT AQTVTLQGET MGTTYTVKYL
51  SNNRDKLPSP AEIQKRIDDA LKEVNRQMSY YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVHLNRLTH GALDVTGGL VNLWGFDPK SVTREPSPEQ
151 IKQAASYTGI DKIIKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPR IGIEQPNIVQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKSG KRLSHIINPN NKRPIHNLAS SISVADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

m111/a111 97.7% identity in 351 aa overlap

m111.pep	10	20	30	40	50	60
	MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLQGETMGTTYXVKYLSNNRDKLPSP					
a111	MPSETRLPNFIRTLIFALSFIFLNACSEQTAQTVTLQGETMGTTYTVKYLSNNRDKLPSP					
	10	20	30	40	50	60
m111.pep	70	80	90	100	110	120
	AEIXKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVRLNRLTH					
a111	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVHLNRLTH					
	70	80	90	100	110	120
m111.pep	130	140	150	160	170	180
	GALDVTGGLVNLWGFDPKSVTREPSPEQIKQAASYTGIDKIIKQKGDYASLSKTHPK					
a111	GALDVTGGLVNLWGFDPKSVTREPSPEQIKQAASYTGIDKIIKQKGDYASLSKTHPK					
	130	140	150	160	170	180
m111.pep	190	200	210	220	230	240
	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHGKGKNARGEPRIGIEQPNIVQ					
a111	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHGKGKNARGEPRIGIEQPNIVQ					
	190	200	210	220	230	240
m111.pep	250	260	270	280	290	300
	GGNTQIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPIHNLASISVADSAM					
a111	GGNTQIIVPLNNRSLATSGDYRIFHVDKSGKRLSHIINPNKRPIHNLASISVADSAM					
	250	260	270	280	290	300
m111.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
a111	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 399>:

g111-1.seq

```

1  ATGCCGCTCTG AACACGCCT GCCGAACCTT ATCCGCGCCT TGATATTTGC
51  CCTGGGTTTC ATCTTCCTGA ACGCTGTTC GGAACAAACC GCGCAAaCCG
101 TTACCCTGCA AGGCGAAACG ATGGGTACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCCCCT GCCAAATAC AAAAGCGCAT
201 TGATGATGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TACCAGACCG

```

```

251 ATTCGGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ATTTGCGACA CGTTACCGCC GAAGCCGTCC GCCTGAACCG
351 CCTGACTCAC GGGCGACTGG ACGTAACCGT CGGCCCTTTG GTCAACCTTT
401 GGGGGTTTCG CCCCACAAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTGCAACA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGCGGAA
601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCggcGAGTT
651 GCACGGCAAA GGCAAAAATG CGCACGGCGA ACCGTGGCGC ATCGGTATAG
701 AGCAACCCAA TATcatccaa ggcggaataa cgcAGattat cgtcccgtg
751 aaCaaccgtt cgcttgccac ttccggcgAT taccgtaTT tccacgtcgA
801 TAAAACGGG Aaaccgcttt cccacATCAT CAATCCCAAC AACAAACGAC
851 CCATCAGcCA CAaccctgcc tcCATCAgCg TGGTCTCAGA CAGTGCAATG
901 ACGGCGGACG GTTTATCCAC AGGATTATTT GTTTAGGCG AAACCGAAGC
951 CTTAAGGCTG GCAGAACAA GAAAACTCGC TGTTCCTTA ATTGTCCGGG
1001 ATAAGGACGG CTACCGCACC GCCATGTCTT CCGAATTGTC CAAGCTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 400; ORF 111-1.ng>:

g111-1.pep

```

1 MPSETRLPLNL IRALIFALGF IFLNACSEQT AQTVTLOGET MGTITYVKYL
51 SNNRDKLPSP AKIQKRIDDA LKEVNRQMSY YQTDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFPGDK SVTREPSPQ
151 IKQAASVTGI DKIIKQGGK YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNHAGPWR IGIEQPNIIQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKNG KRLSHIINPN NKRPIHNLA SISVVSDDAM
301 TADGLSTGLF VLGETEALRL AEQEKLAFLV IVRDKDGYRT AMSSEFAKLL
351 R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 401>:

m111-1.seq

```

1 ATGCCGCTCTG AAACACGCCT GCCGAACCTT ATCCGCGTCT TGATATTTGC
51 CCTGGGTTTC ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCCTGCA AGGCGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCGGAAATAC AAAAAACGAT
201 CGATGACGCG CTTAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC GCCTGAACCG
351 CCTGACACAC GGCAGCTGG ACGTAACCGT CGGCCCTTTG GTCAACCTTT
401 GGGGATTTCG CCCCACAAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTGAAACA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGCGGAA
601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCGTGGCGC ATCGGTATCG
701 AGCAGCCCAA TATCGTCCAA GCGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAACGGC AAACGCCTCT CCCATATCAT CAACCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGAGA CAGTGCGATG
901 ACGGCGGACG GCTTGTCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAGCTG GCAGAGCGCG AAAAACTCGC TGTTCCTG ATTGTAGGG
1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTGTA AAAACTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 402; ORF 111-1>:

m111-1.pep

```

1 MPSETRLPLNF IRVLIFALGF IFLNACSEQT AQTVTLOGET MGTITYVKYL
51 SNNRDKLPSP AEIQKRIDDA LKEVNRQMSY YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFPGDK SVTREPSPQ
151 IKQAASVTGI DKIIKQGGK YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPR IGIEQPNIVQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKNG KRLSHIINPN NKRPIHNLA SISVVSDDAM
301 TADGLSTGLF VLGETEALKL AEREKLAFLV IVRDKGGYRT AMSSEFEKLL
351 R*

```

m111-1/g111-1 96.6% identity in 351 aa overlap

```

          10      20      30      40      50      60
m111-1.pep MPSETRLPLNFIRVLIFALGFIFLNACSEQTAQTVTLOGETMGTITYVKYLSNNRDKLPSP
          |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
g111-1      MPSETRLPLNLIRALIFALGFIFLNACSEQTAQTVTLOGETMGTITYVKYLSNNRDKLPSP

```

326

	10	20	30	40	50	60
m111-1.pep	70	80	90	100	110	120
	AEIQKRIDDALKEVNRQMSTYQPDSEISRNFQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
g111-1	AKIQKRIDDALKEVNRQMSTYQTDSEISRNFQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
	70	80	90	100	110	120
m111-1.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFGPDKSVTREPSPEQIKQAASYTGIDKIILKQGKDYASLSKTHPK					
g111-1	GALDVTVGPLVNLWGFGPDKSVTREPSPEQIKQAASYTGIDKIILKQGKDYASLSKTHPK					
	130	140	150	160	170	180
m111-1.pep	190	200	210	220	230	240
	AYLDLSSIAKGFVDKVGAGELEKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQ					
g111-1	AYLDLSSIAKGFVDKVGAGELEKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIIQ					
	190	200	210	220	230	240
m111-1.pep	250	260	270	280	290	300
	GGNTQIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNNKRPISHNLASISVVADSAM					
g111-1	GGNTQIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNNKRPISHNLASISVVSAM					
	250	260	270	280	290	300
m111-1.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLVFLIVRDKGGYRTAMSSEFEKLLRX					
g111-1	TADGLSTGLFVLGETEALRLAEQEKLVFLIVRDKGGYRTAMSSEFAKLLRX					
	310	320	330	340	350	

g111-1/p44550

sp|P44550|YOJL HAEIN HYPOTHETICAL LIPOPROTEIN HI0172 PRECURSOR >gi|1074292|pir||C64144
 hypothetical protein HI0172 - Haemophilus influenzae (strain Rd KW20) >gi|1573128 (U32702)
 lipoprotein, putative [Haemophilus influenzae Rd] Length = 346
 Score = 349 bits (885), Expect = 2e-95
 Identities = 177/328 (53%), Positives = 240/328 (72%), Gaps = 4/328 (1%)

Query: 23 LNACSEQTAQVTTLQGETMGTTYXVKYLSNNRDKLPSPAEIXKRIDDALKEVNRQMSTYQ 82
 L AC ++T + ++L G+TMGTTY VKYL + S + + I+ LK+ N MSTY+
 Sbjct: 17 LAACQKET-KVISLSGKTMGTTYHVKYLDGGSITATS-EKTHEEIEAILKDVNAKMSTYK 74

Query: 83 PDSEISRNFQHT-AGKPLRISSDFAHVTAEAVRLNRLTHGALDVTVGPLVNLWGFGPDKS 141
 DSE+SRNFQ+T P+ IS+DFA V AEA+RLN++T GALDVTVG+VNLWGFGP+K
 Sbjct: 75 KDELSESRNFQNTQVNTPIEISADFAKVLAELRLNKVTEGALDVTVGPPVNLWGFGPEKR 134

Query: 142 VTREPSPEQIKQAASYTGIDKIILKQGKDYASLSKTHPKAYLDLSSIAKGFVDKVGAGEL 201
 ++P+PEQ+ + ++ GIDKI L K+ A+LSK P+ Y+DLSSIAKGFVD+VA +L
 Sbjct: 135 PEKQPTPEQAERQAWVGIDKITLDTNKEKATLSKALPQVYVDLSSIAKGFVDQVAEKL 194

Query: 202 EKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQGGNTQIIVPLNNRSLATSGDY 261
 E+ QNY+VEIGGE+ KGKN G+PW+I IE+P + ++ LNN +A+SGDY
 Sbjct: 195 EQLNAQNYMVEIGGEIRAKGKNIEGKPWQIAIEKPTTTGERAVEAVIGLNNMGMASSGDY 254

Query: 262 RIFHVDKNGKRLSHIINPNNKRPISHNLASISVVADSAMTADGLSTGLFVLGETEALKLA 321
 RI+ ++NGKR +H I+P PI H+LASI+V+A ++MTADGLSTGLFVLGE +AL++A
 Sbjct: 255 RIY-FEENGKRFAHEIDPKTGYPHQHLLASITVLAPTSMTADGLSTGLFVLGEDKALEVA 313

Query: 322 EREKLVFLIVRDKGGYRTAMSSEFEKL 349
 E+ LAV+LI+R G+ T SS F+KL
 Sbjct: 314 EKNNLAVYLIIRTDNGFVTKSSSAFKKL 341

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 403>:

a111-1.seq

```

1  ATGCCGTCTG AAACACGCCT GCCGAACCTT ATCCGCACCT TGATATTTCG
51  CCTGAGTTTT ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCTTGCA AGGTGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAGCGCAT
201 CGATGACGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCGCCG
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC ACCTGAACCG

```



```

351 CCTGACACAC GCGCGCTGG ACGTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTTCGG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAAG CAGCATCTTA TACGGGCATA GACAAAATCA TTTTGAAACA
501 AGGCAAAGAT TACGTTCCCT TGAGCAAAAC CCACCCAAG GCCTATTTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TGCGGGCGAA
601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCTTGCGCG ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GCGGCGAATA CGCAGATTAT CGTCCCGCTG
751 AACAACCGTT CGCTTGCCAC TTCCGGCGAT TACCGTATT TCCACGTCGA
801 TAAAAGCGGC AAACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCATG
901 ACGGCGGACG GCTTGTCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAAGTCGC TGTTCCTG ATTGTCAGGG
1001 ATAAAGCGG CTACCGCACC GCCATGTCTT CCGAATTGA AAAAGTCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 404; ORF 111-1.a>:

a111-1.pep

```

1  MPSETRLPNF IRTLIFALSF IFLNACSEQT AQTVTLOGET MGTITYTVKYL
51  SNNRDKLPSP AEIQKRIDDA LKEVNRQMST YQPDSEISR F NQHTAGKPLR
101 ISSDFAHVTA EAVHLNRLTH GALDVTVGPL VNLWGFGDPK SVTREPSPEQ
151 IKQAASYTGI DKIIKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIONYL VEIGGELHGK GKNARGEPRW IGIEQPNIVQ GGNTQIIIVPL
251 NNRLATSGD YRIFHVDKSG KRLSHIINPN NKRPIHNLAS SISVVDASAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

a111-1/m111-1 98.9% identity in 351 aa overlap

	10	20	30	40	50	60
a111-1.pep	MPSETRLPNFIRTLIFALSFI	FLNACSEQTAQVTVTLOGET	MGTITYTVKYL	SNNRDKLPSP		
m111-1	MPSETRLPNFIRVLIFALGF	IFLNACSEQTAQVTVTLOGET	MGTITYTVKYL	SNNRDKLPSP		
	10	20	30	40	50	60
	70	80	90	100	110	120
a111-1.pep	AEIQKRIDDALKEVNRQMST	YQPDSEISR F NQHTAGKPLR	ISSDFAHVTA	EAVHLNRLTH		
m111-1	AEIQKRIDDALKEVNRQMST	YQPDSEISR F NQHTAGKPLR	ISSDFAHVTA	EAVRLNRLTH		
	70	80	90	100	110	120
	130	140	150	160	170	180
a111-1.pep	GALDVTVGPLVNLWGFGDPK	SVTREPSPEQIKQAASYTG	IDKIIKQKGD	YASLSKTHPK		
m111-1	GALDVTVGPLVNLWGFGDPK	SVTREPSPEQIKQAASYTG	IDKIIKQKGD	YASLSKTHPK		
	130	140	150	160	170	180
	190	200	210	220	230	240
a111-1.pep	AYLDLSSIAKGFGVDKVAGE	LEKYGIONYLVEIGGELHGK	GKNARGEPRW	IGIEQPNIVQ		
m111-1	AYLDLSSIAKGFGVDKVAGE	LEKYGIONYLVEIGGELHGK	GKNARGEPRW	IGIEQPNIVQ		
	190	200	210	220	230	240
	250	260	270	280	290	300
a111-1.pep	GGNTQIIIVPLNNRSLATSG	DYRIFHVDKSGKRLSHIIN	PNNKRPIHNLAS	SISVVDASAM		
m111-1	GGNTQIIIVPLNNRSLATSG	DYRIFHVDKNGKRLSHIIN	PNNKRPIHNLAS	SISVVDASAM		
	250	260	270	280	290	300
	310	320	330	340	350	
a111-1.pep	TADGLSTGLFVLGETEALKL	AEREKLAVFLIVRDKGGYRT	AMSSEFEKLLRX			
m111-1	TADGLSTGLFVLGETEALKL	AEREKLAVFLIVRDKGGYRT	AMSSEFEKLLRX			
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 405>:

g114.seq

```

1  ATGGCTTCCA TCACTTCGCC GCTGCACGGG GCGCAGCAGG AATGCAGCAA
51  GACTTTTTTA TGTCCGCCGG GCGGACGAG TATGGGGCGG TCAATGTCCG

```

```

101 TAACGGTAGG TTTGTTTTGT GTTTCATTA ACTTAACAAT ATCTGTCGAA
151 TACGGTCAAA GCGGCTATTT TACCAGAGCC GCCGAATGTA AAACAGGGTG
201 TCAGGGCATC AGCCCGAGCT GCCTGAACGA ACGGACGGTT TGCGAGGTAA
251 CGATAAAATG GTCGAGCAGC GAAACATCAA CCAGCGACAT GGCCTGTGCC
301 AGCCGCCTTG TGAACATGAT GTCTTCCTGC GAAGGTTGAG GCGAGCCGCC
351 CGGATGGTTG TGCGCGATAA TCAGGCTGTC GGCATATTCG TCCAATGCCA
401 GTTTGACGAT TTCGCGGATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 406; ORF 114.ng>:

```

g114.pep
  1 MASITSPLHG AQQECSKTFL CPPGGTSMGR SMSVTVGLFC VSINLTISVE
 51 YGQSGYFTRA AECKTGCGI SPSCLNERTV CEVTIKWSSS ETSTSDMACA
101 SRLVNMSSC EGSGEPPGWL CAIIRLSAYS SNASLTISRM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 407>:

```

m114.seq
  1 ATGGCTTCCA TCACTTCGCC GCTGCACGGG GCGCACAGAG AATGCAGCAA
 51 GACTTTTTTA TGTCCACCGG GCGGGACGAG TATAGGGCGG TCAATGTCGG
101 TAACGGTAGG TTTGTTTTGT GTTTCATTA ACTTAACAAT ATCTGTGAA
151 TACGGTTGAA GCGGCTATTT TATCAGAGCC GCCGCATGTA AAACAGAGTG
201 TCAGGGCATC AAGCCGAGCT GTCTGAACGA ACAGACGCTT TGCGAKGTAA
251 CGATAAAATG GTCGAGCAGC GACACATCGA CCAGCGACAT TGCCTGTGCC
301 AGCCGCCTTG TGAACATGAT GTCTTCCTGC GAAGGTTGAG GCGAGCCGCC
351 CGGATGGTTG TGCGCAATAA TCAGGCTGTC GGCATATTCG TCCAATGCCA
401 GTTTGACGAT TTCGCGGATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 408; ORF 114>:

```

m114.pep
  1 MASITSPLHG AHRECSKTFL CPPGGTSIGR SMSVTVGLFC VSINLTISVE
 51 YGXSGYFIRA AACKTECQGI NPSCLINEQTL CXVTIKWSSS DTSTSDIACA
101 SRLVNMSSC EXSGEPPGWL CAIIRLSAYS SNASLTISRM *

```

m114/g114 90.0% identity over a 140 aa overlap

	10	20	30	40	50	60
m114.pep	MASITSPLHGAHRECSKTFLCPPGGTSIGRSMVTVGLFCVSINLTISVEYGXSGYFIRA					
	::: : : : : : :					
g114	MASITSPLHGAQQECSKTFLCPPGGTSMGRSMVTVGLFCVSINLTISVEYQSGYFTRA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m114.pep	AACKTECQGINPSCLINEQTLXVTIKWSSSDTSTSDIACASRLVNMSSCEXSGEPPGWL					
	: : : : : : : :					
g114	AECKTGCGISPSCLNERTVCEVTIKWSSSETSTSDMACASRLVNMSSCEGSGEPPGWL					
	70	80	90	100	110	120
	130	140				
m114.pep	CAIIRLSAYSSNASLTISRMX					
	: : :					
g114	CAIIRLSAYSSNASLTISRMX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 409>:

```

a114.seq
  1 ATGCCGGAGG CAAGCATCGC CTCCATCACT TCGCCGCTGC ACGGGGCGCA
 51 ACAGGAATGC AGCAAGACTT TTTATGTCC GCCGGGCGGG ACGAGTATGG
101 GGCGGTCAAT GTCGGTAACG GTAGGTTTGT TTTGTGTTTC CATTAACCTA
151 ACGATATCTG TCGAATACGG TTGAAGCGGC TATTTTATCA GAGCCGCCGC
201 ATGTAAACA GGTGTGTCAG GCATCAGCCC GAGCTGCCTG AACGAACGGA
251 CGGTTTGCGC CGTTACGATA AAATGGTCGA GCAGCGACAC ATCGACCAGC
301 GACATTGCCT GTGCCAGCCG CCTTGTGAAC ATGATGTCTT CCTGCGAAGG
351 TTCGGGCGAG CCGCCCGGAT GGTGTGCGC GATAATCAGG CTGTCGGCAT
401 ATTCGTCCAA TGCCAGTTTG ACAATTTAC GGATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 410; ORF 114.a>:

a114.pep

```

1  MPEASIASIT SPLHGAQQEC SKTFLCPPGG TSMGRSMSVT VGLFCVSINL
51  TISVEYG*SG YFIRAAACKT GCQGISPSC L NERTVCAVTI KWSSSDTSTS
101 DIACASRLVN MMSSCEGSGE PPGWLCAIR LSAYSSNASL TISRM*

```

m114/a114 92.9% identity in 140 aa overlap

```

              10      20      30      40      50
m114.pep      MASITSPLHGAHRECSKTFLCPPGGTSMGRSMSVTVGLFCVSINLTISVEYGXSG
              :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114           MPEASIASITSPLHGAQQECSKTFLCPPGGTSMGRSMSVTVGLFCVSINLTISVEYGXSG
              10      20      30      40      50      60

              60      70      80      90      100     110
m114.pep      YFIRAAACKTECQGINPSC LNEQTL CXVTIKWSSSDTSTSDIACASRLVNMSSCEXSGE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114           YFIRAAACKTGCQGISPSC L NERTVCAVTIKWSSSDTSTSDIACASRLVNMSSCEGSGE
              70      80      90      100     110     120

              120     130     140
m114.pep      PPGWLCAIIRLSAYSSNASLTISRMX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114           PPGWLCAIIRLSAYSSNASLTISRMX
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 411>:

g117.seq

```

1  atggtcgacg aactcgacCT GCTGCCCGAT GCCGTCGCCG CCACCCTGCT
51  TGCCGACATC GGACGCTACG TCCCCGATTG GAACCTATTG GTTTCGAGC
101 GCTGCAACAG CACCGTCGCC GAGCTGGTCA AAGGTGtgga CGAAGTGCAG
151 AAACTTACCC ACTTCGCCCG GGTGACAGC CTCGCCACGC CGGAAGAACG
201 CGCACAGCAA GCGGAAACCA TCGGAAAAT GCTGCTGGCg atggttaccg
251 Acatccgcgt cgtatTAATC AAATGGCGA TCGGTacgcg caccCTGeta
301 tttTTtaagCA ACGCCCCGA CAGCCCTGAA AAACgcgcgC TCgcaaAga
351 aacccTCGAC ATCTTCGCC CGCTCGCCAA CCGCTTGGG GTGTGGCAGC
401 TCAAAATGCA GCTCGAAGAT TTGGGCTTCC GCCATCAAGA ACCCGAAAAA
451 TACCGCGAAA TCGCCCTGCT TTTGGACGAA AAACGCACCG AACGCCTCGA
501 ATACATCGAA AACTTCCTCG ATATCCTGCG TACGGAATC AAAAAATACA
551 ATATCCACTT TGAAGTCGCC GGCCGTCCGA AACACATCTA CTCCATTTAC
601 AAAAAAATGG TGAAGAAAAA ACTCAGCTTC GACGgccTGT TCGACATCCG
651 CGCCGTGCGG ATTCTGGTCG ATACCGTCCC CGaGTGTAC ACCACGCTGG
701 gcaTCGTCCA CAGCCTCTGG CAGCCCATTC CCGCGagtt CGAcgactAC
751 ATCGCCAACC CCAAAGgcaA CGgttATAAA AGtTTGCACA CCGTCATCGT
801 cggcccGGAA gacaaaggtg tggaaGtgCA AATCCGCACC TTCGAtatGC
851 accAATTcAa CgaatTcggT gtcgcccCCC ACTGGCGtta caaagaaggc
901 ggcaaaaggcg attccGCcTA cgaacaaAAA ATcgccTggt TGCgccaACT
951 CTTGGACTGG CGCGAAAATA TGGCGGAAAG CGGCAAGGAA GACCTCGCCG
1001 CCGCCTTCAA AACCAGAGCTT TTCAACGACA CGATTTATGT TTTGACCCCG
1051 CACGGCAAAG TCCTCTCTCT GCCAACGGGC GCAACCCCA TCGACTTCGC
1101 CTACGCCCTG CACAGCAGCA TcggCGACCG CTGCCGGGGC GCGAAAGTCG
1151 AaggGCAGAT TGTGCCGCTG TCCACCCCGC TCGAAAACGG ACAGCGCGTC
1201 GAAATcatta cCGCcaaAGA AGGGCATCCT TCCGTCAACT GGCTTTACGA
1251 AGGctgGGtc aaATCCGGCA AGGCCATCGG caaAATCCGC GCCTAcatCC
1301 GCCAGcaaAa cgCgaCACC GTGCGGAAG AAGGCCGTGT CCAACTCGAC
1351 AAGCAGCTTG CAAACTCAC GCCCAAACCC AACCTGCAAG AGCTTgccaag
1401 aaATCTCGGC taaaaAAGC cagaagacct ctacacCGCc gtcggacaag
1451 gcgaaatttc caaccgcgcc atCaaaaaag cctgcggcac GCTgaacgaa
1501 ccgccccCCG TGCCCGTCAG CGCAACCACC ATCGTCAAAC AGTCCAAAAA

```

```

1551 CAAAAAAGGT GGCAAAACCG GCGTGCTCAT CGACGGCGAA GACGGCTTGA
1601 TGACCACGCT TGCCAAATGC TGCAAACCCG CGCCGCCCGA CGATATTGCC
1651 GGCTTCGTTA CCCGCGAGCG CGGCATTTC GTCCACCGCA AAACCTGCCC
1701 CTCTTTCCGA CACCTTGCCG AACACGCGCC CGAAAAAGTA CTGGACGCAA
1751 GTTGGGCGGC GTTGCAGGAA GGGCAAGTGT TCGCCGTCGA TATCGAAATC
1801 CGCGCCCAAG ACCGCTCCG GCTTTTGCGC GACGTATCCG ACGCGCTCGC
1851 CCGCCACAAA CTCAACGTTA CCGCCGTGCA AACCCAGTCC CGCGACTTGG
1901 AAGCCAGCAT GAGGTTACAG CTCGAAGTCA AACAAGtCAA CGacTCCCG
1951 CGCGTCCTCG CCGGCCTCGG CGATGTCAA GCGGTATTGA GCGTTACCCG
2001 GCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 412; ORF 117.ng>:

g117.pep

```

1 MVDELDLLPD AVAATLLADI GRYVPDWNLL VSERCNSTVA ELVKGVDEVQ
51 KLTHFARVDS LATPEERAQQ AETMRKMLLA MVTDIRVCLI KLAMRTRTLL
101 FLSNAPDSPE KRAVAKETLD IFAPLANRLG VWQLKWQLED LGFRHQEPEK
151 YREIALLLDE KRTERLEYIE NFLDILRTEL KKYNHFEVA GRPKHIYSIY
201 KKMVKKKLSF DGLFDIRAVR ILVDTVPECY TTLGIVHSLW QPIPGFDDY
251 IANPKNGYK SLHTVIVGPE DKGVEVQIRT FDMHQFNEFG VAAHWRYKEG
301 GKGDSAYEQK IAWLRQLLDW RENMAESGKE DLAAAFKTEL FNDTIYVLTP
351 HGKVLSLPTG ATPIDFAYAL HSSIGDRCRG AKVEGQIVPL STPLENGQRV
401 EIITAKEGHP SVNWLYEGWV KSGKAIGKIR AYIRQONADT VREEGRVQLD
451 KQLAKLTPKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTLNE
501 PPPVPVSATT IVKQSKIKKG GKTGVLIDGE DGLMTTLAKC CKPAPDDIA
551 GFVTRERGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GQVFAVDIEI
601 RAQDRSGLLR DVSDALARHK LNVTAQTQS RDLEASMRFT LEVKQVNDLP
651 RVLAGLGDVK GVLSVTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 413>:

m117.seq (partial)

```

1 ..GTGAAACTCA AGAAATACAA TGTCCATTTC GAAGTCGCCG GCCGCCCGAA
51 ACACATCTAC TCCATTTACA AAAAAATGGT GAAGAAAAAA CTCAGCTTCG
101 ACGGCTCTT TGACATCCGC GCCGTGCGAA TTCTGGTTGA TACCGTCCCC
151 GAGTGTTACA CCACGCTGGG TATCGTCCAC AGCCTCTGGC AGCCCATTC
201 CGGCGAGTTC GACGACTACA TCGCCAATCC CAAAGGCAAC GGCTATAAAA
251 GTTTGCACAC CGTCATCGTC GGCCCGAAG ACAAGGCGT GGAAGTACAA
301 ATCCGCACCT TCGATATGCA CCAATTCAAC GAATTGCGTG TCGCCGCCCA
351 CTGgCGTTAC AAAGAGGGCG GCAAGGGCGA TTCCGCCTAC GAACAGAAAA
401 TCGCCTGGTT GCGCCAATC TTGGACTGGC GCGAAAACAT GGCGGAAAGC
451 GGCAAGGAAG ACCTCGCCGC CGCCTTCAAA ACCGAGCTTT TCAACGACAC
501 GATTTATGTT TTGACCCCGC ACGGCAAAGT CCTCTCCCTG CCCACGGGCG
551 CGACCCCAT CGACTTCGCC TACGCCCTGC ACAGCAGCAT CGGCGACCGT
601 TGCCGCGGTG CGAAAGTCGA AGGGCAGATT GTGCCGCTGT CCACCCCGCT
651 CGAAACCGGA CAGCGCGTCG AAATCATTAC CGCCAAAGAA GGGCATCCTT
701 CCGTCAACTG GCTTTACGAA GGCTGGGTCA AATCCAACAA GGCAATCGGC
751 AAAATCCGCG CTTACATCCG CCAGCAAAAC GCCGACACCG TCGCGAAGA
801 AGGCCGCGTC CAACTCGACA AACAGCTTGC CAAACTCACG CCCAAACCCA
851 ACCTGCAAGA GCTTGCCGAA AATCTCGGT ACAAAAAGCC AGAAGACCTC
901 TACACCGCCG TCGGACAAGG CGAAATTTCC AACCGCGCCA TCCAAAAGC
951 CTGCGGCACg CTGAACGAAC CGCCGCCGT ACCCGTCAGC GAAACCACCA
1001 TCGTCAAACA GTCCAAAATC AAAAAAGGCG GCAAAAACGG CGTGCTCATC
1051 GACGGCGAAG ACGGTCTGAT GACCACGCTT GCCAAATGCT GCAAACCCGC
1101 GCCGCCGAC GATATTATCG GCTTCGTTAC CCGCGAGCGC GgCATTTAG
1151 TGCACCGCAA AwyyTkCyCG TCTTTCCAAC ACCTCGCCGA ACACGCGCCC
1201 GAwAAAGTGC TGGACGCAAG CTGGGCGGCA TTGCAGGAAG GACAAGTATT
1251 CGCCGTCGAT ATCGAAATCC GCGCCCAAGA CCGCTCCGGG CTTTTCGCGC
1301 ACGTATCCGA CGCGCTCGCC CGCCACAAAC TCAACGTTAC CGCCGTGCAA
1351 ACCCAGTCCC GCGACTTGA AGCCAGCATG AGGTTACGC TCGAAGTCAA
1401 ACAAGTCAAC GACCTCCGC GCGTCTCGC CAGCCTCGGC GACGTCAAAG
1451 GCGTATTGAG CGTTACCCGG CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 414; ORF 117>:

m117.pep (partial)

```

1...VKLKKYNVHF EVAGRPKHIY SIYKKMVKKK LSFGLFDIR AVRILVDTVP
51  ECYTTLGIVH SLWQPIPGF DDYIANPKGN GYKSLHTVIV GPEDKGVEVQ
101 IRTFDMHQFN EFGVAHWRY KEGGKGDSAY EQKIAWLRQL LDWRENMAES
151 GKEDLAAAFK TELFNDTIYV LTPHGKVLSL PTGATPIDFA YALHSSIGDR
201 CRGAKVEGQI VPLSTPLENG QRVETITAKE GHPSVNWLYE GWVKSNAIG
251 KIRAYIRQQN ADTVREEGRV QLDKQLAKLT PKPNLQELAE NLGYKKPEDL
301 YTAVGQGEIS NRAIQKACGT LNEPPVPVVS ETTIVKQSKI KKGKNGVLI
351 DGEDGLMTTL AKCKPAPPD DIIGFVTRER GISVHRKXXX SFQHLAEHAP
401 XKVLDASWAA LQEGQVFAVD IEIRAQDRSG LLRDVSDALA RHKLNVTAVQ
451 TQSRDLEASM RFTLEVQVN DLPRVLASLG DVKGVLVTR L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 117 shows 97.6% identity over a 490 aa overlap with a predicted ORF (ORF 117.ng) from *N. gonorrhoeae*:

m117/g117

m117.pep				10	20	30
				VKLKKYNVHF	EVAGRPKHIY	SIYKKMVKKK
g117	EKYREIALLLDEKRTERLEYIENFLDILRTELKKYNIHFEVAGRPKHIY	SIYKKMVKKK				
	150	160	170	180	190	200
m117.pep		40	50	60	70	80
		SFDGLFDIRAVRILVDTVP	ECYTTLGIVHSLWQPIPGF	DDYIANPKNGYKSLHTVIVG		
g117		SFDGLFDIRAVRILVDTVP	ECYTTLGIVHSLWQPIPGF	DDYIANPKNGYKSLHTVIVG		
	210	220	230	240	250	260
m117.pep		100	110	120	130	140
		PEDKGVEVQIRTFDMHQFNEFGVAHWRYKEGGKGDSAYEQKIAWLRQLLDWRENMAESG				
g117		PEDKGVEVQIRTFDMHQFNEFGVAHWRYKEGGKGDSAYEQKIAWLRQLLDWRENMAESG				
	270	280	290	300	310	320
m117.pep		160	170	180	190	200
		KEDLAAAFKTELFNDTIYVLTPHGKVL	SLPTGATPIDFAYALHSSIGDR	CRGAKVEGQIV		
g117		KEDLAAAFKTELFNDTIYVLTPHGKVL	SLPTGATPIDFAYALHSSIGDR	CRGAKVEGQIV		
	330	340	350	360	370	380
m117.pep		220	230	240	250	260
		PLSTPLENGQ	RVETITAKEGHPSVNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQ			
g117		PLSTPLENGQ	RVETITAKEGHPSVNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQ			
	390	400	410	420	430	440
m117.pep		280	290	300	310	320
		LDKQLAKLTPKPNLQELAENLG	YKKPEDLYTAVGQGEISNRAIQKACGT	LNEPPVPVSE		
g117		LDKQLAKLTPKPNLQELAENLG	YKKPEDLYTAVGQGEISNRAIQKACGT	LNEPPVPVSA		
	450	460	470	480	490	500
m117.pep		340	350	360	370	380
		TTIVKQSKI	KKGKNGVLIDGEDGLMTTLAKCKPAPPDDIIGFVTRERGISVHRKXXXS			
g117		TTIVKQSKI	KKGKNGVLIDGEDGLMTTLAKCKPAPPDDIAGFVTRERGISVHRKTCPS			
	510	520	530	540	550	560
m117.pep		400	410	420	430	440
		FQHLAEHAPXK	VLDASWAAALQEGQVFAVDIEIRAQDRSGLLRDVSDAL	RHKLNVTAVQT		
	400	410	420	430	440	450

a117.seq

1	ATGGTTCATG	AAC TCGACCT	GCTCCCGCAT	GCCGTGCGCG	CCACCTGTCT
51	TGCCGACATC	GGACGCTACG	TCCCCGACTG	GAACCTATTG	GTTTCCGAAC
101	GCTGCAACAG	TACCGTCGCC	GAGCTGGTCA	AAGGTGTGGA	CGAAGTGCAG
151	AAACTCACCC	ACTTCGCCCC	GGTGGACAGC	CTCGCCACGC	CGGAAGAAGC
201	CGCCCCAGAG	GCAGAAACTA	TGCGGAAAAA	GCTGCTGGCG	ATGGTTACCG
251	ACATCCGCGT	CGTGTTAATC	AAACTGCGGA	TGCGTACCGC	CACCTCGCAA
301	TTTTTAAGCA	ACGCCCCCGA	CAGCCCCGAA	AAACGCGCCG	TCGCCAAAGA
351	AACCCCTGAC	ATCTTCGCCC	CGCTCGCCAA	CCGTTTGGGC	GTGTGGCAGC
401	TCAAATGGCA	GCTCGAAGAT	TTGGGCTTCC	GCCATCAAGA	ACCCGAAAAA
451	TACCCGGA	TCGCCCTGCT	TTTGAGACGA	AAACGCACCG	AACGCCCTCGA
501	ATACATCGAA	AAC TCTCCTTA	ATATCCTGCG	TACGGAACTC	AAAAAATACA
551	ATATCCACTT	TGAAGTCGCC	GGCCGTCCGA	AACACATCTA	CTCCATTAC
601	AAAAAAATGG	TGAAGAAAAA	ACTCAGCTTG	GACGGGTGTG	TCGACATCCG
651	CGCCGTGCGG	ATTCTGGTTG	ATACCGTCCC	CGAGTGTAC	ACCACACTGG
701	GCATTGTCCA	CAGCCTCTGG	CAGCCCATTG	CCGGCGAGTT	CGACGACTAC
751	ATCGCAACC	CGAAAGGCAA	CGGTATAAA	AGTTTGACAC	CCGTATCGT
801	CGGCCCGGAA	GACAAAGGCG	TGGAAGTGCA	AATCCGCACC	TTGATATGC
851	ACCAATTCAA	CGAATTTCGT	GTCGCCGCGC	ACTGCGGTTA	CAAAGAGGGC
901	GGCAAAGCGG	ATTCGCGCTA	CGAACAAAAA	ATCGCTGGT	TACGCCAACT
951	TTTGAGACTG	CGCGAAAAAC	TGGCGGAAAG	CGGCAAGGAA	GACCTCGCCG
1001	CGGCTTCAA	AACCGAGCTT	TTCAACGACA	CGATTTATGT	TTTGACCCCG
1051	CACGGCAAAG	TCCTCTCCCT	GCCACAGGC	GCGACCCCA	TCGACTTCGC
1101	CTACGCCCTG	CACAGCAGCA	TCGGCGACCG	TTGCCGCGGT	GCGAAAGTCG
1151	AAGGGCAGAT	TGTGCCGCTG	TCCACCCCGC	TCGAAAACGG	ACAGCGTGTC
1201	GAAATCATTA	CCGCCAAAGA	AGGGCATCTT	TCCGTCAACT	GGCTTTACGA
1251	AGGCTGGGTC	AAATCCAACA	AGGCAATCGG	CAAAATCCCG	GGCTACATCC
1301	GCCAGCAAAA	CGCGCAGACC	GTCGCGGAAG	AAGGCCGCGT	CCAACCTGAC
1351	AAACAGCTTG	CCAAACTCAC	GCCCAAACCC	AACCTGCAAG	AGCTTGCCGA
1401	AAATCTCGGC	TACAAAAAGC	CAGAAGACCT	CTACACCGCC	GTCGGACAAG
1451	GCGAAATTTT	CAACCGCGCC	ATCCAAAAAG	CCTGCGGCAC	GCTGAACGAA
1501	CCGCCGCCCC	TACCCGTCAG	CGAAACCACC	ATCGTCAAAC	AGTCCAAAAAT
1551	CAAAAAAGGC	GGCAAAAAAG	TGCTGCTCAT	CGACGGCGAA	GACGGTCTGA
1601	TGACCACGCT	TGCCAAATGC	TGCAAAACCCG	CGCCGCCCGA	CGACATTGTC
1651	GGCTTCGTTA	CCCGCATGCG	CGGCATTTTC	GTACACCGCA	AAACCTGCCC
1701	CTCTTTCCGA	CACCTCGCCG	AACACGCGCC	CGAAAAAGTA	CTGGACGCAA
1751	GTTGGGCGGC	GTTGCAGGAA	GGACAAGTGT	TCGCCGTCGA	TATCGAAATC
1801	CGCGCCCAAG	ACGCTCCGG	GCTTTTGCGC	GACGTATCCG	ACGCGCTCGC
1851	CCGCCACAAA	CTCAACGTTA	CCGCCGTGCA	AACCCAGTCC	CGCGACTTGG
1901	AAGCGGACAT	GAGGTTACAG	CTCGAAGTCA	AACAAGTTAC	CGACCTCCCA
1951	CGCGTCTCTG	CCAGCCTCGG	CGACGTCAA	GGCGTATTGA	GCGTTACCCG
2001	GCTTTAA				

a117.pap

1	MVHELDLLPD	AVAATLLADI	GRYPDPWNL	VUSERCSTVA	ELVKGVDVQ
51	KLTHFARVDS	LATPEERAQQ	<u>AETMRKMLLA</u>	<u>MVTDIRVLI</u>	KLAMRTRTLQ
101	FLSNAPDSPE	KRAVAKETLD	IFAPLANRLG	VWQLKWQLED	LGFRHQEPEK
151	YREIALLDE	KRTERLEYIE	NFLNIIRTEL	KKYNTHFEVA	GRPKHIYSIY
201	KKMVKKKLSF	DGLFDIRAVR	ILVDTVPECY	TTLGIVHSLW	QPIPGFDDY
251	IANPKGNSYK	SLHTVIGLDE	DKGVEVQIRT	FDMHQFNEFG	VAHWRYKEG
301	GKGDSAYEQK	IAWLRQLQDW	RENNASEGKE	DLAAAFKTEL	FNDTHVLTPT
351	HGKVLSLPTG	ATPIDFAYAL	HSSIGDRCRG	AKVEQIQIVPL	STPLENGQRV

333

401 EIITAKEGHP SVNWLYEGWV KSNKAIGKIR AYIRQQNADT VREEGRVQLD
 451 KQLAKLTPKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTLNE
 501 PPPVPVSETT IVKQSKI KKG GKNGLVIDGE DGLMTTLAKC CKPAPPDDIV
 551 GFVTRDRGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GQVFAVDIEI
 601 RAQDRSGLLR DVSDALARHK LNVTAQTQS RDLEASMRFT LEVKQVTDLP
 651 RVLASLGDKV GVLSTRL*

m117/a117 98.0% identity in 490 aa overlap

m117.pep				10	20	30
				VKLKKYNVHFEVAGRPKHIYSIYKKMVKKKL		
a117	EKYREIALLLDEKRTERLEYIENFLNILRTELKKYNHFEVAGRPKHIYSIYKKMVKKKL					
	150	160	170	180	190	200
m117.pep		40	50	60	70	80
	SFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQPIPGEFDDYIANPKNGYKSLHTVIVG					
a117	SFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQPIPGEFDDYIANPKNGYKSLHTVIVG					
	210	220	230	240	250	260
m117.pep		100	110	120	130	140
	PEDKGVEVQIRTFDMHQFNEFGVAAHWRYKEGKGDSAYEQKIAWLRQLLDWRENMAESG					
a117	PEDKGVEVQIRTFDMHQFNEFGVAAHWRYKEGKGDSAYEQKIAWLRQLLDWRENMAESG					
	270	280	290	300	310	320
m117.pep		160	170	180	190	200
	KEDLAAAFKTELFNDTIYVLTPHGKVLSPGATPIDFAYALHSSIGDRCRGAKVEGQIV					
a117	KEDLAAAFKTELFNDTIYVLTPHGKVLSPGATPIDFAYALHSSIGDRCRGAKVEGQIV					
	330	340	350	360	370	380
m117.pep		220	230	240	250	260
	PLSTPLENGQREIITAKEGHP SVNWLYEGWV KSNKAIGKIRAYIRQQNADTVREEGRVQ					
a117	PLSTPLENGQREIITAKEGHP SVNWLYEGWV KSNKAIGKIRAYIRQQNADTVREEGRVQ					
	390	400	410	420	430	440
m117.pep		280	290	300	310	320
	LDKQLAKLTPKPNLQELAENLG YKKPEDLYTAVGQGEISNRAIQKACGTLNEPPPVPVSE					
a117	LDKQLAKLTPKPNLQELAENLG YKKPEDLYTAVGQGEISNRAIQKACGTLNEPPPVPVSE					
	450	460	470	480	490	500
m117.pep		340	350	360	370	380
	TTIVKQSKI KKG GKNGLVIDGE DGLMTTLAKCKPAPPDDIIGFVTRERGISVHRKXXXS					
a117	TTIVKQSKI KKG GKNGLVIDGE DGLMTTLAKCKPAPPDDIVGFVTRDRGISVHRKTCPS					
	510	520	530	540	550	560
m117.pep		400	410	420	430	440
	FQHLAEHAPXKVLDA SWAALQEGQVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAQT					
a117	FRHLAEHAPEKVLDA SWAALQEGQVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAQT					
	570	580	590	600	610	620
m117.pep		460	470	480	490	
	QSRDLEASMRFTLEV KQVNDLPRVLASLGDKV KGLSVTRLX					
a117	QSRDLEASMRFTLEV KQVTDLPRVLASLGDKV KGLSVTRLX					
	630	640	650	660		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 417>:

g117-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CCCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCGC CGCTCTGCCG GACAACGATA
101 AAAACCTCAT CGGTACCGCA TGGTCGCTGG CGCAGGAACA TTATCCTGCC
151 GATGCCGCCA CGCCGTATGG CGAGCCGCTG CCCGACCACT TCCTCGGCGC
201 GGCAGCAATG GTCGACGAAC TCGACCTGCT GCCCGATGCC GTCGCCGCCA
251 CCCTGCTTGC CGACATCGGA CGCTACGTCC CGGATTGGAA CCTATTGGTT
301 TCCGAGCGCT GCAACAGCAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTTACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401 AAGAACGCGC ACAGCAAGCG GAAACCATGC GGAAAAATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCTG ATTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCTGCAATTT TTAAGCAACG CCCCAGACAG CCCTGAAAAA CGCGCCGTCG
551 GCCAAGAAAA CCTCGACATC TTCGCCCGCG TCGCCAACCG CTTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTG GGTTCGCGC ATCAAGAACC
651 CGAAAAATAC CGCGAAATCG CCCTGCTTTT GGACGAAAAA CGCACCGAAC
701 GCCTCGAATA CATCGAAAAC TTCTCGATA TCCTGCGTAC GGAACCTCAA
751 AAATACAAAT TCCACTTTGA AGTCGCCGCG CGTCCGAAAC ACATCTACTC
801 CATTTACAAA AAAATGGTGA AGAAAAAACT CAGCTTCGAC GGCCTGTTTCG
851 ACATCCGCGC CGTGCGGATT CTGGTCGATA CCGTCCCGCA GTGTTACACC
901 ACGCTGGGCA TCGTCCACAG CCTCTGGCAG CCCATTCCCG GCGagttCGA
951 cgactACATC GCCAACCCTA AAGcaACGg ttATAAAAGt TTGCACACCG
1001 TCATCGTcgg cccGGAagaa aaaggtgtgg aagtgcAAAT CCGCACCTTC
1051 GATATGCacc AATTCAaCga ATTCCGTGTC GCCGCCCACT GGCGTTACAA
1101 AGAAGGCGGC AAAGGCGATT CCGCCTACGA AAAAAAATC GCCTGGTTGC
1151 GCCAACTCTT GGACTGGCGC GAAAATATGG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCGCGCG CCTTCAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAAGTCC TCTCTCTGCC AACGGGCGCA ACCCCCATCG
1301 ACTTCGCTTA CGCCCTGCAC AGCAGCATCG GCGACCGCTG CCGGGGCGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCCGACTC AAAACGGACA
1401 GCGCGTCGAA ATCATTACCG CCAAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAA TCCGGCAAGG CCATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGTGTCCA
1551 ATCTGCACAA GAGCTTGCCA AACTCACGCG CAACCCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGTAC AAAAAAGCCAG AAGACCTCTA CACCGCCGTC
1651 GGACAAGCGG AAATTTCCAA CCGCGCCATC CAAAAAGCCT GCGGCACGCT
1701 GAACGAACCG CCGCCCGTGC CCGTCAGCGC AACCACCATC GTCAAACAGT
1751 CCAAAATCAA AAAAGGTGGC AAAACCGGCG TGCTCATCGA CGGCGAAGAC
1801 GGCTTGATGA CCACGCTTGC CAAATGCTGC AAACCGCGCG CGCCCGACGA
1851 TATTGCCGCG TTCGTTACCC GCGAGCGCGG CATTTCGTC CACCGCAAAA
1901 CTGCCCCCTC TTTCGACAC CTGCGCGAAC ACGCGCCCGA AAAAGTACTG
1951 GACGCAAGTT GGGCGGCGTT GCAGGAAGGG CAAGTGTTCC CCGTCGATAT
2001 CGAAATCCCG GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAATC AACGTTACCG CCGTGCAAAC CCAGTCCCGC
2101 GACTTGGAAG CCAGCATGAG GTTACGCTC GAAGTCAAAC AAGTCAACGA
2151 CCTCCGCGC GTCCTCGCCG GCCTCGCGCA TGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 418; ORF 117-1.ng>:

g117-1.pep

```

1  MTAISPIQDT QSATLQELRE WFDSYCAALP DNDKNLIGTA WSLAQEHYPA
51  DAATPYGEPL PDHFLGAAQM VDELDLPLDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLDILRTELK
251 KYNIHFEVAG RPKHIYSIYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKGNGYKS LHTVIVGPEE KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESGKED
401 LAAAFKTELF NDTIYVLTPH GKVLSTPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGQVE IITAKEGHP S VNWLYEGWVK SGKAIGKIRA
501 YIRQONADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSATTI VKQSKIKKGG KTGVLIDGED
601 GLMTTLAKCC KPAPPDDIAG FVTRERGISV HRKTCPSFRH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVNDLPR VLAGLGDVKG VLSVTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 419>:

m117-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA

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```

51  ATTGCGCGAA  TGGTTCGACA  GCTACTGCGC  CGCTCTGCCG  GACAACGATA
101  AAAACCTCAT  CGGTACCGCA  TGGTTGCTGG  CGCAGGAACA  TTACCCCGCC
151  GATGCCGCCA  CGCCGTATGG  CGAGCCGCTG  CCCGACCACT  TCCTCGGCGC
201  GCGCGAAATG  GTTCATGAAC  TCGACCTGCT  CCCCGATGCC  GTCGCGGCCA
251  CCCTGCTTGG  CGACATCGGA  CGCTACGTCC  CCGACTGGAA  CCTATTGGTT
301  TCCGAACGCT  GCAACAGTAC  CGTCGCCGAG  CTGGTCAAAG  GTGTGGACGA
351  AGTGCAGAAA  CTCACCCACT  TCGCCCGGGT  GGACAGCCTC  GCCACGCCGG
401  AAGAACGCGC  CCAGCAGGCA  GAAACTATGC  GGAAAATGCT  GCTGGCGATG
451  GTTACCGACA  TCCGCGTCTG  GTTAATCAAA  CTGGCGATGC  GTACGCGCAC
501  CCTGCAATTT  TTAAGCAACG  CCCCCGACAG  CCCCCGAAAA  CGCGCCGTCG
551  CCAAAGAAAC  CCTCGACATC  TTCGCCCCGC  TCGCCAACCG  TTTGGGCGTG
601  TGGCAGCTCA  AATGGCAGCT  CGAAGATTG  GGCTTCCGCC  ATCAAAGGCC
651  GCGGAAATAC  CGCGAAATCG  CGCTGCTTTT  GGACGAAAAA  CGCACCGAAC
701  GCCTCGAATA  CATCGAAAC  TTCCTCAACA  TCCTGCGCGG  TGAATCAAG
751  AAATACAATG  TCCATTTTCA  AGTCGCCGGC  CGCCCCGAAAC  ACATCTACTC
801  CATTTACAAA  AAAATGGTGA  AGAAAAAAGT  CAGCTTCGAC  GGCCTCTTTG
851  ACATCCGACC  CGTGCGAATT  CTGGTTGATA  CCGTCCCGCA  GTGTTACACC
901  ACGCTGGGTA  TCGTCCACAG  CCTCTGGCAG  CCCATTCCCG  GCGAGTTCGA
951  CGACTACATC  GCCAATCCCA  AAGGCAACGG  CTATAAAAGT  TTGCACACCG
1001  TCATCGTCGG  CCCGGAAGAC  AAAGGCGTGG  AAGTACAAAT  CCGCACCTTC
1051  GATATCGACC  AATTCAACGA  ATTCGGTGTC  GCCGCCCACT  GCGGTTACAA
1101  AGAGGGCGGC  AAGGGCGATT  CCGCCTACGA  ACAGAAAATC  GCCTGGTTGC
1151  GCCAACTCTT  GGACTGGCGC  GAAAACATGG  CGGAAAGCGG  CAAGGAAGAC
1201  CTCGCCCGCC  CCTTCAAAAC  CGAGCTTTTC  AACGACACGA  TTTATGTTTT
1251  GACCCCGCAC  GGCAAAAGTCC  TCTCCCTGCC  CACGGGCGCG  ACCCCCATCG
1301  ACTTCGCTTA  CGCCCTGCAC  AGCAGCATCG  GCGACCGTTG  CCGCGGTGCG
1351  AAAGTCGAAG  GGCAGATTGT  GCCGCTGTCC  ACCCCGCTCG  AAAACGGACA
1401  GCGCGTCGAA  ATCATTACCG  CCAAAGAAGG  GCATCCTTCC  GTCAACTGGC
1451  TTTACGAAG  CTGGGTCAAA  TCCAACAAGG  CAATCGGCAA  AATCCGCGCC
1501  TACATCCGCC  AGCAAAACGC  CGACACCGTG  CGCGAAGAAG  GCCGCGTCCA
1551  ACTCGACAAA  CAGCTTGCCA  AACTCAGGCC  CAAACCCAAC  CTGCAAGAGC
1601  TTGCCGAAAA  TCTCGGCTAC  AAAAAGCCAG  AAGACCTCTA  CACCGCCGTC
1651  GGACAAGGCG  AAATTTCCAA  CCGCGCCATC  CAAAAAGCCT  CGGCGACGCT
1701  GAACGAACCG  CCGCCCGTAC  CCGTCAGCGA  AACCACCATC  GTCAAAACGT
1751  CCAAAATCAA  AAAAGGCGGC  AAAAACGGCG  TGCTCATCGA  CGGCGAAGAC
1801  GGTCTGATGA  CCACGCTTGC  CAAATGCTGC  AAACCCGCGC  CGCCCGACGA
1851  TATTATCGGC  TTCGTTACCC  GCGAGCGCGG  CATTTCAGTG  CACCGCAAAA
1901  CCTGCCCGTC  TTTCCAAAC  CTCGCCGAAC  ACGCGCCCGA  AAAAGTGCTG
1951  GACGCAAGCT  GGGCGGCATT  GCAGGAAGGA  CAAGTATTCG  CCGTCGATAT
2001  CGAAATCCCG  GCCCAAGACC  GCTCCGGGCT  TTTGCGCGAC  GTATCCGACG
2051  CGCTCGCCCG  CCACAAACTC  AACGTTACCG  CCGTGCAAA  CCAGTCCCGC
2101  GACTTGGAAG  CCAGCATGAG  GTTCACGCTC  GAAGTCAAAC  AAGTCAACGA
2151  CCTCCGCGCG  GTCCTCGCCA  GCCTCGGCGA  CGTCAAAGGC  GTATTGAGCG
2201  TTACCCGGCT  TTAA

```

This corresponds to the amino acid sequence <SEQ ID 420; ORF 117-1>:

m117-1.pep

```

1  MTAISPIQDT  QSATLQELRE  WFDSYCAALP  DNDKNLIGTA  WLLAQEHYPA
51  DAATPYGEPL  PDHFLGAAQM  VHEL DLLPDA  VAATLLADIG  RYVPDWNLLV
101  SERCNSTVAE  LVKGDEVQK  LTHFARVDSL  ATPEERAQQA  ETMRKMLLAM
151  VTDIRVVLIK  LAMRTRTLQF  LSNAPDSPEK  RAVAKETLDI  FAPLANRLGV
201  WOLKWQLEDL  GFRHQKPEKY  REIALLLDEK  RTERLEYIEN  FLNILRGELK
251  KYNVHFEVAG  RPKHIYSIYK  KMKVKKLSFD  GLFDIRAVRI  LVDTVPECYT
301  TLGIVHSLWQ  PIPGEFDDYI  ANPKNGYKYS  LHTVIVGPED  KGVEVQIRTF
351  DMHQFNEFGV  AAHWRYKEGG  KGDSAYEQKI  AWLRQLLDWR  ENMAESGKED
401  LAAAFKTELF  NDTIYVLTPH  GKVLSLPTGA  TPIDFAYALH  SSIGDRCRGA
451  KVEGQIVPLS  TPLENGQORV  IITAKEGHPS  VNWLYEGWVK  SNKAIGKIRA
501  YIRQQNADTV  REEGRVQLDK  QLAKLTPKPN  LQELAENLGY  KKPEDLYTAV
551  QGGEISNRAI  QKACGTLNEP  PPVPVSETTI  VKQSKIKKGG  KNGVLIDGED
601  GLMTTLAKCC  KPAPPDDIIG  FVTRERGISV  HRKTCPSFQH  LAEHAPEKVL
651  DASWAALQEG  QVFAVDIEIR  AQDRSGLLRD  VSDALARHKL  NVTAVQTQSR
701  DLEASMRFTL  EVKQVNDLPR  VLASLGDVKG  VLSVTRL*

```

m117-1/g117-1 98.2% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFDSYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
g117-1	MTAISPIQDTQSATLQELREWFDSYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
	10	20	30	40	50	60
	70	80	90	100	110	120

m117-1.pep	PDHFLGAAQMVHEDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK
g117-1	PDHFLGAAQMVDELDDLDPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK
	70 80 90 100 110 120
m117-1.pep	130 140 150 160 170 180
g117-1	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEK
	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEK
	130 140 150 160 170 180
m117-1.pep	190 200 210 220 230 240
g117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQKPEKYREIALLLDEKRTERLEYIEN
	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQEPEKYREIALLLDEKRTERLEYIEN
	190 200 210 220 230 240
m117-1.pep	250 260 270 280 290 300
g117-1	FLNILRGELKKYNVHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT
	FLDILRTELKKYNIHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT
	250 260 270 280 290 300
m117-1.pep	310 320 330 340 350 360
g117-1	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV
	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEEKGVEVQIRTFDMHQFNEFGV
	310 320 330 340 350 360
m117-1.pep	370 380 390 400 410 420
g117-1	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH
	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH
	370 380 390 400 410 420
m117-1.pep	430 440 450 460 470 480
g117-1	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS
	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS
	430 440 450 460 470 480
m117-1.pep	490 500 510 520 530 540
g117-1	VNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY
	VNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY
	490 500 510 520 530 540
m117-1.pep	550 560 570 580 590 600
g117-1	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKIKKGGKNGVLIDGED
	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSATTIVKQSKIKKGGKTGVLIDGED
	550 560 570 580 590 600
m117-1.pep	610 620 630 640 650 660
g117-1	GLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDAASWAALQEG
	GLMTTLAKCKPAPPDDIAGFVTRERGISVHRKTCPSFRHLAEHAPEKVLDAASWAALQEG
	610 620 630 640 650 660
m117-1.pep	670 680 690 700 710 720
g117-1	QVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAQTQSRDLEASMRFTLEVQVNDLPR
	QVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAQTQSRDLEASMRFTLEVQVNDLPR
	670 680 690 700 710 720
m117-1.pep	730
g117-1	VLASLGDKVGLSVTRLX
	VLASLGDKVGLSVTRLX
	730
m117-1/RelA	

sp|P55133|RELA_VIBSS GTP PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) >gi|537617 (U13769) ppGpp synthetase I [Vibrio sp.] Length = 744
Score = 536 bits (1366), Expect = e-151
Identities = 288/685 (42%), Positives = 432/685 (63%), Gaps = 31/685 (4%)

Query: 74 LDLLPDAVAATLLADI---GRYVPDWNLLVSERCNSTVAELVKGVDEVQKLTHFARVDSL 130
L + D + A LL + G Y D + E + T+ LV+GV+++ ++ ++ S
Sbjct: 68 LSMADADTLIAALLYPLVEGGCYSTD---ALKEEYSGTILHLVQGVQMC AIS---QLKST 121

Query: 131 ATPEERAQQAETMRKMLLAMVTDIRVVLIKLAMRTRLQFLSNAPDSPEKRAVAKETLDI 190
A +A Q + +R+MLL+MV D R V+IKLA R L+ + + PD +RA A+E +I
Sbjct: 122 AEETAQAQVDNIRRMLLSMVDDFRVCVVIKLAERICNLREVQDQDEV-RRAAAQECANI 180

Query: 191 FAPLANRLGVWLKWLQLEDLGRHOKPEKYREIALLLDEKRTRELEYIENFLNIRLGEK 250
+APLANRLG+ QLKW++ED FR+Q P+ Y++IA L E+R +R +YI +F++ L +K
Sbjct: 181 YAPLANRLGIGQLKWEIEDYAFRYQHPDQTYKQIAQLSERRIDREDYITHFVDDLSDAMK 240

Query: 251 KYNVHFEVAGRPKHIYSIYKKMVKKKLSFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQ 310
N+ EV GRPKHIYSI++KM KK L FD LFD+RAVRI+ + + +CY LG+VH+ ++
Sbjct: 241 ASNIRAEVQGRPKHIYSIWRKMQKKSLEFDELFDVRAVRIVAEELQDCYAALGVVHTKYR 300

Query: 311 PIPGEFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTQDMHGFNEFGVAHWRYKEG- 369
+P EFDDY+ANPK NGY+S+HTV++GPE K +E+QIRT MH+ +E GVAHW+YKEG
Sbjct: 301 HLPKEFDDYVANPKNGYQSIHTTVVLGPEGKTIEIQIRTQMHEESELGVAHWKYKEGT 360

Query: 370 --GKGDSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPHGKVLSP 427
G SAY++KI WLR+LL W+E M++SG ++ +++++F+D +Y TP G V+ LP
Sbjct: 361 ASGGAQSAYDEKINWLRKLLAWQEEMSDSG--EMLDELRSQVFDREVYAFTPKGDVVDLP 418

Query: 428 TGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPSVNWLYE- 486
+ ATP+DFAY +HS +G RC GAKVEG+IVP + L+ G +VEIIT KE +PS +WL
Sbjct: 419 SNATPLDFAYHIHSEVGHRCIGAKVEGRIVPFTYHLQMGDQVEIITQKEPNPSRDWLNPN 478

Query: 487 -GWVKSNAIGKIRAYIROQNADTVREEGRVQLDKQLAKL--TPKPNLQELAENLGYPK 543
G+V S++A K+ A+ R+Q+ D G+ L+ +L K+ T K A+ K P
Sbjct: 479 LGFVTSSRARAKVHAWFRKQDRDKNIIAGKEILEALVKIHATLKDAQYYAARKFNKSP 538

Query: 544 EDLYTAVGQGEIS-NRAIQKACGTLEPPVPVSETTIVKQSKI-----KKGGKNGV 594
E+LY +G G++ N+ I +N+P + + K S+ KK ++ V
Sbjct: 539 EELYAGIGSGDLRINQVINHINALVNKPTAEEDQQLLEKLSEASNKQATSHKKPQRDAV 598

Query: 595 LIDGEDGLMTTLAKCCCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDAW 654
+++G D LMT LA+CC+P P DDI GFVT+ RGISVHR C + L HAPE+++D W
Sbjct: 599 VVEGVDNLMTHLARCCQPIPGDDIIGFVTQGRGISVHRMDCEQLEELRHAPERIIDTVW 658

Query: 655 AALQEQGVFAVDIEIRAQDRSGLLRDVSALARHKLNVTAQTQ--SRDLEASMRFTLEV 712
G + + + + A +R+GLL++++ L K+ V +++ + + M F LE+
Sbjct: 659 GGGFVGN-YTITVRVTASERNGLKELTNLMNEKVKVAGMKSRVDYKKQMSIMDFEEL 717

Query: 713 KQVNDLPRVLASLGDVKGVLVSVTRL 737
+ L RVL + VK V RL
Sbjct: 718 TDLEVLGRVLKRIEQVKDVAEAKRL 742

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 421>:

all17-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCAC CGCGCTGCCG AACAAACGATA
101  AAAAATTGT CTTAGCCGCC CGTTCGCTGG CGGAAGCACA TTACCCCGCC
151  GATGCCGCCA CGCCGTATGG CGAACCGCTG CCCGACCACT TCCTCGGCGC
201  GCGCAAATG GTTCATGAAC TCGACCTGCT CCCGATGCC GTCGCGCCA
251  CCTGTGCTGC CGACATCGGA CGTACGTC CCGACTGGAA CCTATTGGTT
301  TCCGAACGCT GCAACAGTAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351  AGTCAGAAA CTCACCCACT TCGCCCGGGT GGACAGCTC GCCACGCCGG
401  AAGAACGCGC CCAGCAGGCA GAACTATGC GGAAATGCT GCTGGCGATG
451  GTTACCGACA TCCGCGTCGT GTTAATCAAA CTGGCGATGC GTACGCGCAC
501  CCTGCAATTT TTAAGCAACG CCCCAGACAG CCCCAGAAAA CGCGCCGTCG
551  CCAAAGAAAC CCTCGACATC TTCGCCCGCG TCGCCAACCG TTTGGGCGTG
601  TGGCAGCTCA AATGGCAGCT CGAAGATTTG GGCTTCCGCC ATCAAGAACC
651  CGAAAAATAC CGCGAAATCG CCCTGCTTTT GGACGAAAAA CGCACCGAAC
701  GCCTCGAATA CATCGAAAC TTCCTTAATA TCCTGCGTAC GGAACCTAAA
751  AAATACAATA TCACTTTGA AGTCGCCGCG CGTCCGAAAC ACATCTACTC
801  CATTTACAAA AAAATGGTGA AGAAAAACT CAGCTTCGAC GGGTTGTTCC

```

```

851 ACATCCGCGC CGTGGCGGATT CTGGTTGATA CCGTCCCCGA GTGTTACACC
901 ACACCTGGGCA TTGTCCACAG CCTCTGGCAG CCCATTCCCG GCGAGTTCGA
951 CGACTACATC GCCAACCCGA AAGGCAACGG CTATAAAAGT TTGCACACCG
1001 TCATCGTCGG CCCGGAAGAC AAAGGCGTGG AAGTGCAAAT CCGCACCTTC
1051 GATATGCACC AATTCAACGA ATTCGGTGTC GCCGCGCACT GGCCTTACAA
1101 AGAGGGCGGC AAAGGCGGAT CCGCCTACGA ACAAAAAATC GCCTGGTTAC
1151 GCCAACTTTT GGAATGGCGC GAAAACATGG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCGCGC CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAAGTCC TCTCCCTGCC CACAGGCGCG ACCCCATCG
1301 ACTTCGCCTA CGCCCTGCAC AGCAGCATCG GCGACCGTTG CCGCGGTGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCGCTCGC AAAACGGACA
1401 GCGTGTGCGA ATCATTACCG CCAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAA TCCAACAAGG CAATCGGCAA AATCCGCGCC
1501 TACATCGGCC AGCAAAACGC CGACACCGTG CGCGAAGAA GCGCGCTCCA
1551 ACTCGACAAA CAGCTTGCCA AACTCACGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCCGTC
1651 GGACAAGGCG AAATTTCCAA CCGCGCCATC CAAAAAGCCT GCGGCACGCT
1701 GAACGAACCG CCGCCGTAC CCGTCAGCGA AACCACCATC GTCAAACAGT
1751 CCAAAATCAA AAAAGGCGGC AAAAAGCGCG TGCTCATCGA CGGCGAAGAC
1801 GGTCTGATGA CCACGCTTGC CAAATGTGTC AAACCCGCGC CGCCGACGCA
1851 CATTGTGCGC TTCGTTACCC GCGATCGCGG CATTTCGGTA CACCGCAAAA
1901 CCTGCCCTTC TTTCCGACAC CTCGCCGAAC ACGCGCCCGA AAAAGTACTG
1951 GACGCAAGTT GGGCGGCGTT GCAGGAAGGA CAAGTGTTTC CCGTCGATAT
2001 CGAAATCCGC GCCCAAGACC GTCGCGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAATC AACGTTACCG CCGTGCAAAC CCAGTCCCGC
2101 GACTTGGAA GACGATGAG GTTCACGCTC GAAGTCAAAC AAGTTACCGA
2151 CCTCCACGC GTCCTCGCCA GCCTCGGCGA CGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 422; ORF 117-1.a>:

a117-1.pep

```

1  MTAISPIQDT QSATLQELRE WFDSYCTALP NNDKKLVLA RSLAEAHYPA
51  DAATPYGEPL PDHFLGAAQM VHELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLNLRTELK
251 KYNHFVEVAG RPKHIYSIYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKNGYKYS LHTVIVGPED KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWRQLLDWR ENMAESGKED
401 LAAAFKTELF NDTIYVLTTPH GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGQORVE IITAKEGHPS VNWLYEGWVK SNKAIGKIRA
501 YIRQONADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSETTI VKQSKIKKGG KNGVLIDGED
601 GLMTTLAKKC KPAPPDDIVG FVTRDRGISV HRKTCPSFRH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVTDLPR VLASLGDKVG VLSVTRL*

```

a117-1/m117-1 97.7% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFD SYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
a117-1	MTAISPIQDTQSATLQELREWFD SYCTALPNNDKKLVLAARSLAEAHYPADAATPYGEPL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m117-1.pep	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK					
a117-1	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m117-1.pep	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEK					
a117-1	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m117-1.pep	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGRHQEPEKYREIALLLDEKRTERLEYIEN					
a117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGRHQEPEKYREIALLLDEKRTERLEYIEN					
	190	200	210	220	230	240

m117-1.pep	250	260	270	280	290	300
	FLNILRGELKKYNVHFEVAGRPKHIYSIYKKMVKKKLSFDGLFDIRAVRILVDTVPECYT					
a117-1	250	260	270	280	290	300
	FLNILRTELKKYNIHFEVAGRPKHIYSIYKKMVKKKLSFDGLFDIRAVRILVDTVPECYT					
m117-1.pep	310	320	330	340	350	360
	TLGIVHSLWQPIPGFDDYIANPKGNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV					
a117-1	310	320	330	340	350	360
	TLGIVHSLWQPIPGFDDYIANPKGNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV					
m117-1.pep	370	380	390	400	410	420
	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPH					
a117-1	370	380	390	400	410	420
	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPH					
m117-1.pep	430	440	450	460	470	480
	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS					
a117-1	430	440	450	460	470	480
	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS					
m117-1.pep	490	500	510	520	530	540
	VNWLYEGWVKSNAIGKIRAYIRQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY					
a117-1	490	500	510	520	530	540
	VNWLYEGWVKSNAIGKIRAYIRQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY					
m117-1.pep	550	560	570	580	590	600
	KKPEDLYTAVGQGEISNRAIQKACGTLENEPPVPVSETTIVKQSKIKKGGKNGVLIDGED					
a117-1	550	560	570	580	590	600
	KKPEDLYTAVGQGEISNRAIQKACGTLENEPPVPVSETTIVKQSKIKKGGKNGVLIDGED					
m117-1.pep	610	620	630	640	650	660
	GLMTTLAKCKKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDAASWAALQEG					
a117-1	610	620	630	640	650	660
	GLMTTLAKCKKPAPPDDIIGFVTRDRGISVHRKTCPSFRHLAEHAPEKVLDAASWAALQEG					
m117-1.pep	670	680	690	700	710	720
	QVFAVDIEIRAQDRSGLLRDVSALARHKLNVAVQTQSRDLEASMRFTLEVQVNDLPR					
a117-1	670	680	690	700	710	720
	QVFAVDIEIRAQDRSGLLRDVSALARHKLNVAVQTQSRDLEASMRFTLEVQVNTDLPR					
m117-1.pep	730					
	VLASLGDKGVLSVTRLX					
a117-1	730					
	VLASLGDKGVLSVTRLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 423>:

```

g118.seq
1   ATGTGCGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
51  TGACGAAAAT TCATTTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAGCTG GAGAATGATT TAATcgaGGT TAGGAGAAAA
151 TATCCTTATC CGATGGATAT ACCAAGGGAT ATTGTGATTG GAATCGGTAC
201 CATTATTGAT TTTTAAATGG TTCCAAATTG GGAGCTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCCTGAT AGCGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAaCA AAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 424; ORF 118.ng>:

```

g118.pep
1   MCEFKDFRRN IPCFEEYDEN SFIGKWYDDG VWDDEEYWKI ENDLIEVRRK
51  YPYPMIDIPRD IVIGIGTIID FLMVPNWELF EIKASPWLPD SVGIHERYER
101 FTTMLRYIFT EKDIVNVRFD YYNKK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 425>:

```
m118.seq
  1 ATGTGTGAGT TCAAGGATAT TATAAGAAAC GTTCCTTATT TTGAGGGGTA
  51 TGACGAAAAT TCATTTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
 101 ATGAAGAATA TTGGAAGTTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
 151 TATCCTTATC CGATGGACAT ACCAAGATAT GTTGTGATTG GAATCGGTAC
 201 CATTATTGAT TTCTTAATGG TTCCAAATTG GAAACTTTTT GAAATTAAAG
 251 CTTCCCTTGT GTTGCCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
 301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
 351 GCGATTTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 426; ORF 118>:

```
m118.pep
  1 MCEFKDIIRN VPFYFEGYDEN SFIGKWYDDG VWDDEEYWKLENDLIEVRKK
  51 YPYPM DIPRY VVIGIGTIID FLMVPNWKL EIKAS PWLPD SVGIHERYER
 101 FTTMLRYIFT EKDIVNVREFD YYNKK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 118 shows 92.8% identity over a 125 aa overlap with a predicted ORF (ORF 118.ng) from *N. gonorrhoeae*:

```
m118/g118

      10      20      30      40      50      60
m118.pep MCEFKDIIRNVPFYFEGYDENSFIGKWYDDGVWDDEEYWKLENDLIEVRKKYPYPMDIPRY
          |||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||:|||||
g118      MCEFKDFRRNIPCFEEDENSFIGKWYDDGVWDDEEYWKLENDLIEVRKKYPYPMDIPRD
          10      20      30      40      50      60

      70      80      90      100     110     120
m118.pep VVIGIGTIIDFLMVPNWKLFEIKAS PWLPDSVGIHERYERFTTMLRYIFTEKDIVNVREFD
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g118      IVIGIGTIIDFLMVPNWELFEIKAS PWLPDSVGIHERYERFTTMLRYIFTEKDIVNVREFD
          70      80      90      100     110     120

m118.pep YYNKKX
          |||||
g118      YYNKKX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 427>:

```
a118.seq
  1 ATGTGTGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
  51 TGACGAAAAT TCATTTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
 101 ATGAAGAATA TTGGAATTTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
 151 TATCCTTATC CGATGGATAT ACCAAGGGAT ATTGTGATTG GAATCGGTAC
 201 CATTATTGAT TTTTAAATGG TTCCAAATTG GGAGCTTTTT GAAATTAAAG
 251 CTTCCCTTGT GTTGCCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
 301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
 351 GCGATTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 428; ORF 118.a>:

```
a118.pep
  1 MCEFKDFRRN IPCFEEYDEN SFIGKWYDDG VWDDEEYWKLENDLIEVRKK
  51 YPYMDIPRD IVIGIGTIID FLMVPNWELF EIKAS PWLPD SVGIHERYER
 101 FTTMLRYIFT EKDIVNVREFD YYNKK*
```

m118/a118 93.6% identity in 125 aa overlap

```
      10      20      30      40      50      60
m118.pep MCEFKDIIRNVPFYFEGYDENSFIGKWYDDGVWDDEEYWKLENDLIEVRKKYPYPMDIPRY
          |||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||
a118      MCEFKDFRRNIPCFEEDENSFIGKWYDDGVWDDEEYWKLENDLIEVRKKYPYPMDIPRD
          10      20      30      40      50      60
```

341

	70	80	90	100	110	120
m118.pep	VVIGIGTIIDFLMVPNWKLF EIKAS PWLPDSVGIHERYERFTT MLRYIFTEKDIVNVRFD					
	: : : : : : :					
a118	IVIGIGTIIDFLMVPNWELFEIKAS PWLPDSVGIHERYERFTT MLRYIFTEKDIVNVRFD					
	70	80	90	100	110	120
m118.pep	YYNKKX					
a118	YYNKKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 429>:

```

g120.seq
1  ATGATGAAGA CTTTTAAAAA TATATTTTCC GCCGCCATTT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAAGGCTACC CCAATCCGCC GTGCTGCACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTTGA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAATCC GGCGGTACGG TTGTCGGCAA TACCCTGCAC CCTGCCTACT
251 ATAAAGACAT ACGCAGGGGC AAACGTATG CGGAAGCCAA ATTCCCGGAC
301 GGCAGCGTAA CCTACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTTGTTCA CGCTTGCCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGTCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGCC TGAATAAGGC GGGTACGGGA AAATACAGCA Taggcggcgt
501 gGAAACCGAA GTCGTCAAAT ATCGGGTGCG GCGCGGCGAC GATACGGTAA
551 CGTATTTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGAcgaCG GCAAAACCTA TACGCTGAAG CTCAAATCGG TGCAGATCAA
651 CGGACAGGCC GCCAAACCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 430; ORF 120.ng>:

```

g120.pep
1  MMKTFKNIFS AAILSAAALPC AYAARLPQSA VLHYSGSYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNTLH PAYYKDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DTVTYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 431>:

```

m120.seq
1  ATGATGAAGA CTTTTAAAAA TATATTTTCC GCCGCCATTT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGmACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTTGA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAGTCC GGCGGTACGG TTGTCGGCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AAACGTATG CGGAAGCcAA ATTCCCGGAC
301 GGCAGCGTAA CTTACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTTGTTCA CGCTTGCCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGGCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGTT TGAATAAGGC GGGTACAGGA AAATACAGCA TAGGCGGCGT
501 GGAAACCGAA GTCGTCAAAT ATCGGGTGCG GCGCGGCGAC GATGCGGTAA
551 TGTATTTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAAACCTA TACGCTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCG

```

This corresponds to the amino acid sequence <SEQ ID 432; ORF 120>:

```

m120.pep
1  MMKTFKNIFS AAILSAAALPC AYAAGLPQSA VLXYSYSGYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNTLH PTYYRDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DAVMYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 120 shows 97.3% identity over a 223 aa overlap with a predicted ORF (ORF 120.ng) from *N. gonorrhoeae*:

m120/g120

	10	20	30	40	50	60
m120.pep	MMKTFKNIFS	AAILSAA	LPCAYA	AGLPQSA	VLHYS	SGSYGI
g120	MMKTFKNIFS	AAILSAA	LPCAYA	ARLPQSA	VLHYS	SGSYGI
	10	20	30	40	50	60
	70	80	90	100	110	120
m120.pep	VPLYNIRFES	GGTVVGN	TLHPTYY	RDIRRG	KLYAEAK	FADGSV
g120	VPLYNIRFES	GGTVVGN	TLHPAYY	KDIRRG	KLYAEAK	FADGSV
	70	80	90	100	110	120
	130	140	150	160	170	180
m120.pep	DLFTLAWQLA	ANDAKLP	PGLKITN	GKKLYS	VGGLNK	AGTGKYS
g120	DLFTLAWQLA	ANDAKLP	PGLKITN	GKKLYS	VGGLNK	AGTGKYS
	130	140	150	160	170	180
	190	200	210	220		
m120.pep	DAVMYFFAP	SLNNIPA	QIGYTDD	GKTYTL	KLKSVQ	INGQA
	:					
g120	DTVTYFFAP	SLNNIPA	QIGYTDD	GKTYTL	KLKSVQ	INGQA
	:					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 433>:

a120.seq

```

1  ATGATGAAGA CTTTAAAAA TATATTTTCC GCCGCCATTT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGCACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTTGA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAGTCC GGCGGTACGG TTGTCCGGCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AAATGTATG CGGAAGCCAA ATTCGCCGAC
301 GGCAGCGTAA CCTACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAAAGCCC
351 CAAGGCTATG GATTTGTTCA CGCTTGCC TGAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGGCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGTT TGAATAAGGC GGGTACAGGA AAATACAGCA TAGGCGGCGT
501 GGAAACCGAA GTCGTCAAAT ATCGGGTGCG GCGCGGCGAC GATGCGGTAA
551 TGTATTTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAAACCTA TACGCTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 434; ORF 120.a>:

a120.pep

```

1  MMKTFKNIFS AAILSAA LPCAYA AYAAGLPQSA VLHYS GSYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGN TLHPTYYRDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLP PGLKITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DAVMYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP*

```

m120/a120 99.6% identity in 223 aa overlap

	10	20	30	40	50	60
m120.pep	MMKTFKNIFS	AAILSAA	LPCAYA	AGLPQSA	VLHYS	SGSYGI
a120	MMKTFKNIFS	AAILSAA	LPCAYA	AGLPQSA	VLHYS	SGSYGI

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	10	20	30	40	50	60
m120.pep	70	80	90	100	110	120
	VPLYNIRFESGGTVVGN	TLHPTYYRDIRRGKLYAEAKFADGS	SVTYGKAGESKTEQSPKAM			
a120	70	80	90	100	110	120
	VPLYNIRFESGGTVVGN	TLHPTYYRDIRRGKLYAEAKFADGS	SVTYGKAGESKTEQSPKAM			
m120.pep	130	140	150	160	170	180
	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE	VVKYRVRRGD				
a120	130	140	150	160	170	180
	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE	VVKYRVRRGD				
m120.pep	190	200	210	220		
	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAKPX					
a120	190	200	210	220		
	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAKPX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 435>:

g121.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATTATG TCGGGAACCA GTATGGACGG
51  GGCGGATGCC GTGCTGGTAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCTGACC GGTTCGCGCG CAAATTGCTG
151 GATTTCAGG ACACAGGCAC AGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCTCCGTGC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTtac AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACtGa cgcggatttt TACCGTCggc gacttcCGCA
401 GCCGCGACCT TGCTGCCGGC GGacaAGGTG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCCGCGA TGACAGGGAA ACACGCGTGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCGCCTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGAcgcgtg gacgcaggca
601 cacTGGcagc TGCCTTACGA CAAAAacggt gcAAAGgcgg cacAAGGCAA
651 catatTGCcg cAACTGCTCG gcaggctGCT CGCCcaccCG TATTTCTCAC
701 AACCCcacc aaAAAGCACG GGgcGCCaac Tgtttgccct AAattggctc
751 gaaacctAcc ttgacggcgg cgaaaaccga tacgacgtat tgcggacgct
801 ttcccgattc accgcgcaaA ccgTttggga cgccgtctca CACGAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCTCAATG GGTGGAGGCG gccgCATttg
1001 cgtggttgC GCGTGTtGG ATTAACGCA TTCCCGGTAG TCCGCACAAA
1051 GCGACCGGCG CATCCAAACC GTGTATTCTG GGCGGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 436; ORF 121.ng>:

g121.pep

```

1  METQLYIGIM SGTSMDGADA VLVRMDGGKW LGAEGHAFTP YPDRLRRKLL
51  DLQDTGTDEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPC DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AELTRIFTVG DFRSRDLAAG GQGAPLVPFAP
151 HEALFRDDRE TRVVLNIGGI ANISVLPPGA PAFGFDTPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLGRLLAHP YFSQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVWDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AFAFWLAACW INRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 437>:

m121.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTACGCGC CCAATTGCTG

```

```

151 GATTTGCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTG
201 GCAAGAACTC AGCCGCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCCTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATAACAGC TTGCCGATT
351 GCCGTGCTG GCGxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxGAGC TTCCTTACGA CAAAACGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACGCCACCC TAAAGACACG GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCCGTCTCA CACGACGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 438; ORF 121>:

m121.pep

```

1 METQLYIGIM SGTSMGDGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRQLL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPHEGY SIQLADLPLL Axxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
151 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDAYS HAAADARQMY ICDGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDGADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLLDLQDTGADEL					
g121	METQLYIGIMSGTSMGDGADAVLVRMDGGKWLGAEGHAFTPYPDRLLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
m121.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPHEGYYSIQLADLPLL					
g121	HRSRMLSQELSRLYAQTAAELLCSQNLAPCDITALGCHGQTVRHAPHEGYYSIQLADLPLL					
	70	80	90	100	110	120
m121.pep	AXXX					
g121	AELTRIFTVGDFRSRDLAGGQGAPLVPAFHEALFRDDRETRVVLNIGGIANISVLPPGA					
	130	140	150	160	170	180
m121.pep	XXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
g121	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST					
	190	200	210	220	230	240
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDAYSHAAADARQMYICDGGIRNPV					
g121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDAYSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
g121	LMADLAECFGTRVSLHSTAE LNLDPOWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYYX					
g121	GAGYYYYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 439>:

```

a121.seq
1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTACGCCG CAAATTGCTG
151 GATTTGCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGGCGCCGC GGACAAGGCG CGCCGCTCGT CCGCGCCTTT
451 CACGAAGCCC TGTTCGCGCA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCGCGACGCA CCGGCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCCG TATTTTCGCAC
701 AACCCACACC TAAAGACACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATTG ACCGCGCAAA CCGTTTTTCG CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCG
1001 CATGGATGGC GGCGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG GGCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 440; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRRLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPESHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPGP NMLMDAWMQA
201 HWQLPYDKNG AKAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AFAWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

m121/a121 74.0% identity in 366 aa overlap

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL					
a121	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL					
	10	20	30	40	50	60
m121.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPESHSYQLADLPLL					
a121	HRSRMLSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPESHSYQLADLPLL					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m121.pep	XX					
a121	: : : :					
	130	140	150	160	170	180
	AERTQIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	190	200	210	220	230	240
m121.pep	XXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
a121	: : : : : :					
	190	200	210	220	230	240
	PAFGFDTGPGNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	250	260	270	280	290	300
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADARQMYICDGGIRNPV					
a121	: : : : :					
	250	260	270	280	290	300
	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVFVDAVSHAAADARQMYICGGGIRNPV					
	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
a121	: : : : :					
	310	320	330	340	350	360
	LMADLAECFGTRVSLHSTAE LNLDPOWVEAAAFWMAACWVNRI PGSPHKATGASKPCIL					
m121.pep	XAGYYYY					
a121						
	GAGYYYY					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 441>:

m121-1.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCAGCG CTTTACCCCC TACCCCGGCA GGTACGCCG CCAATTGCTG
151 GATTTGCAGG ACACAGCGCG AGACGAAC TG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATAACG TTGCCGATTT
351 GCCGTGCTG GCGGAACGGA CGCGGATTTT TACCGTCGCG GACTTCCGCA
401 GCCGCGACCT TGCGGCCGCG GGACAAGGCG CGCCACTCGT CCCC GCCTTT
451 CACGAAGCCC TGTTCGCGCA CAACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCC GACGCA CCGCCTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGACGCGTG GACGCGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACCCACCC TAAAAGCAGC GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGCGCG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCCGTCTCA CACGCGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGNATTG
1001 CGTGGTTGGC GCGGTGTTG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGCGC CATCCAAACC GTGTATTCTG ANCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 442; ORF 121-1>:

m121-1.pep

```

1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLRRQLL
51  DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPHEGY SIQLADLPLL AERTRIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNLW
251 ETYLDGGENR YDVLRTLSRF TAQTVCDVSH AAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

m121-1/g121 95.6% identity in 366 aa overlap

10 20 30 40 50 60

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```

m121-1.pep  METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTFPYGRRLRRQLLDLQDTGADEL
              |||||
g121         METQLYIGIMSGTSMGDADAVLVRMDGGKWLGAEGHAFTFPYDRLRRKLLDLQDTGTDEL
              10      20      30      40      50      60

              70      80      90      100     110     120
m121-1.pep  HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL
              |||||
g121         HRSRMLSQELSRLYAQTAAELLCSQNLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL
              70      80      90      100     110     120

              130     140     150     160     170     180
m121-1.pep  AERTRIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDNRETRAVLNIGGIANISVLPPDA
              |||||
g121         AELTRIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDDRETRVVLNIGGIANISVLPPGA
              130     140     150     160     170     180

              190     200     210     220     230     240
m121-1.pep  PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST
              |||||
g121         PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST
              190     200     210     220     230     240

              250     260     270     280     290     300
m121-1.pep  GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADARQMYICGGGIRNPV
              |||||
g121         GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDVSHAAADARQMYICGGGIRNPV
              250     260     270     280     290     300

              310     320     330     340     350     360
m121-1.pep  LMADLAECFGTRVSLHSTADLNLDPPQWVEAAFAWLAACWINRIPGSPHKATGASKPCIL
              |||||
g121         LMADLAECFGTRVSLHSTAE LNLDPPQWVEAAFAWLAACWINRIPGSPHKATGASKPCIL
              310     320     330     340     350     360

m121-1.pep  XAGYYYYX
              |||||
g121         GAGYYYYX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 443>:

```

a121-1.seq
1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCCG CAAATTGCTG
151 GATTTCGAGG ACACAGGCGC GGACGAAC TG CACCGCAGCA GGATGTGTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TGCGGCCGGC GGACAAGGCG CGCCGCTCGT CCCC GCCTTT
451 CACGAAGCCC TGTTCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGGAT GCCAACATCA GCGTACTCCC CCCC GACGCA CCGCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCGG TATTTGCGAC
701 AACCCACCCC TAAAAGCACG GGGCGCGAAC TGTTCGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGATTC ACCGCGCAAA CCGTTTTCGA CGCCGTCTCA CACGACGCGG
851 CAGATGCCCC TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCTG
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCAAAC GTGTATTCTG GGGCGGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 444; ORF 121-1.a>:

```

a121-1.pep
1  METQLYIGIM SGTSMDGADA VLIRMDGGKW LGAEGHAFTF YPGRRLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWMQA

```

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201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
 251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
 301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK
 351 ATGASKPCIL GAGYYY*

m121-1/a121-1 96.4% identity in 366 aa overlap

m121-1.pep	10	20	30	40	50	60
	METQLYIGIMSGTSM	DGADAVLIRMDGGK	WLGAEGHAFTPYPG	RRLRRQLLDLQDT	GADEL	
a121-1	METQLYIGIMSGTSM	DGADAVLIRMDGGK	WLGAEGHAFTPYPG	RRLRRQLLDLQDT	GADEL	
	10	20	30	40	50	60
m121-1.pep	70	80	90	100	110	120
	HRSRILSQELSR	LYAQTAELLCSQNL	APSDITALGCHGQ	TVRHAPEHGYSIQ	LADLPLL	
a121-1	HRSRILSQELSR	LYAQTAELLCSQNL	APSDITALGCHGQ	TVRHAPEHGYSIQ	LADLPLL	
	70	80	90	100	110	120
m121-1.pep	130	140	150	160	170	180
	AERTRIFTVGDF	RSRDLAAGGQGA	PLVPAPFHEALFR	DNRETRAVLNIG	GIANISVLP	PPDA
a121-1	AERTRIFTVGDF	RSRDLAAGGQGA	PLVPAPFHEALFR	DDRETRAVLNIG	GIANISVLP	PPDA
	130	140	150	160	170	180
m121-1.pep	190	200	210	220	230	240
	PAFGFDTGPGN	MLMDAWTQAHWQ	LPYDKNGAKAAQ	GNILPQLLDRL	LAHPYFAQPH	PKST
a121-1	PAFGFDTGPGN	MLMDAWTQAHWQ	LPYDKNGAKAAQ	GNILPQLLDRL	LAHPYFAQPH	PKST
	190	200	210	220	230	240
m121-1.pep	250	260	270	280	290	300
	GRELFALNWLE	TYLDGGENRYD	VLRTLSRFTAQ	TVCDVASHAA	ADARQMYICG	GGGIRNPV
a121-1	GRELFALNWLE	TYLDGGENRYD	VLRTLSRFTAQ	TVFVASHAA	ADARQMYICG	GGGIRNPV
	250	260	270	280	290	300
m121-1.pep	310	320	330	340	350	360
	LMADLAECFG	TRVSLHSTAD	LNLDLPQWVEA	AXFAWLAAC	WINRIPGSP	HKATGASKPCIL
a121	LMADLAECFG	TRVSLHSTAE	LNLDLPQWVEA	AAFAWMAAC	WVNRIPGSP	HKATGASKPCIL
	310	320	330	340	350	360
m121-1.pep	XAGYYYYX					
a121	GAGYYYYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 445>:

g122.seq

```

1  ATGGCTTTAC TGAGCATCCG CAAGCTGCAC AAACAATACG GCAGCGTAAC
51  CGCCATCCAA TCCTTAGACT TGGACTTGGA AAAAGGCGAA GtcatCGTAC
101 TGCTGGGCCC gTccggctgc ggCAAATCCA CCTCctgcg ctgcgtaaaC
151 GGTTTGGAGC CGCACCAagg cgGCAGCATC GTGATGGACG GTgtcgGCGA
201 ATTcggcAAA GACGTTTCCT GGCAAACCGC CCGGCAAAAa gtcggtatgg
251 tctttcaaaag taacgAactg Tttgcccaca tgaccgtcat cgAaaacatc
301 ttcttAggcC CGGTAAagga aCAAAAcGgc gaccgtgccg aagcaGAGGC
351 gCAAGCCGGC AAactGttgg aacgcgTCGG actgctAGAC CGCAAAAACG
401 CCTATCCGCG CGAACTTTCC GGCGGTCAGA AACAGCGCAT CGCCATTGTC
451 CGCGCCCTGT GCCTGAATCC GGAAGTCATC CTGCTGGACG AAATCACCGC
501 CGCACTTGAC CCCGAAATGG TGC GCGAAGT CTTGGAAGTG GTTTTGAAC
551 TCGCCCGCGA AGGGATGAGT ATGCTCATCG TAACCCACGA AATGGGGTTC
601 GCACGCAAAG TTGCCGACCG CATCGTCTTT ATGGACAAAG GCGGCATCGT
651 CGAATCGTCC GACCCCGAAA CCTTTTTC CGACCAAAA AGCGAACGCG
701 CCCGCCAATT TCTGGCAGGT ATGACTACT GA
```

This corresponds to the amino acid sequence <SEQ ID 446; ORF 122.ng>:

g122.pep
 1 MALLSIRKLH KQYGSVTAIQ SLDLDLEKGE VIVLLGPSGC GKSTLLRCVN
 51 GLEPHQGGSI VMDGVGEFGK DVSWQTARQK VGMVFQSNEL FAHMTVIENI
 101 FLGPVKEQNR DRAEAEAQAG KLLERVGLLD RKNAYPRELS GGQKQRIAI
 151 RALCLNPEVI LLDEITAALD PEMVREVLEV VLELAREGMS MLIVTHEMGF
 201 ARKVADRIVE MDKGGIVESS DPETFFSAPK SERARQFLAG MDY*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 447>:

m122.seq
 1 GTTGTTCATGA TTAAATCCG CAATATCCAT AAGACCTTTG GCGAAAACAC
 51 TATTTTGGCG GGCATCGATT TGGATGTGTG CAAAGGGCAG GTGGTCGTCA
 101 TCCTCGGGcC TTCCGGCTCA GGCAAAACGA CGTTTCTGCG ATGCCTAAAC
 151 GCGTTGGAAA TGCCCGAAGA CGGACAAATC GAGTTCGACA ACGAGCGACC
 201 GCTGAAAATC GATTTTCTA AAAAACCAAG CAAACACGAT ATTTTGGCAC
 251 TGCGCCGCAA ATCAkGCATG GTGTTTCAAC AATACAyCT CTTTCCGCAC
 301 AAAACCGCCT TGGAAAACGT AATGGAAGGA CCGGTTGCCG TACAgGGCAA
 351 GCCTGCCGCC CAAGCGCGCG AAGAGGCTCT GAAACTGCTG GAAAAAGTCG
 401 GCTTGGGCGA CAAAGTGGAT TTGTATCCCT ACCAGCTTTC CGGCGGTCAG
 451 CAGCAGCGCG TCGGCATTGC CCGCGCATTG GCGATTCAGC CTGAAGTATG
 501 GCTGTTTGAC GAACCGACTT CCGCGCTCGA TCCTGAATTG GTGCAAGATG
 551 TTTTGGATmC CATGAAGGAA TTGGCGCAAG AAGGCTGGAC CATGGTTGTC
 601 GTTACGCATG AAATCAAGTT CGCCTTAGAA GTGGCAACCA CCGwCGTCGT
 651 GATGGACrGC GCGGTTATTG TCGAACAGG CAGCCCGCAA GATTGTTCG
 701 ACCACCCCAA ACACGAACGG ACGCGGAGAT TTTTAAGCCA AATCCAATCT
 751 ACCAAGATTT GA

This corresponds to the amino acid sequence <SEQ ID 448; ORF 122>:

m122.pep
 1 VVMIKIRNIH KTFGENTILR GIDL DVCKGQ VVILGPSGS GKTTFLRCLN
 51 ALEMPEDGQI EFDNERPLKI DFSKKPSKHD ILALRRKSXM VFQQYNLFPH
 101 KTALENVMEG PVAVQGPAA QAREEALKLL EKVGLGDKVD LYPYQLSGGQ
 151 QQRVGIARAL AIQPELMLFD EPTSALDPEL VQDVLDMKE LAQEGWTMVV
 201 VTHEIKFALE VATTXVMDX GVIVEQGSPO DLFDPKHER TRRFLSQIQS
 251 TKI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 122 shows 47.2% identity over a 246 aa overlap with a predicted ORF (ORF 122.ng) from *N. gonorrhoeae*:

m122/g122

	10	20	30	40	50	60
m122.pep	VVMIKIRNIHKTFFGENTILRGIDL DVCKGQVVILGPSGSGKTTFLRCLNALEMPEDGQI					
g122	MALLSIRKLHKQYGSVTAIQSLDLDLEKGEVIVLLGPSGCGKSTLLRCVNGLEPHQGGSI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m122.pep	EFDNERPLKIDFSKKPSKHDILALRRKSXMVFQQYNLFPHKTALENVMEGPAVAVQGPAA					
g122	VMDGVGEFGKDVSWQTA-----RQKVMVFQSNELFAHMTVIENIFLGPVKEQNRDRA					
	70	80	90	100	110	
	130	140	150	160	170	180
m122.pep	QAREEALKLLEKVGLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSALDPEL					
g122	EAEAQAGKLLERVGLLDKRNAYPRELSGGQKQRIAIVRALCLNPEVILLDEITAALDPEM					
	120	130	140	150	160	170
	190	200	210	220	230	240
m122.pep	VQDVLDMKELAQEGWTMVVVTHEIKFALEVATTXVMDXGVIVEQGSPODLFDHPKHER					
g122	VREVLEVLELAREGMSMLIVTHEMGFARKVADRIVFMDKGGIVESSDPETFFSAPKSER					

350

	180	190	200	210	220	230
		250				
m122.pep	TRRFLS	QIQSTKIX				
	:	:	:	:	:	:
g122	ARQFLAGMDYX					
	240					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 449>:

```

a122.seq
1   GTTGTTCATGA TTAAATCCG CAATATCCAT AAGACCTTCG GCAAAAATAC
51  CATTTTGC GC CATCAATT TGGATGTGTG CAAAGGGCAG GTGGTCGTCA
101 TCCTCGGGCC TTCCGGCTCA GGCAAAACGA CGTTTCTGCG ATGCCTAAAC
151 GCGTTGGAAG TGCCCGAAGA CGGACAAATC GAGTTCGACA ACGAGCGACC
201 GCTGAAAATC GATTTTCTA AAAAACCAAG CAAACACGAT ATTTTGGCAC
251 TGCGCCGCAA ATCAGGCATG GTGTTTCAAC AATACAACCT CTTTCCGCAC
301 AAAACCGCCT TGGAAAACGT GATGGAAGGA CCGGTTGCCG TACAGGGCAA
351 GCCTGCCGCC CAAGCGCGCG AAGAGGCTCT GAAACTGCTG GAAAAAGTCG
401 GCTTGGGCGA CAAAGTGGAT TTGTATCCCT ACCAGCTTTC CGGCGGTCAG
451 CAGCAGCGCG TCGGCATTGC CCGAGCATTG GCGATTACAG CCGAGCTGAT
501 GTTGTTTGAC GAACCCACTT CCGCGCTTGA CCCCAGATTG GTGCAAGACG
551 TGTTGAACGC CATGAAGGAA TTGGCGCGGG AAGGTTGGAC GATGGTCGTC
601 GTTACCCACG AAATCAAGTT CGCGCTGGAA GTTGCCACGA CCGTTGTCGT
651 GATGGACGGC GCGGTTATCG TAGAGCAGGG CAGCCCGAAA GAGTTGTTTCG
701 ACCACCCCAA ACACGAACGG ACGCGGAGAT TTTTAAGCCA AATCCAATCT
751 ACCAAGATTT GA

```

This corresponds to the amino acid sequence <SEQ ID 450; ORF 122.a>:

```

a122.pep
1   VVMIKIRNIH KTFGKNTILR GINLDVCKGQ VVILGPSGS GKTTFLRCLN
51  ALEMPEDGQI EFDNERPLKI DFSKKPSKHD ILALRRKSGM VFQQYNLFPH
101 KTALENVMEG PVAVQGKPAA QAREEALKLL EKVGLGDKVD LYPYQLSGGQ
151 QQRVGIARAL AIQPELMLFD EPTSALDPEL VQDVNLAMKE LAREGWTMVV
201 VTHEIKFALE VATTVVVMDG GVIVEQGS PK ELFDHPKHER TRRFLS QIQS
251 TKI*

```

m122/a122 96.0% identity in 253 aa overlap

	10	20	30	40	50	60
m122.pep	VVMIKIRNIHKT	FGENTILRGID	LDVCKGQVVV	ILGPSGSGKT	TFRLCLNALE	MPEDGQI
a122	VVMIKIRNIHKT	FGKNTILRGIN	LDVCKGQVVV	ILGPSGSGKT	TFRLCLNALE	MPEDGQI
	70	80	90	100	110	120
m122.pep	EFDNERPLKID	FSKKPSKHDIL	ALRRKSXMVF	QQYNLFPHKTA	LENVMEG	PVAVQGKPAA
a122	EFDNERPLKID	FSKKPSKHDIL	ALRRKSGMVF	QQYNLFPHKTA	LENVMEG	PVAVQGKPAA
	130	140	150	160	170	180
m122.pep	QAREEALKLLE	KEVGLGDKVD	LYPYQLSGGQ	QQRVGIARAL	AIQPELMLFD	EPTSALDPEL
a122	QAREEALKLLE	KEVGLGDKVD	LYPYQLSGGQ	QQRVGIARAL	AIQPELMLFD	EPTSALDPEL
	190	200	210	220	230	240
m122.pep	VQDVLDMKELA	QEGWTMVVV	THEIKFALE	VATTXVMDXG	VIVEQGS	PQDLFDHPKHER
a122	VQDVNLAMKE	LAREGWTMVVV	THEIKFALE	VATTVVVMDG	GVIVEQGS	PKELFDHPKHER
	250					
m122.pep	TRRFLS	QIQSTKIX				

351

a122 |||||
 TRRFLSQIQSTKIX
 250

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 451>:

g122-1.seq
 1 ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACCATTTT
 51 GCGCGGCATC GATTTGATG TGGGCAAAGG GCAGGTGGTC GTCATCCTCG
 101 GGCCTTCCGG CTCGGGTAAA ACAACATTTC TGCCTGCCT AAACGCGTTG
 151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGCGC GGCCGTTACG
 201 CATTGATTTT TCCAAAAAAA CAAGCAAACA CGATATTTTG GCACTGCGCC
 251 CCAAGTCCGG AATGGTATTC CAACAATACA ACCTCTTCCC GCATAAAACC
 301 GTGTTGAAA ACGTGATGGA AGGGCCGGT GCCGTACAGG GCAAGCCTGC
 351 CGCCCAAGCG CGCGAAGAGG CTTTGAAACT GCTGGA AAAA GTCGGCTTGG
 401 GCGATAAAGT GGATTGTAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG
 451 CGTGTCGGTA TCGCCCGCGC ACTGGCGATT CAGCCTGAAT TGATGCTGTT
 501 TGACGAACCC ACTTCCGCGC TGGACCCCGA GTTGGTGCAA GACGTGTTGG
 551 ACGCCATGAA GGAATTGGCG CGGGAAGGTT GGACGATGGT CGTCGTTACC
 601 CACGAAATCA AGTTCACGCT GGAAGTTGCC ACGAACGTCG TCGTGATGGA
 651 CGGCGGCGTT ATCGTAGAGC AGGGCAGCCC GAAAGAGTTG TTCGACCACC
 701 TCAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTGCCAAG
 751 ATTTGA

This corresponds to the amino acid sequence <SEQ ID 452; ORF 122-1.ng>:

g122-1.pep
 1 MIKIRNIHKT FGENTILRGI DLDVGKGQVV VILGPSGSGK TTFLRCLNAL
 51 EMPEDGQIEF DNARPLRIDF SKKTSKHDIL ALRRKSGMVF QQYNLFPHKT
 101 VLENVMEGPV AVQGKPAAQA REEALKLLEK VGLGDKVDLY PYQLSGGQQQ
 151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDMKELA REGWTMVVVT
 201 HEIKFTLEVA TNVVVMDGGV IVEQGSPKEL FDHLKHERTR RFLSQIQSAK
 251 I*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 453>:

m122-1.seq
 1 ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA AACTATTTT
 51 GCGCGGCATC GATTTGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG
 101 GGCCTTCCGG CTCAGGCAAA ACGACGTTTC TGCATGCCT AAACGCGTTG
 151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGAGC GACCGCTGAA
 201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTTG GCACTGCGCC
 251 GCAATCAGG CATGGTGTTC CAACAATACA ACCTCTTCCC GCACAAAACC
 301 GCCTTGAAA ACCTAATGGA AGGACCGGTT GCCGTACAGG GCAAGCCTGC
 351 CGCCCAAGCG CGCGAAGAGG CTCTGAAACT GCTGGA AAAA GTCGGCTTGG
 401 GCGACAAAGT GGATTGTAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG
 451 CGCGTCGGCA TTGCCCGCGC ATTGGCGATT CAGCCTGAAC TGATGCTGTT
 501 TGACGAACCG ACTTCCGCGC TCGATCCTGA ATTGGTGCAA GATGTTTGG
 551 ATACCATGAA GGAATTGGCG CAAGAAGGCT GGACCATGGT TGTGTTTACG
 601 CATGAAATCA AGTTCGCCTT AGAAGTGGCA ACCACCGTCG TCGTGATGGA
 651 CGGCGGCGTT ATTGTGCAAC AAGGCAGCCC GCAAGATTG TTCGACCACC
 701 CCAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTACCAAG
 751 ATTTGA

This corresponds to the amino acid sequence <SEQ ID 454; ORF 122-1>:

m122-1.pep
 1 MIKIRNIHKT FGENTILRGI DLDVCKGQVV VILGPSGSGK TTFLRCLNAL
 51 EMPEDGQIEF DNERPLKIDF SKKPSKHDIL ALRRKSGMVF QQYNLFPHKT
 101 ALENVMEGPV AVQGKPAAQA REEALKLLEK VGLGDKVDLY PYQLSGGQQQ
 151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDTMKELA QEGWTMVVVT
 201 HEIKFALEVA TTVVVMDGGV IVEQGSPQDL FDHPKHERTR RFLSQIQSTK
 251 I*

m122-1/g122-1 94.8% identity in 251 aa overlap

	10	20	30	40	50	60
m122-1.pep	MIKIRNIHKT	FGENTILRGI	DLDVCKGQVV	VILGPSGSGK	TTFLRCLNAL	EMPEDGQIEF
g122-1	MIKIRNIHKT	FGENTILRGI	DLDVGKGQVV	VILGPSGSGK	TTFLRCLNAL	EMPEDGQIEF

352

	10	20	30	40	50	60
m122-1.pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFFQYNLFPHKTALENVMEGPPVAVQGKPAAQA					
g122-1	DNERPLRIDFSKKTSKHDILALRRKSGMVFFQYNLFPHKTVLENVMEGPPVAVQGKPAAQA					
	70	80	90	100	110	120
m122-1.pep	130	140	150	160	170	180
	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSAIDPELVQ					
g122-1	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSAIDPELVQ					
	130	140	150	160	170	180
m122-1.pep	190	200	210	220	230	240
	DVLDTMKELAQEGWTMVVVTHEIKFALEVATTVVVMDGGVIVEQGSQDLFDHPKHERTR					
g122-1	DVLDTMKELAQEGWTMVVVTHEIKFTLEVATNVVMDGGVIVEQGSQDLFDHPKHERTR					
	190	200	210	220	230	240
m122-1.pep	250					
	RFLSQIQSTKIX					
g122-1	RFLSQIQSAKIX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 455>:

a122-1.seq

```

1  ATGATTAAAA TCCGCAATAT CCATAAGACC TTCGGCAAAA ATACCATTTT
51  GCGCGGCATC AATTGGGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCAGGCAAA ACGACGTTTC TGCGATGCCT AAACGCGTTG
151 GAAATGCCCG AAGACGGGACA AATCGAGTTC GACAACGAGC GACCGCTGAA
201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTTG GCACTGCGCC
251 GCAAATCAGG CATGGTGTTC CAACAATACA ACCTCTTTCC GCACAAAACC
301 GCCTTGGAAG ACGTGATGGA AGGACCGGTT GCCGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCGAAGAGG CTCTGAAACT GCTGGAAAAA GTCGGCTTGG
401 GCGACAAAGT GGATTGTGAT CCCTACCAGC TTTCCGCGCG TCAGCAGCAG
451 CGCGTCGGCA TTGCCCGAGC ATTGGCGATT CAGCCCGAGC TGATGTGTGT
501 TGACGAACCC ACTTCCGCGC TTGACCCCGA GTTGGTGCAA GACGTGTGTA
551 ACGCCATGAA GGAATTGGCG CGGGAAGGTT GGACGATGGT CGTCGTTACC
601 CACGAAATCA AGTTCGCGCT GGAAGTTGCC ACGACCGTTG TCGTGATGGA
651 CGGCGGCGTT ATCGTAGAGC AGGGCAGCCC GAAAGAGTTG TTCGACCACC
701 CCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTACCAAG
751 ATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 456; ORF 122-1.a>:

a122-1.pep

```

1  MIKIRNIHKT FGKNTILRGI NLDVCKGQVV VILGPSGSGK TFLRCLNAL
51  EMPEDGQIEF DNERPLKIDF SKKPSKHDIL ALRRKSGMVF QQYNLFPHKT
101 ALENVMEGPV AVQGKPAAQA REEALKLLEK VLGDKVDLY PYQLSGGQQQ
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLNAMKELA REGWTMVVVT
201 HEIKFALEVA TTVVMDGGV IVEQGSPEL FDHPKHERTR RFLSQIQSTK
251 I*

```

a122-1/m122-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
a122-1.pep	MIKIRNIHKTFGKNTILRGINLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
m122-1	MIKIRNIHKTFGKNTILRGIDLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
	10	20	30	40	50	60
a122-1.pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFFQYNLFPHKTALENVMEGPPVAVQGKPAAQA					
m122-1	DNERPLKIDFSKKPSKHDILALRRKSGMVFFQYNLFPHKTALENVMEGPPVAVQGKPAAQA					
	70	80	90	100	110	120
a122-1.pep	130	140	150	160	170	180
	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSAIDPELVQ					
m122-1	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSAIDPELVQ					


```

851 ACATTTCCGC GCGTTTTCGC GAAACACCCG TCGCTGTCrG CGTTACCCTG
901 ATCGGCACGG TACTTGCCGT CATGCTGCCC GTTACCGAAT ATGAAAACCTT
951 CCTGCTGCTT ATCGGCTCGG TATTTGCGCC GATGGCGGgC GGTTTTGATT
1001 GCCGACTTTT TCGTCTTGAA ACGGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 460; ORF 125>:

```

m125.pep
  1 MSGNASSPSS SSAIGLIWFG AAVSIAEIST GTLLAPLGWQ RGLAALLLGH
 51 AVGGALFFAA AYIGALTGRS SMESVRLSFG KRGSVLFSVA NMLQLAGWTA
101 VMIYAGATVS SALGKVLWDG ESFVWWALAN GALIVLWLVF GARKTGGLKT
151 VSMLLMLLAV LWLSAEVFST AGSTAAQVSD GMSFGTAVEL SAVMPLSWLP
201 LAADYTRHAR RPFATLTAT LAYTLTGCWM YALGLAAALF TGETDVAKIL
251 LGAXLGAAGI LAVVLSTVTT TFLDAYSAGA SANNISARFA ETPVAVXVTL
301 IGTVLAVMLP VTEYENFLLL IGSVFAPMAG GFDCRLFRLE TA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 125 shows 92.1% identity over a 343 aa overlap with a predicted ORF (ORF 125.ng) from *N. gonorrhoeae*:

```

m125/g125

      10      20      30      40      50      60
m125.pep  MSGNASSPSSSSAIGLIWFGAAVSIAEISTGTLLAPLGWQ RGLAALLLGHAVGGALFFAA
          |||||:||||:|||||
g125       MSGNASSPSSSSAIGLVWFGAAVSIAEISTGTLLAPLGWQ RGLAALLLGHAVGGALFFAA
          10      20      30      40      50      60

      70      80      90      100     110     120
m125.pep  AYIGALTGRSSMESVRLSFGKRGSVLFSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG
          |||||:||||:|||||
g125       AYIGALTGRSSMESVRLSFGKCGSVLFSVANMLQLAGWTAVMIYVGVATVSSALGKVLWDG
          70      80      90      100     110     120

      130     140     150     160     170     179
m125.pep  ESFVWWALANGALIVLWL VFGARKTGGLKTVSMLLM LLA VLWLSAEVFSTAGSTAAQ-VS
          |||||:||||:|||||
g125       ESFVWWALANGALIVLWL VFGARRTGGLKTVSMLLM LLA VLWLSVEVFASSGTNAAPAVS
          130     140     150     160     170     180

      180     190     200     210     220     230     239
m125.pep  DGMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCWMYALGLAAAL
          |||:|||||:|||||
g125       DGMTFGTAVELSAVMPLSWLPLAADYTRQARRPFAATLTATLAYTLTGCWMYALGLAAAL
          190     200     210     220     230     240

      240     250     260     270     280     290     299
m125.pep  FTGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVT
          |||||:||||:|||||
g125       FTGETDVAKILLGAGLGITGILAVVLSTVTTTFLDTYSAGASANNISARFAEIPVAVGVT
          250     260     270     280     290     300

      300     310     320     330     340
m125.pep  LIGTVLAVMLPVTEYENFLL LIGSVFAPMAGGFDCRLFRLETAX
          || |||||:||||| ||:||||| ||:|||
g125       LIRTVLAVMLPVTEYKNFLL LIRSVFGPMAGGFDCRLFCLKTAX
          310     320     330     340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 461>:

```

a125.seq
  1 ATGTCGGGCA ATGCCTCCTC TCCTTCATCT TCCGCCGCCA TCGGGCTGAT
 51 TTGGTTCGGC GCGGCGGTAT CGATTGCCGA AATCAGCACG GGTACACTGC
101 TTGCGCCTTT GGGCTGGCAG CGCGGTCTGG CGGCTCTGCT TTTGGGTCAT

```

a125.pep

1	<u>MSGNASSPSS</u>	<u>SAAIGLIWFG</u>	<u>AAVSIAEIST</u>	<u>GTLLAPLWQ</u>	<u>RGLAALLLGH</u>
51	<u>AVGGALFFAA</u>	<u>AYIGALTGRS</u>	<u>SMESVRLSFG</u>	<u>KRGSVLFSVA</u>	<u>NMLQLAGWTA</u>
101	<u>VMIYAGATVS</u>	<u>SALGKVLWDG</u>	<u>ESFVWWALAN</u>	<u>GALIVLWLVF</u>	<u>GARKTGGLKT</u>
151	<u>VSMLLMLLAV</u>	<u>LWLSAEVFST</u>	<u>AGSTAAQVSD</u>	<u>GMSFGTAVEL</u>	<u>SAVMPLSWLP</u>
201	<u>LAADYTRHAR</u>	<u>RPFAAATLAT</u>	<u>LAYTLTGCMW</u>	<u>YALGLAAALF</u>	<u>TGETDVAKIL</u>
251	<u>LGAGLGAAGI</u>	<u>LAVVLSTVTT</u>	<u>TFLDAYSAGV</u>	<u>SANNISAKLS</u>	<u>EIPIAVAVAV</u>
301	<u>VGTLGAVLLP</u>	<u>VTEYENFLLL</u>	<u>IGSVFAPMAX</u>	<u>GFDRCRLERLE</u>	<u>TA*</u>

	10	20	30	40	50	60
m125.pep	MSGNASSPSSSSAIGLIWFGAAVSI AEISTGTLLAPLGWQRGLAALLGHAVGGALFFAA					
a125	MSGNASSPSSSSAIGLIWFGAAVSI AEISTGTLLAPLGWQRGLAALLGHAVGGALFFAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m125.pep	AYIGALTGRSSMESVRLSFGKRGSVLFSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG					
a125	AYIGALTGRSSMESVRLSFGKRGSVLFSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m125.pep	ESFVWWALANGALIVLWL VFGARKTGGLKTVSMLMLLAVLWLSAEVFSTAGSTAAQVSD					
a125	ESFVWWALANGALIVLWL VFGARKTGGLKTVSMLMLLAVLWLSAEVFSTAGSTAAQVSD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m125.pep	GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTG CWMYALGLAAALF					
a125	GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTG CWMYALGLAAALF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m125.pep	TGETDVAKILLGAGLGAAGILAVVLSTVTTTTFLDAYSAGASANNISARFAETPVAVXVTL					
a125	TGETDVAKILLGAGLGAAGILAVVLSTVTTTTFLDAYSAGVSANNISAKLSEIPIAVAVV					
	250	260	270	280	290	300
	310	320	330	340		
m125.pep	IGTVLAVMLPVTEYENFLLLIGSVFAPMAGGFDCRLFRLETAX					
a125	VGTVLAVMLPVTEYENFLLLIGSVFAPMAXGFDCRLFRLETAX					

310 320 330 340

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 463>:

```
g126.seq
  1  AtgccgctcTG AAaccCcaaaa ggcACGCCGC CGGCTTTCAG ACGGCATCGC
 51  GTCCGACAAC CATACCAAAG AATCCATCAT GCTCACCctg tacggcGAAA
101  CTTTCCCTTC GCGGCTGCTg ctcggcacgG cggcctacCC GACCCCTGAA
151  ATCCTCAAAC AATCCGTCCG AACCGCCCGG CCCGCGATGA ttaccGTCTC
201  GCTGCGCCGC ACGGGATGCG GCGGCGAGGC GCACGGTCAG GGGTTTTGGT
251  CGCTGCTTCA AGAAACCGGC GTTCCCGTCC TGCCGAACAC GGCAGGCTGC
301  CAAAGCGTGC AGGAAGCGGT AACGACGGCG CAAATGGCGC GCGAAGTGTT
351  TGAAACCGAT TGGATAAAAT TGGAACTCAT CGGCGACGAC GACACCTTGC
401  AGCCGGACGT GTTCCAATC GTCGAAGCGG CGGAAATCCT GATTAAAGAC
451  GGCTTCAAAG TGCTGCCTTA TTGCACCGAA GACCTGATTG CCTGCCGCCG
501  CCTGCTCGAT GCGGGCTGTC AGGCGTTGAT GCCGTGGGCG GCTCCCATCG
551  GCACGGGTTT GGGGGCGGTT CACGCCTATG CGCTCAAAAT CCTGCGCGAA
601  CGCCTGCCCG ACACGCCGCT GATTATCGAC GCGGGCTTGG GTTTGCCTTC
651  CCAAGCGGCA CAAGTGATGG AATGGGGTTT TGACGGCGTA TTGTTAAACA
701  CCGCCGTTTC CCGCAGCGGC GACCCCGTCA ACATGGCGCG CGCCTTCGCA
751  CTCGCCGTCG AATCCGGACG GCTGGCATTT GAAGCCGGGC CGGTCGAAGC
801  GCGAACCAAA GCCCAAGCCA GCACGCCGAC AGTCGGACAA CCGTTTTGGC
851  ATTGCGCGGA ATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 464; ORF 126.ng>:

```
g126.pep
  1  MPSETPKARR RLSGDIASDN HTKESIMLT L YGETFPSRL LGTAAYPTPE
 51  ILKQSVRTAR PAMITVSLRR TGCGGEAHGQ GFWSLLQETG VPVLPNTAGC
101  QSVQEAHTTA QMAREVFETD WIKLELIGDD DTLQPDVFQL VEAEEILIKD
151  GFKVLPYCTE DLIACRRLD AGCQALMPWA APIGTGLGAV HAYALKILRE
201  RLPDTPLIID AGLGLPSQAA QVMEWGFQDV LLNTAVSRSG DPVNMARAF
251  LAVESGRLAF EAGPVEARTK AQASTPTVGQ PFWHSAEY*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 465>:

```
m126.seq (partial)
  1  ..CACTATACAA AGGAACCCAT TATGCTCACC CTATACGGCG AAACCTTTCCC
 51  CTCGCGGCTG CTGCTCGGCA CGGCTGCCTA CCCGACCCCG GAAATCCTCA
101  AACAATCCAT CCAAACCGCC CAGCCTGCGA TGATTACCGT CTCGCTGCGC
151  CGCGCGGGAA GCGGCGGCGA GGCGCACGGT CAGGGGTTTT GTTCGCTGCT
201  TCAAGAAACC GCGGTTCCTG TCCTGCCGAA CACGGCAGGC TGCCAAAGCG
251  TGCAGGAAGC GGTAAACGAC GCGCAATATG CCGCGGAAGT GTTTGAAACC
301  GATTGGATAA AATTGGAAC TATCGGAGAT GACGACACCT TGCAGCCGGA
351  TGTGTTCCAG CTTGTCGAAG CGGCGGAAAT CCTGATTAAA GACGGCTTCA
401  AAGTGCTGCC TTATTGCACC GAAGACCTGA TTGCCTGCCG CCGCCTGCTC
451  GACGCGGGCT GTCAGGCGTT GATGCCGTGG GCGGCCCGGA TCGGCACGGG
501  TTTGGGCGCG GTTACGCCT ACAGGTTGAA CGTCCTGCGC GAACGCCTGC
551  CCGACACGCC GCTGATTATC GACGCGGGCT TGGGTTTGCC CTCACAGGCG
601  GCACAAGTGA TGGAATGGGG CTTTGACGGC GTGCTTTTGA ATACTGCCGT
651  TTCCGCAGC GGCATCCGG TCAATATGGC ACGGCCTTC GCACTCGCCG
701  TCGAATCCGG ACGGCTGGCA TTTGAAGCCG GACCGGTCGA AGCACGCGAC
751  AAAGCGCAAG CCAGCACGCC GACAGTCGGA CAACCGTTTT GGCATTCCGC
801  GGAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 466; ORF 126>:

```
m126.pep (partial)
  1  ..HYTKEPIMLT LYGETFPSRL LLGTAAYPTP EILKQSIQTA QPAMITVSLR
 51  RAGSGGEAHG QGFWSLLQET GVPVLPNTAG CQSVQEAHTT AQMAREVFET
```

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```

101 DWIKLELIGD DDTLQPDVFQ LVEAAEILIK DGFKVLPYCT EDLIACRRL
151 DAGCQALMPW AAPIGTGLGA VHAYALNVLR ERLPDTPLII DAGLGLPSQA
201 AQVMEWGF DG VLLNTAVSRS GDPVNMAF ALAVESGRLA FEAGPVEARD
251 KAQASTPTVG QPFWHSAEY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 126 shows 95.9% identity over a 269 aa overlap with a predicted ORF (ORF 126.ng) from *N. gonorrhoeae*:

m126/g126

```

                                10      20      30      40
m126.pep      .  HYTKFIMLTLYGETFP SRLLLGTAA YPTPEILKQSIQTAQ
                  :| | | | | | | | | | | | | | | | | | | | | | | |
g126      MPSETPKARRRLSDGIASDNHTKESIMLTLYGETFP SRLLLGTAA YPTPEILKQSVRTAR
                   10      20      30      40      50      60

                                50      60      70      80      90     100
m126.pep      PAMITVSLRRAGSGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
                  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g126      PAMITVSLRRRTGCGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
                   70      80      90     100     110     120

                                110     120     130     140     150     160
m126.pep      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
                  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g126      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
                   130     140     150     160     170     180

                                170     180     190     200     210     220
m126.pep      APIGTGLGAVHAYALNVLRERLPDTP LIIDAGLGLPSQAAQVMEWGF DG VLLNTAVSRSRG
                  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g126      APIGTGLGAVHAYALKILRERLPDTP LIIDAGLGLPSQAAQVMEWGF DG VLLNTAVSRSRG
                   190     200     210     220     230     240

                                230     240     250     260     270
m126.pep      DPVNMAFALAVESGRLAFEAGPVEARDKAQASTPTVGQPFWHSAEYX
                  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g126      DPVNMAFALAVESGRLAFEAGPVEARTKAQASTPTVGQPFWHSAEYX
                   250     260     270     280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 467>:

a126.seq

```

1   TTGTTAATCC ACTATACAAA GGAACCCATT ATGCTCACCC TGTACAGCGA
51  AACTTTCCCT TCGCGGCTGC TGCTCGGCAC AGCCGCCTAC CCGACCCCTG
101 AAATCCTCAA ACAATCCGTC CGAACCGCCC GGCCCGCGAT GATTACCGTC
151 TCGCTGCGCC GCGCGGGATG CGGCGGCGAG GCGCACGGTC AGGGGTTTGT
201 GTCGCTGCTT CAAGAAACCG GCGTTCCTCG CCTGCCGAAC ACGGCAGGCT
251 GCCAAAGCGT GCAGGAAGCG GTAACGACGG CGCAAATGGC GCGCGAAGTG
301 TTTGAAACCG ATTGGATTAA ACTCGAATC ATCGGCGACG ACGACACCTT
351 GCAGCCGGAT GTGTTCCAAC TTGTCGAAGC GCGGGAATC CTGATTAAAG
401 ACGGCTTCAA AGTGCTGCCT TATTGCACCG AAGACCTGAT TGCCTGCCGC
451 CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG ATGCCGTGGG CGGCCCGAT
501 CGGCACGGGT TTGGGCGCGG TTCACGCCTA CGCGTTGAAC GTCCTGCCGC
551 AACGCCTGCC CGACACGCCG CTGATTATCG ACGCGGGCTT GGGTTTGCCC
601 TCACAGGCGG CACAAGTGAT GGAATGGGGC TTTGACGGCG TGCTTTTGAA
651 TACTGCCGTT TCCCGCAGCG GCGATCCGGT CAATATGGCA CGCGCTTCG
701 CACTCGCCGT CGAATCCGGA CGGCTGGCAT TTGAAGCCGG ACCGGTCGAA
751 GCACGCGACA AAGCGCAAGC CAGCACGCCG ACAGTCGGAC AACCGTTTGT
801 GCATTGCGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 468; ORF 126.a>:

```
a126.pep
  1  LLIHYTKEPI MLTYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV
 51  SLRRAGCGGE AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV
101  FETDWIKLEL IGDDDTLQPD VFQLVEAAEI LIKDGFKVLP YCTEDLIACR
151  RLLDAGCQAL MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP
201  SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE
251  ARDKAQASTP TVGQPFWHS EY*
```

m126/a126 98.1% identity in 269 aa overlap

	10	20	30	40	50	
m126.pep	HYTKEPIMLTLYGETFPSRLLLGTAAYPTPEILKQSIQTAQPAMITVSLRRAGSGGE					
a126	LLIHYTKEPIMLTLYSETFPSRLLLGTAAYPTPEILKQSVRTARPAMITVSLRRAGCGGE					
	10	20	30	40	50	60
m126.pep	AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREVFETDWIKLELIGDDDTLQPD					
a126	AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREVFETDWIKLELIGDDDTLQPD					
	70	80	90	100	110	120
m126.pep	VFQLVEAAEILIKDGFKVLPYCTEDLIACRRLDAGCQALMPWAAPIGTGLGAVHAYALN					
a126	VFQLVEAAEILIKDGFKVLPYCTEDLIACRRLDAGCQALMPWAAPIGTGLGAVHAYALN					
	130	140	150	160	170	180
m126.pep	VLRERLPDTP LIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSGDPVNMA RAFALAVESG					
a126	VLRERLPDTP LIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSGDPVNMA RAFALAVESG					
	190	200	210	220	230	240
m126.pep	RLAFEAGPVEARDKAQASTPTVGQPFWHS <u>EY</u> X					
a126	RLAFEAGPVEARDKAQASTPTVGQPFWHS <u>EY</u> X					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 469>:

```
g126-1.seq
  1  ATGCTCACCC TGTACGGCGA AACTTTCCTT TCGCGGCTGC TGCTCGGCAC
 51  GGCCGCTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACC GCCC
101  GGCCCGCAT GATTACCGTC TCGCTGCGCC GCACGGGATG CGGCGGCGAG
151  GCGCACGGTC AGGGGTTTGT GTCGCTGCTT CAAGAAACCG GCGTTCCCGT
201  CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251  CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATTGGAATC
301  ATCGGCGACG ACGACACCTT GCAGCCGGAC GTGTTCACAC TCGTCGAAGC
351  GGCGGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401  AAGACCTGAT TGCTGCGCGC CGCCTGCTCG ATGCGGGCTG TCAGGCGTTG
451  ATGCGGTGGG CGGCTCCCAT CGGCACGGGT TTGGGGGCGG TTCACGCCTA
501  TCGCTCAAAA ATCTGCGCG AAGCCTGACC CGACACGCCG CTGATTATCG
551  ACGCGGGCTT GGGTTTGCCT TCCCAAGCGG CACAAGTGAT GGAATGGGGT
601  TTTGACGGCG TATTGTTAAA CACCGCCGTT TCCCGCAGCG GCGACCCCGT
651  CAACATGGCG CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701  TTGAAGCCGG GCCGGTCGAA GCGCGAACCA AAGCCCAAGC CAGCACGCCG
751  ACAGTCGGAC AACCGTTTTG GCATTGCGCG GAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 470; ORF 126-1.ng>:

```
g126-1.pep
  1  MLTYLYGETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE
```


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```

51  AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQLVEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALK ILRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARTKAQASTP
251 TVGQPFWSHA EY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 471>:

m126-1.seq

```

1  ATGCTCACCC TATACGGCGA AACTTTCCCC TCGCGGCTGC TGCTCGGCAC
51  GGCTGCCTAC CCGACCCCGG AAATCCTCAA ACAATCCATC CAAACCGCCC
101 AGCCTGCGAT GATTACCGTC TCGCTGCGCC GCGCGGGAAG CGGCGGCGAG
151 GCGCACGGTC AGGGGTTTTG GTCGCTGCTT CAAGAAACCG GCGTTCCTCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATTGGAATC
301 ATCGGAGATG ACGACACCTT GCAGCCGGAT GTGTTCCAGC TTGTGGAAGC
351 GCGCGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCTTGCCGC CGCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCCCGGAT CGGCACGGGT TTGGGCGCGG TTCACGCCCTA
501 CGCGTTGAAC GTCTGCGCG AACGCCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCG TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTGCGCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCGTTTGT GCATTGCGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 5; ORF 126-1>:

m126-1.pep

```

1  MLTLYGETFP SRLLLGTAAY PTPEILKQSI QTAQPAMITV SLRRAGSGGE
51  AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQLVEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALN VLRRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWSHA EY*

```

m126-1/g126-1 96.9% identity in 262 aa overlap

	10	20	30	40	50	60
m126-1.pep	MLTLYGETFPSRLLLGTAAYPTPEILKQSIQTAQPAMITVSLRRAGSGGEAHGQGFWSLL					
g126-1	MLTLYGETFPSRLLLGTAAYPTPEILKQSVRTARPAMITVSLRRAGSGGEAHGQGFWSLL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m126-1.pep	QETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDTLQPD VFQLVEAAEI					
g126-1	QETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDTLQPD VFQLVEAAEI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m126-1.pep	LIKDGFKVLPYCTEDLIACR RLLDAGCQAL MPWAAPIGTGLGAVHAYALN VLRRERLPDTP					
g126-1	LIKDGFKVLPYCTEDLIACR RLLDAGCQAL MPWAAPIGTGLGAVHAYALK ILRERLPDTP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m126-1.pep	LIIDAGLGLPSQAAQVMEWGF DGVLLNTAVSRSGDPVNMA RAFALAVESG RLAFEAGPVE					
g126-1	LIIDAGLGLPSQAAQVMEWGF DGVLLNTAVSRSGDPVNMA RAFALAVESG RLAFEAGPVE					
	190	200	210	220	230	240
	250	260				
m126-1.pep	ARDKAQASTPTVGQPFWSHA EYX					
g126-1	ARTKAQASTPTVGQPFWSHA EYX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 473>:

a126-1.seq

```

1  ATGCTCACCC TGTACAGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
51  AGCCGCCTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACCGCCC
101 GGCCCGCGAT GATTACCGTC TCGCTGCGCC GCGCGGGATG CGGCGGCGAG

```

```

151 GCGCACGGTC AGGGGTTTTG GTCGCTGCTT CAAGAAACCG GCGTTCCTGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATTAA ACTCGAACTC
301 ATCGGCGACG ACACACCTT GCAGCCGGAT GTGTTCCAAC TTGTGGAAGC
351 GCGCGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCCCCGAT CGGCACGGGT TTGGGCGCGG TTCACGCTTA
501 CGCGTTGAAC GTCCTGCGCG AACGCCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGGCT GGGTTTGCCC TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCCTTTTG GCATTGCGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 474; ORF 126-1.a>:

```

a126-1.pep
  1 MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE
 51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWWSA EY*

```

a126-1/m126-1 98.1% identity in 262 aa overlap

	10	20	30	40	50	60
a126-1.pep	MLTLYSETFP	SRLLLGTAAY	PTPEILKQSV	RTARPAMITV	SLRRAGCGGE	AHGQGFWSLL
m126-1	MLTLYGETFP	SRLLLGTAAY	PTPEILKQSI	QTAQPAMITV	SLRRAGSGGE	AHGQGFWSLL
	10	20	30	40	50	60
	70	80	90	100	110	120
a126-1.pep	QETGVPVLP	NTAGCQSVQEA	VTTAQMAREV	FETDWIKLEL	IGDDDTLQPD	VFQVLEAAEI
m126-1	QETGVPVLP	NTAGCQSVQEA	VTTAQMAREV	FETDWIKLEL	IGDDDTLQPD	VFQVLEAAEI
	70	80	90	100	110	120
	130	140	150	160	170	180
a126-1.pep	LIKDGFKVLP	YCTEDLIACR	RLLDAGCQAL	MPWAAPIGTG	LGAVHAYALN	VLRERLPDTP
m126-1	LIKDGFKVLP	YCTEDLIACR	RLLDAGCQAL	MPWAAPIGTG	LGAVHAYALN	VLRERLPDTP
	130	140	150	160	170	180
	190	200	210	220	230	240
a126-1.pep	LIIDAGLGLP	SQAAQVMEWG	FDGVLLNTAV	SRSGDPVNMA	RAFALAVESG	RLAFEAGPVE
m126-1	LIIDAGLGLP	SQAAQVMEWG	FDGVLLNTAV	SRSGDPVNMA	RAFALAVESG	RLAFEAGPVE
	190	200	210	220	230	240
	250	260				
a126-1.pep	ARDKAQASTP	TVGQPFWWSA	EYXX			
m126-1	ARDKAQASTP	TVGQPFWWSA	EYXX			
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 475>:

```

g127.seq
  1 ATGGAAATAT GGAATATGTT GAACACTTGG CCCGATGCCG TCCCAGATACG
 51 CGCGGAGGCG GCCGAATCCG TGGCGGCGGT CGCGGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAGAC GGCATCCGGA TTCGGGCATC
151 GAAAGCAAGC GCGGGTTTTT GGTTGCCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GGCGCAAAAT CAAACGCTGG
251 CTTTGTGCAT GTTTGCGGTG GCGGCGGCGG TCGTCGTGGC GACAAAAGAA
301 CTGATTATGT GTCTGTGCGG CAGTATTTTA aggtctGCCA CCCAGCAATA
351 CTCGGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAATCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGGACAGC TTGCGGGAAC CACCGTTTCT TTCCCAACA GCCTGTTGTT
501 GAGCCACCCC GTGCGCCGCG ACAATATTTT GGGCGACTAT GTCATCCATA

```

```

551  CGGTCGAAAT  CCCCCTTCCC  ATCCATTGG  ATTCGGATGA  AGCCGTATGC
601  CGTCTGAAAG  CCGTACTCGA  GCCCTTGTGC  GCGCCCTACA  TCCCCGCCAT
651  TCAGCGGTAT  TTGGAACG  TGCAGGCGGA  AAACTGTTT  ATCACGCCCCG
701  CCGCCAGGCC  GCGCGTTACC  CGCGTACCGT  ACGACGACAA  GGCATACCGC
751  ATCATCGTCC  GCTTCGCCTC  CCCCCTTTCA  AAGCGGCTGG  AAATCCAACA
801  GGCGGTTATG  GACGAATTTT  TGCGCGTACA  ATACCGCCTG  TTAAATCATC
851  CCGCCGgctc  cgAAACACTT  TAA

```

This corresponds to the amino acid sequence <SEQ ID 476; ORF 127.ng>:

```

g127.pep
1  MEIWNMLNTW  PDAVPIRAEA  AESVAAVAAL  LLARALLLNI  HFRRHPDFGI
51  ESKRRFLVAS  RNITLLLVLF  SLAFIWSAQI  QTLALSMFAV  AAHVVVATKE
101 LIMCLSGSIL  RSATQQYSVG  DYIEINGLRG  RVVDINLLNT  LMMQVGNPL
151 VGQLAGTTVS  FPNSLLLSHP  VRRDNILGDY  VIHTVEIPVP  IHLDSDEAVC
201 RLKAVLEPLC  APYIPAIQRY  LENVQAEKLF  ITPAARPRVT  RVPYDDKAYR
251 IIVRFASPVS  KRLEIQQAVM  DEFLRVQYRL  LNHPAGSETL  *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 477>:

```

m127.seq
1  ATGGAAATAT  GGAATATGTT  GGACACTTGG  CTCGGTGCCG  TCCCGATACG
51  TCGGAGGCG  GTCGAATCCG  TGGCGGCGGT  TCGCGCTTTG  CTGCTGGCGC
101 GCGCCCTTCT  GTTGAATATC  CACTTCAAAC  GGCATCCGGA  TTTCGGCATC
151 GAAAGCAAGC  GGCGGTTTTT  GGTGCGCAGC  CGCAATATAA  CGCTGCTTTT
201 GGTGCTGTTT  TCGCTGGCAT  TTATCTGGTC  GGCGCAAATC  CAAACGCTGG
251 CTTTGTGAT  GTTGTGCGTG  GCGGCGGCGG  TCGTCTGGC  GACGAAGGAA
301 CTGATTATGT  GTCTGTGCGG  CAGTATTTTA  AGGTCTGCCA  CCCAGCAATA
351 CTCGGTCGGC  GACTATATCG  AAATCAACGG  CCTGCGCGGG  CGCGTGGTCG
401 ACATCAACCT  GTTGAACACG  CTGATGATGC  AGGTCGGTCC  GAACCCCTTG
451 GTCGGACAGC  TTGCGGGAAC  CACCGTTTCT  TTCCCAACA  GCCTGTTGTT
501 GAGCCACCCC  GTGCGCCGCG  ACAATATTTT  GGGCGACTAT  GTCATCCATA
551 CGGTCGAAAT  CCCCCTTCCC  ATCCATTGG  ATTCGGATGA  AGCCGTATGC
601 CGTCTGAAAG  CCGTACTCGA  GCCCTTGTGC  GCGCCCTACA  TCCCCGCCAT
651 CCAACGGsAT  TTGGAACG  TGCAGGCGGA  AAACTGTTT  ATCACGCCCCG
701 CCGCCAGACC  GCGCGTTACC  CGCGTGCCGT  ACGATGACAA  GGCATACCGC
751 ATCATCGTCC  GCTTCGCTTC  CCCCCTTTCA  AAGCGGCTGG  AAATCCAACA
801 GGCGGTTATG  GACGAATTTT  TGCGCGTACA  ATACCGCCTG  TTAAATCACC
851 CCGCCGCTC  CGAAACACTT  TAA

```

This corresponds to the amino acid sequence <SEQ ID 478; ORF 127>:

```

m127.pep
1  MEIWNMLDTW  LGAVPIRAEA  VESVAAVAAL  LLARALLLNI  HFKRHPDFGI
51  ESKRRFLVAS  RNITLLLVLF  SLAFIWSAQI  QTLALSMFAV  AAHVVVATKE
101 LIMCLSGSIL  RSATQQYSVG  DYIEINGLRG  RVVDINLLNT  LMMQVGNPL
151 VGQLAGTTVS  FPNSLLLSHP  VRRDNILGDY  VIHTVEIPVP  IHLDSDEAVC
201 RLKAVLEPLC  APYIPAIQRY  LENVQAEKLF  ITPAARPRVT  RVPYDDKAYR
251 IIVRFASPVS  KRLEIQQAVM  DEFLRVQYRL  LNHPAGSETL  *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 127 shows 97.9% identity over a 290 aa overlap with a predicted ORF (ORF 127.ng) from *N. gonorrhoeae*:

```

m127/g127
          10      20      30      40      50      60
m127.pep  MEIWNMLDTWLGAVPIRAEAVESVAAVAALLLARALLLNIHFKRHPDFGIESKRRFLVAS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g127       MEIWNMLNTWPDVPIRAEAAESVAAVAALLLARALLLNIHFRRHPDFGIESKRRFLVAS
          10      20      30      40      50      60
          70      80      90      100     110     120
m127.pep  RNITLLLVLFSLAFIWSAQIQTALALSMFAVAAHVVVATKELIMCLSGSILRSATQQYSVG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g127       RNITLLLVLFSLAFIWSAQIQTALALSMFAVAAHVVVATKELIMCLSGSILRSATQQYSVG

```

	70	80	90	100	110	120
	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGQLAGTTVSFPNSLLLSHPVRRDNILGDY					
g127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGQLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSDEAVCRLKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
g127	VIHTVEIPVPIHLDSDEAVCRLKAVLEPLCAPYIPAIQRYLENVQAEKLFITPAARPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVS KRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
g127	RVPYDDKAYRIIVRFASPVS KRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 479>:

a127.seq	1	ATGGAAATAT	GGAATATGTT	GGACACTTGG	CTCGGTGCCG	TCCCGATACG
	51	TGCGGAGGCG	GTCGAATCCG	TGCGGTGGT	CGCGGCTTTG	CTGCTGCGCG
	101	GCGCCCTTCT	GTTGAATATC	CACTTCAAAC	GGCATCCGGA	TTTCGGCATC
	151	GAAAGCAAGC	GGCGGTTTT	GGTTGCCAGC	CGCAATATAA	CGCTGCTTTT
	201	GGTGCTGTTT	TCGCTGGCAT	TTATCTGGTC	GGCGCAAATC	CAAACGCTGG
	251	CTTTGTCGAT	GTTTGC GTG	GCGGCGCGG	TCGTCTGGC	GACGAAGGAA
	301	CTGATTATGT	GTCTGTCTGG	CAGCATTTTA	AGGTCTGCCA	CCCAGCAATA
	351	CTCGGTCTGCG	GACTATATCG	AAATCAACGG	CCTGCGCGGG	CGCGTGCTCG
	401	ACATCAACCT	GTTGAACACG	CTGATGATGC	AGGTCTGGTCC	GAACCCCTTG
	451	GTCGGACAGC	TTGCGGGAAC	CACCGTTTCT	TTCCCAACA	GCCTGTTGTT
	501	GAGCCACCCC	GTGCGCCGCG	ACAATATTTT	GGGCGACTAC	GTCATCCATA
	551	CGGTCTGAAAT	CCCGGTTCCC	ATCCATTTGG	ATTCGGATGA	AGCCGTATGC
	601	CGTCTGAAAG	CCGTACTCGA	GCCCTTGTGC	GCGCCCTACA	TCCCCGCCAT
	651	CCAACGGCAT	TTGGAAAACG	TGCAGGCGGA	AAACTGTTT	ATCACGCCCG
	701	CCGCCAAACC	GCGCGTTACC	CGCGTGCCGT	ACGATGACAA	GGCATAACCG
	751	ATCATCGTCC	GCTTCGCCTC	CCCCGTTTCA	AAGCGGCTGG	AAATCCAACA
	801	GGCGGTTATG	GACGAATTTT	TGCGGTACA	ATACCGCTG	TTAAATTACC
	851	CCGCCGGCTC	CGAAACACTT	TAA		

This corresponds to the amino acid sequence <SEQ ID 480; ORF 127.a>:

a127.pep	1	MEIWNMLDTW	LGAVPIRAEA	VESVAVVAAL	LLARALLNI	HFKRHPDFGI
	51	ESKRRLVAS	RNITLLLVL	SLAFIWSAQI	QTLALSMFAV	AAVVVATKE
	101	LIMCLSGSIL	RSATQQYSVG	DYIEINGLRG	RVVDINLLNT	LMMQVGNPL
	151	VGQLAGTTVS	FPNSLLLSHP	VRRDNILGDY	VIHTVEIPVP	IHLDSDEAVC
	201	RLKAVLEPLC	APYIPAIQRH	LENVQAEKLF	ITPAKPRVT	RVPYDDKAYR
	251	IIVRFASPVS	KRLEIQQAVM	DEFLRVQYRL	LNYPAGSETL	*

m127/a127 98.6% identity in 290 aa overlap

	10	20	30	40	50	60
m127.pep	MEIWNMLDTWLGAVPIRAEAVESVAVVAALLARALLNIHFKRHPDFGIESKRRLVAS					
a127	MEIWNMLDTWLGAVPIRAEAVESVAVVAALLARALLNIHFKRHPDFGIESKRRLVAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m127.pep	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAVVVATKELIMCLSGSILRSATQQYSVG					
a127	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAVVVATKELIMCLSGSILRSATQQYSVG					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
a127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSDEAVCRLKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
a127	VIHTVEIPVPIHLDSDEAVCRLKAVLEPLCAPYIPAIQRHLENVQAEKLFITPAARPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
a127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 481>:

g128.seq

```

1  atgattgaca acgCActgct ccacttgggc gaagaaccCC GTTTTaatca
51  aatccaaacc gaagACatca AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTGT
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCG GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTGCA ACGCTTTCCC CCGCACAAAA AACCAAGCTC GATCACGACC
401 TCGCGGATTT CGTATTGAGC GGCGCGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCCGG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGccaaa cTGCTCGGCT TTAATAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACGCCG GAACAGGTTT TAAACTTCCT GCACGACCTC
901 GCGCGCCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCGCCCCG GAACACCTCG GTCTCGCCGA CCCGCAGCCG TGGGACTTGA
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTTCTGGCAG GCCTGTTCCG
1101 CCAAATCAA AACTCTACG GCATCGGATT CGCCGAAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCAAAACC
1201 ATCGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGActaca AAGGCCGCCG CCGCTTTGCC GACGgcacGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCGCGTCGGC
1351 GGCAAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACCC TCTTCCACGA
1401 AacCGGCCAC GGAAGTGCAC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGGCAT CAacggcgTA GAATGGGACG CGGTCGAACT GCCCAGCCAG
1501 TTTATGGAAA ACTTCGTTTG GGAATACAAT GTATTGGCAC AAATGTCCGC
1551 CCACGAAGAA AccgGCGAGC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TcgCGCCAA AACTTCCAG CGCGGTATGT TCCTCGTCCG GCAATGGAG
1651 TTCGCCCTCT TCGATATGAT GATTACAGT GAAAGCGACG AATGCCGTCT
1701 GAAAAACTGG CAGCAGGTTT TAGACAGCGT GCGCAAAGAA GTcGCCGTCA
1751 TCCAACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCacatctTC
1801 GCcggcGGCT ATTCCGAGG CTATTACAGC TACGCATGGG CCGAAGTCCT
1851 cAGCACCGAT GCCTACGCCG CTTTGAAGA AAGcGACGac gtcGCCGCCA
1901 CAGGCAAACG CTTCTGGCAA GAAAtccttg cgtcgggcg ctCCCGCAGC
1951 gcgGCGGAAT CCTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC

```

2001 ACTGCTGCGC CAaagcggtT TCGACAACGC gGcttgA

This corresponds to the amino acid sequence <SEQ ID 482; ORF 128.ng>:

g128.pep

```

1  MIDNALLHLG  EEPRFNQIQT  EDIKPAVQTA  IAEARGQIAA  VKAQHTTGWA
51  NTVERTLGIT  ERVGRIWGVV  SHLNSVVDTP  ELRAVYNELM  PEITVFFTEI
101 GQDIELYNRF  KTIKNSPEFA  TLSPAQKTKL  DHDLRDFVLS  GAELPPERQA
151 ELAKLQTEGA  QLSAKFSQNV  LDATDAFGIY  FDDAAPLAGI  PEDALAMFAA
201 AAQSEGKTGY  KIGLQIPHYL  AVIQYAGNRE  LREQIYRAYV  TRASELSNDG
251 KFDNTANIDR  TLENALKTAK  LLGFKNYAEL  SLATKMADTP  EQVLNFLHDL
301 ARRAKPYAEK  DLAEVKAFAR  EHLGLADPQP  WDLSYAGEKL  REAKYAFSET
351 EVKKYFPVGK  VLAGLFAQIK  KLYGIGFAEK  TVPVWHKDVR  YFELQQNGKT
401 IGGVYMDLYA  REGKRGGAWM  NDYKGRRRFA  DGTQLQLPTAY  LVCNFAPPVG
451 GKEARLSHDE  ILTLFHETGH  GLHLLTQVD  ELGVSGINGV  EWDAVELPSQ
501 FMENFVWEYN  VLAQMSAHEE  TGEPLPKELF  DKMLAAKNFQ  RGMFLVRQME
551 FALFDMMIYS  ESDECRLKNW  QQVLDSVRKE  VAVIQPPEYN  RFANSFGHIF
601 AGGYSAGYYS  YAWAEVLSTD  AYAAFEESDD  VAATGKRFWQ  EILAVGGSRS
651 AAESFKAFRG  REPSIDALLR  QSGFDNAA*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 483>:

m128.seq (partial)

```

1  ATGACTGACA  ACGCACTGCT  CCATTTGGGC  GAAGAACCCC  GTTTTGATCA
51  AATCAAAACC  GAAGACATCA  AACCCGCCCT  GCAAACCGCC  ATCGCCGAAG
101 CGCGCGAACA  AATCGCCGCC  ATCAAAGCCC  AAACGCACAC  CGGCTGGGCA
151 AACACTGTCT  AACCCCTGAC  CGGCATCACC  GAACGCGTCG  GCAGGATTTG
201 GGGCGTGGTG  TCGCACCTCA  ACTGCGTCGC  CGACACGCCC  GAACTGCGCG
251 CCGTCTATAA  CGAACTGATG  CCCGAAATCA  CCGTCTTCTT  CACCGAAATC
301 GGACAAGACA  TCGAGCTGTA  CAACCGCTTC  AAAACCATCA  AAAATTCCCC
351 CGAATTCGAC  ACCCTCTCCC  CCGCACAAAA  AACCAAACTC  AACCAC
1  TACGCCAGCG  AAAAACTGCG  CGAAGCCAAA  TACGCGTTCA  GCGAAACCGA
51  wGTCAAAAAA  TAyTTCcCyG  TCGGCAAwGT  ATTAACCGGA  CTGTTTCGCC
101 AAmTCAAAAA  ACTmTACGGC  ATCGGATTTA  CCGAAAAAAC  yGTCCCCGTC
151 TGGCACAAAG  ACGTGCGCTA  TTKtGAATTG  CAACAAAACG  GCGAAmCCAT
201 AGGCGGCGTT  TATATGGATT  TGTACGCACG  CGAAGGCAAA  CGCGGCGGCG
251 CGTGATGAA  CGACTACAAA  GGCCGCCGCC  GTTTTTCAGA  CGGCACGCTG
301 CAAYTGCCCA  CCGCCTACCT  CGTCTGCAAC  TTCGCCCCAC  CCGTCGGCGG
351 CAGGGAAGCC  CGCyTGAGCC  ACGACGAAAT  CCTCATCCTC  TTCCACGAAA
401 CCGGACACGG  GCTGCACCAC  CTGCTTACCC  AAGTGGACGA  ACTGGGCGTA
451 TCCGGCATCA  ACGGCGTAKA  ATGGGACGCG  GTCGAACTGC  CCAGCCAGTT
501 TATGGAATAA  TTCGTTTGGG  AATACAATGT  CTTGGCACAA  mTGTCAGCCC
551 ACGAAGAAAC  CGGcgTTCCC  yTGCCGAAAG  AACTCTTsGA  CAAAwTGCTC
601 GCCGCCAAAA  ACTTCCAAsG  CGGCATGTTC  yTsGTCCGCG  AAwtGGAGTT
651 CGCCCTCTTT  GATATGATGA  TTTACAGCGA  AGACGACGAA  GGCCGTCTGA
701 AAAACTGGCA  ACAGGTTTTA  GACAGCGTGC  GCAAAAAAGT  CGCCGTCATC
751 CAGCCGCCCG  AATACAACCG  CTTGCGCTTG  AGCTTCGGCC  ACATCTTCGC
801 AGGCGGCTAT  TCCGCAGCTn  ATTACAGCTA  CGCGTGGGCG  GAAGTATTGA
851 GCGCGGACGC  ATACGCCGCC  TTTGAAGAAA  GCGACGATGT  CGCCGCCACA
901 GGCAAACGCT  TTTGGCAGGA  AATCCTCGCC  GTCGGGGnAT  CGCGCAGCGG
951 nGCAGATCC  TTCAAAGCCT  TCCGCGGCCG  CGAACCAGAG  ATAGACGCAC
1001 TCTTGCGCCA  CAGCGGTTTC  GACAACGCGG  TCTGA
```

This corresponds to the amino acid sequence <SEQ ID 484; ORF 128>:

m128.pep (partial)

```

1  MTDNALLHLG  EEPRFDQIKT  EDIKPALQTA  IAEAREQIAA  IKAQHTTGWA
51  NTVEPLTGIT  ERVGRIWGVV  SHLNCVADTP  ELRAVYNELM  PEITVFFTEI
101 GQDIELYNRF  KTIKNSPEFD  TLSPAQKTKL  NH
```

//

```

1  YASEKLREAK  YAFSETXVKK  YFPVGXVLNG  LFAQXKKLYG  IGfTEKTVPV
51  WHKDVRyxEL  QQNGEXIGGV  YMDLYAREGK  RGGAWMNDYK  GRRRFSdGTL
101 QLPTAYLVCN  FAPPVGGREA  RLSHDEILIL  FHETGHGLHH  LLTQVDELGV
151 SGINGVXWDA  VELPSQFMEN  FVWEYNVLAQ  XSAHEETGVP  LPKELXDKXL
201 AAKNFQXGMF  XVRQXEFALF  DMMIYSEDDE  GRLKNWQQVL  DSVRKKVAVI
251 QPPEYNRFAL  SFGHIFAGGY  SAAXYSYAWA  EVLSADAYAA  FEESDDVAAT
```

301 GKRFWQEILA VGXSRSGAES FKAFRGREPS IDALLRHSGF DNAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng) from *N. gonorrhoeae*:

m128/g128

	10	20	30	40	50	60
g128.pep	MIDNALLHLGEEPRFNQIQTEDIKPAVQTAIAEARGQIAAVKAQTHGTWANTVERLTGIT					
m128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQTHGTWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g128.pep	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130	140	150	160	170	180
g128.pep	TLSPAQKTKLDHDLRDFVLGAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128	TLSPAQKTKLNH					
	130					
	//					
				340	350	360
g128.pep	YAGEKLREAKYAFSETEVKKYFPVGKVLG					
m128	YASEKLREAKYAFSETXVKKYFPVGXVLNG					
				10	20	30
	370	380	390	400	410	420
g128.pep	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWMNDYK					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
	430	440	450	460	470	480
g128.pep	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVDELGV					
m128	GRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILTLFHETGHGLHLLTQVDELGV					
	100	110	120	130	140	150
	490	500	510	520	530	540
g128.pep	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQXGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKMLAAKNFQXGMF					
	160	170	180	190	200	210
	550	560	570	580	590	600
g128.pep	LVRQMEFALFDMMIYSESDCRLKNWQQVLDVSRKEVAVIQPPEYNRFANSFGHIFAGGY					
m128	XVRQXEALFDMMIYSEDEGRKKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
	610	620	630	640	650	660
g128.pep	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRGREPS					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRGREPS					
	280	290	300	310	320	330

```

              670      679
g128.pep      IDALLRQSGFDNAAX
              |||||:|||||:
m128          IDALLRHSGFDNAVX
              340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 485>:

```

a128.seq
1  ATGACTGACA  ACGCACTGCT  CCATTGGGC  GAAGAACCCC  GTTTTGATCA
51  AATCAAAACC  GAAGACATCA  AACCCGCCCT  GCAAACCGCC  ATTGCCGAAG
101 CGCGCGAACA  AATCGCCGCC  ATCAAAGCCC  AAACGCACAC  CGGCTGGGCA
151 AACACTGTCTG  AACCCTGAC  CGGCATCACC  GAACGCGTCG  GCAGGATTTG
201 GGGCGTGGTG  TCGCACCTCA  ACTCCGTCAC  CGACACGCCC  GAACTGCGCG
251 CCGCTACAA  TGAATTAATG  CCCGAAATTA  CCGTCTTCTT  CACCGAAATC
301 GGACAAGACA  TCGAGCTGTA  CAACCGCTTC  AAAACCATCA  AAAACTCCCC
351 CGAGTTCGAC  ACCCTCTCCC  ACGCGCAAAA  AACCAAATC  AACCACGATC
401 TGCGCGATTT  CGTCTCAGC  GGCGCGGAAC  TGCCGCCCGA  ACAGCAGGCA
451 GAATTGGCAA  AACTGCAAA  CGAAGGCGCG  CAACTTTCCG  CCAAATCTC
501 CCAAAACGTC  CTAGACGCGA  CCGACGCGTT  CGGCATTTAC  TTTGACGATG
551 CCGCACCGCT  TGCCGGCATT  CCCGAAGACG  CGCTCGCCAT  GTTGGCCGCT
601 GCCGCGCAAA  GCGAAGGCAA  AACAGGCTAC  AAAATCGGTT  TGAGATTCC
651 GCACTACCTC  GCCGTACATC  AATACGCCGA  CAACCGCAAA  CTGCGCGAAC
701 AAATCTACCG  CGCTACGTT  ACCCGCGCCA  GCGAGCTTTC  AGACGACGGC
751 AAATTCGACA  ACACGCCCAA  CATCGACCGC  ACGCTCGAAA  ACGCCCTGCA
801 AACCGCCAAA  CTGCTCGGCT  TCAAAACTA  CGCCGAATTG  TCGCTGGCAA
851 CCAAAATGGC  GGACACCCCC  GAACAAGTTT  TAAACTTCCT  GCACGACCTC
901 GCCGCGCGCG  CCAAACCCTA  CGCCGAAAAA  GACCTCGCCG  AAGTCAAAGC
951 CTTCGCCCCG  GAAAGCCTCG  GCCTCGCCGA  TTTGCAACCG  TGGGACTTGG
1001 GCTACGCCGG  CGAAAACTG  CGCGAAGCCA  AATACGCATT  CAGCGAAACC
1051 GAAGTCAAAA  AATACTTCCC  CGTCGGCAA  GTATTAAACG  GACTGTTCCG
1101 CCAAATCAAA  AAACCTTACG  GCATCGGATT  TACCGAAAAA  ACCGTCCCCG
1151 TCTGGCACAA  AGACGTGCGC  TATTTTGAAT  TGCAACAAAA  CGGCGAAACC
1201 ATAGGCGGCG  TTTATATGGA  TTTGTACGCA  CGCGAAGGCA  AACGCGGCGG
1251 CGCGTGGATG  AAGGACTACA  AAGGCCGCCG  CCGTTTTTCA  GACGGCACGC
1301 TGCAACTGCC  CACCGCCTAC  CTCGTCTGCA  ACTTCACCCC  GCCCGTCGGC
1351 GGCAAAGAAG  CCCGCTTGAG  CCATGACGAA  ATCCTCACCC  TCTTCCACGA
1401 AACCGGACAC  GGCTGCACC  ACCTGCTTAC  CCAAGTCGAC  GAACTGGGCG
1451 TATCCGGCAT  CAACGGCGTA  GAATGGGACG  CAGTCGAAC  GCCCAGTCAG
1501 TTTATGGA  AATTCGTTT  GGAATACAAT  GTCTTGGCGC  AAATGTCCGC
1551 CCACGAAGAA  ACCGGCGTTC  CCCTGCCGAA  AGAACTCTTC  GACAAAATGC
1601 TCGCCGCCAA  AAACCTCCAA  CGCGGAATGT  TCCTCGTCCG  CCAAATGGAG
1651 TTCGCCCTCT  TTGATATGAT  GATTTACAGC  GAAGACGACG  AAGGCCGTCT
1701 GAAAACTGG  CAACAGGTTT  TAGACAGCGT  GCGCAAAGAA  GTCGCCGTCT
1751 TCCGACCGCC  CGAATACAAC  CGCTTCGCCA  ACAGCTTCGG  CCACATCTTC
1801 GAGGCGGCT  ATTCGCGAGG  CTATTACAGC  TACGCGTGGG  CGGAAGTATT
1851 GAGCGCGGAC  GCATACGCCG  CCTTTGAAGA  AAGCGACGAT  GTCGCGGCCA
1901 CAGGCAAACG  CTTTGGCAG  GAAATCCTCG  CCGTCGGCGG  ATCGCGCAGC
1951 GCGGCAGAAT  CTTCAAAGC  CTTCCGCGGA  CGCGAACCGA  GCATAGACGC
2001 ACTCTTGCGC  CACAGCGGCT  TCGACAACGC  GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 486; ORF 128.a>:

```

a128.pep
1  MTDNALLHLG  EEPRFDQIKT  EDIKPALQTA  IAEAREQIAA  IKAQHTGWGA
51  NTVEPLTGIT  ERVGRIWGVV  SHLNSVTDTP  ELRAAYNELM  PEITVFFTEI
101 QODIELYNRF  KTIKNSPEFD  TLSHAQKTKL  NHDLRDFVLS  GAELPPEQQA
151 ELAKLQTEGA  QLSAKFSQNV  LDATDAFGIY  FDDAAPLAGI  PEDALAMFAA
201 AAQSEGKTGY  KIGLQIPHYL  AVIQYADNRK  LREQIYRAYV  TRASELSDDG
251 KFDNTANIDR  TLENALQTAK  LLGFKNYAEL  SLATKMADTP  EQVLNFLHDL
301 ARRAKPYAEK  DLAEVKAFAR  ESLGLADLQP  WDLGYAGEKL  REAKYAFSET
351 EVKKYFPVGK  VLNLFAFIK  KLYGIGFTEK  TVPVVHKDVR  YFELQONGET
401 IGGVYMDLYA  REGKRGGAWM  NDYKGRRRFS  DGTLLQLPTAY  LVCNFTPPVG
451 GKEARLSHDE  ILTLFHETGH  GLHLLTQVD  ELGVSGINGV  EWDAVELEPSQ
501 FMENFVWEYN  VLAQMSAHEE  TGVPLPKELF  DKMLAAKNFQ  RGMFLVRQME

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551 FALFDMMIYS EDDEGR LKNW QQVLD SVRKE VAVVRPPEYN RFANSFGHIF
 601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRWFQ EILAVGGSRS
 651 AAESFKAFRG REPSIDALLR HSGFDNAA*

m128/a128 66.0% identity in 677 aa overlap

m128.pep	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGTWANTVEPLTGIT					
a128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGTWANTVEPLTGIT					
	10	20	30	40	50	60
m128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
m128.pep	130					
	TLSPAQKTKLNH-----					
a128	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
m128.pep	-----					
a128	FDDAAPLAGIPEDALAMFAAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
	190	200	210	220	230	240
m128.pep	-----					
a128	TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMADTPEQVLNLFHDL					
	250	260	270	280	290	300
m128.pep	-----					
	-----YASEKLREAKYAFSETXVKKYFPVGX					
a128	ARRAKPYAEKDLAEVKAFARESLGLADLPWDLG YAGEKLREAKYAFSETEVKKYFPVGK					
	310	320	330	340	350	360
m128.pep	160	170	180	190	200	210
	VLNGLFAQXKKLYGIGFTEKTPVWHKDVRYXELQQNGEXIGGVYMDLYAREGKRGGAWM					
a128	VLNGLFAQIKKLYGIGFTEKTPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
m128.pep	220	230	240	250	260	270
	NDYKGRRRFS DGTQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD					
a128	NDYKGRRRFS DGTQLPTAYLVCNFAPPVGGKEARLSHDEILILFHETGHGLHLLTQVD					
	430	440	450	460	470	480
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWD AVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAACKNFQ					
a128	ELGVSGINGVEWD AVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAACKNFQ					
	490	500	510	520	530	540
m128.pep	340	350	360	370	380	390
	XGMFXVRQXEFALFDMMIYSEDEGR LKNWQQVLD SVRKKVAVIQPPEYNRFALSFGHIF					
a128	RGMFLVRQMEFALFDMMIYSEDEGR LKNWQQVLD SVRKEVAVVRPPEYNRFANSFGHIF					
	550	560	570	580	590	600

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          400      410      420      430      440      450
m128.pep  AGGYSAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRG
          |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAESFKAFRG
          610      620      630      640      650      660

          460      470
m128.pep  REPSIDALLRHSGFDNAVX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      REPSIDALLRHSGFDNAAX
          670

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 487>:

g128-1.seq (partial)

```

1  ATGATTGACA ACGCACTGCT CCACTTGGGC GAAGAACCCC GTTTTAATCA
51  AATCAAAACC GAAGACATCA AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTG
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCG GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAATGTGA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTGCA ACGCTTTCCC CCGCACAAAA AACCAAGCTC GATCACGACC
401 TGC GCGATT TCGTATTGAGC GCGCGGAAC TGCGGCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAA CGAAGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGT CCGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTGCCGCC
601 GCCGCGCAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCCG CAACCGCAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGCCAAA CTGCTCGGCT TAAAAATTA CGCCGAATG TCGCTGGCAA
851 CCAAATGGC GGACACGCCG GAACAGGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCTTA CGCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCCG GAACACCTCG GTCTCGCCGA CCCGACGCG TGGGACTTGA
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTTCTGGCAG GCCTGTTCGC
1101 CCAAATCAAA AAATCTACG GCATCGGATT CGCGAAAAA ACCGTTCCCG
1151 TCTGGCAGAA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCAAAACC
1201 ATCGGCGCGG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCG CCGCTTTGCC GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACC TCTTCCACGA
1401 AACCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGCAT CAACGGCGTA AAA

```

This corresponds to the amino acid sequence <SEQ ID 488; ORF 128-1.ng>:

g128-1.pep (partial)

```

1  MIDNALLHLG EEPFRNQIKT EDIKPAVQTA IAEARGQIAA VKAQHTGWA
51  NTVRLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY PDAAAPLAGI PEDALAMFAA
201 AAQSEGKTYG KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDSL YAGEKL REAKYAFSET
351 EVKKYFFPVGK VLAGLFAQIK KLYGIGFAEK TVPVVHKDVR YFELQONGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV K

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 489>:

m128-1.seq

```

1  ATGACTGACA ACGCACTGCT CCATTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTG AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTG

```

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201 GGGCGTGGTG TCGCACCTCA ACTCCGTCGC CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCTC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAA AACCAACTC AACACGATC
401 TGCGCGATTT CGTCTCAGC GCGCGGAAC TGCCGCCC GAACAGCAGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTCCG CCAATTCCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCCTG TGCCGGCATT CCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAA GCGAAAGCAA AACAGGCTAC AAAATCGGCT TGCAGATTCC
651 AACTACCTC GCCGTCATCC AATACGCCGA CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAACTTTC AGACGACGCG
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGCAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACGCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAAACCTA CGCCGAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCGCCCGC GAAAGCCTGA ACCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCAG CGAAAACTG CGCGAAGCCA AATACGCGTT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTCGC
1101 CCAAATCAA AAATCTACG GCATCGGATT TACCGAAAA ACCGTCCCGC
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCGAAACC
1201 ATAGGCGCGG TTTATATGGA TTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCGG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCTAC CTCGTCTGCA ACTTCGCCCC ACCCGTCGGC
1351 GGCAGGGAAG CCCGCTGAG CCACGACGAA ATCCTCATCC TCTTCCACGA
1401 AACCGGACAC GGGCTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TATCCGGCAT CAACGCGTA GAATGGGACG CGGTGGAAT GCCAGCCAG
1501 TTTATGGAAA ATTTCTGTTG GGAATACAAT GTCTTGGCAC AAATGTCAGC
1551 CCACGAAGAA ACCGGCGTTC CCTGCGGAA AGAATCTTC GACAAAATGC
1601 TCGCCGCCAA AAATCTCCAA CGCGGCATGT TCCTCGTCCG GCAATGGAG
1651 TTCGCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAAAATGG CAACAGGTTT TAGACAGCGT GCGCAAAAA GTTCGCGTCA
1751 TCCAGCCGCC CGAATACAAC CGCTTGCCT TGAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCGCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCCGCCCA
1901 CAGGCAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 CGGCGAAGT CTTCAAAGC CTTCCGCGCG CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGTT TCGACAACGC GGTCTGA

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This corresponds to the amino acid sequence <SEQ ID 490; ORF 128-1>:

m128-1.pep.

```

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51 NTVPLTGIT ERVGRWGVV SHLNSVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSESKTGY KIGLQIPHYL AVIQYADNRE LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLANALQTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR ESLNLADLQP WDLGYASEKL REAKYAFSET
351 EVKKYFPVKG VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTQLQLPTAY LVCNFAPPVG
451 GREARLSHDE ILILFHETGH GLHLLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAANKFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRLLKNW QQVLDVSRKK VAVIQPPEYN RFALSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAV*

```

m128-1/g128-1 94.5% identity in 491 aa overlap

	10	20	30	40	50	60
g128-1.pep	MIDNALLHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT					
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIAQHTGWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g128-1.pep	ERVGRWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128-1	ERVGRWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120

370

	130	140	150	160	170	180
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
	190	200	210	220	230	240
g128-1.pep	FDDAAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV					
m128-1	FDDAAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV					
	190	200	210	220	230	240
	250	260	270	280	290	300
g128-1.pep	TRASELSNDGKFDNTANIDRTLENALKTAKLLGFKNYAELSLATKMADTPEQVLNFIHDL					
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNFIHDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
g128-1.pep	ARRAKPYAEKDLAEVKAFAREHLGLADPQWDLSVAGEKLREAKYAFSETEVKKYFPVVGK					
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPQWDLGAYASEKLREAKYAFSETEVKKYFPVVGK					
	310	320	330	340	350	360
	370	380	390	400	410	420
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQQNGKTIGGVYMDLYAREGKRGGAWM					
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAPPVVGKEARLSHDEILTLFHETGHGLHLLTQVD					
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVVGREARLSHDEILILFHETGHGLHLLTQVD					
	430	440	450	460	470	480
	490					
g128-1.pep	ELGVSGINGVK					
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 491>:

a128-1.seq

```

1  ATGACTGACA ACGCACTGCT CCATTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCGGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTAC CACACGCCC GAACTGCGCG
251 CCGCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAACTC AACCCAGATC
401 TCGCGGATTT CGTCCTCAGC GGCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTGACGATG
551 CCGCACCCTG TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCATCC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACCTCGAAA ACGCCCTGCA
801 AACCGCAAAA CTGCTCGGCT TCAAAAATA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCGCGCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCGC AAGTCAAAGC
951 CTTCGCCCCG GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTAGCCCGG CGAAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAACG GACTGTTCGC
1101 CCAAAATCAA AAATCTACG GCATCGGATT TACCGAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGCGCG

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1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCGCGTCGGC
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAA ATTTTCGTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AACTTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAAT CCTTCAAAGC CTTCCGCGGA CGCGAACC GAATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 492; ORF 128-1.a>:

a128-1.pep

```
1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51 NTVEPLTGIT ERVGRIWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQQNGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTQLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDDMMIYS EDDEGRLLKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRWFQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAA*
```

m128-1/a128-1 97.8% identity in 677 aa overlap

	10	20	30	40	50	60
a128-1.pep	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT					
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a128-1.pep	ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
m128-1	ERVGRIWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130	140	150	160	170	180
a128-1.pep	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128-1	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
	190	200	210	220	230	240
a128-1.pep	FDDAAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
m128-1	FDDAAPLAGIPEDALAMFAAAQSESKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
	190	200	210	220	230	240
	250	260	270	280	290	300
a128-1.pep	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNLFHDL					
m128-1	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNLFHDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
a128-1.pep	ARRAKPYAEKDLAEVKAFARESLGLADLQPWDLGYAGEKLREAKYAFSETEVKKYFPVGK					
	: :					

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m128-1      ARRAKPYAEKDLAEVKAFARESLNLADLQPWDLGYASEKLREAKYAFSETEVKKYFPVVGK
              310      320      330      340      350      360

              370      380      390      400      410      420
a128-1.pep  VLNGLFAQIKKLYGIGFTEKTPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
              |||||
m128-1      VLNGLFAQIKKLYGIGFTEKTPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
              370      380      390      400      410      420

              430      440      450      460      470      480
a128-1.pep  NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
              |||||
m128-1      NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILTLFHETGHGLHLLTQVD
              430      440      450      460      470      480

              490      500      510      520      530      540
a128-1.pep  ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
              |||||
m128-1      ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
              490      500      510      520      530      540

              550      560      570      580      590      600
a128-1.pep  RGMFLVRQMEFALFDMMIYSEDDEGLKNWQQVLDVRKEVAVVRPPEYNRFANSFGHIF
              |||||
m128-1      RGMFLVRQMEFALFDMMIYSEDDEGLKNWQQVLDVRKKVAVIQPEYNRFALSFGHIF
              550      560      570      580      590      600

              610      620      630      640      650      660
a128-1.pep  AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
              |||||
m128-1      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
              610      620      630      640      650      660

              670      679
a128-1.pep  REPSIDALLRHSGFDNAAX
              |||||
m128-1      REPSIDALLRHSGFDNAVX
              670

```

a128-1/ P44573

sp|P44573|OPDA_HAEIN OLIGOPEPTIDASE A >gi|1075082|pir||C64055 oligopeptidase A (prlC) homolog
 - Haemophilus influenzae (strain Rd KW20)
 >gi|1573174 (U32706) oligopeptidase A (prlC) [Haemophilus influenzae Rd] Length = 681
 Score = 591 bits (1507), Expect = e-168
 Identities = 309/677 (45%), Positives = 415/677 (60%), Gaps = 4/677 (0%)

```

Query: 4  NALLHLGEEPRFDQIKTEDIKPALQTXXXXXXXXXXXXXTHTGWANTVEPLTGITERV 63
          N LL++ P F QIK E I+PA++ H W N + PLT +R+
Sbjct: 5  NPLLNIQGLPPFSQIKPEHIRPAVEKLIQDCRNTIEQVLKQPHFTWENFILPLTETNDRL 64

Query: 64  GRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFDTLS 123
          R W VSHLNSV ++ ELR AY +P ++ + T +GQ LYN + +KNS EF S
Sbjct: 65  NRAWSPVSHLNSVKNSTELREAYQTCLPLLSEYSTWVGQHKGLYNAYLALKNSAEFADYS 124

Query: 124  HAQKTKLNHDLRDFVLSGAELPPEQQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIYFDD 183
          AQK + + LRDF LSG L E+Q ++ ++L+++FS NVLDAT + ++
Sbjct: 125  IAQKKAIEENSLRDFELSGIGLSEKQQRIGEIVARLSELNSQFSNNVLDATMGWEKLIEN 184

Query: 184  AAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYVTRA 243
          A LAG+PE AL +A+S+G GY+ L+IP YL V+ Y +NR LRE++YRAY TRA
Sbjct: 185  EABELAGLPESALQAAQQAESKGLKGYRFTLEIPSYLPVMTYCENRALREEMYRAYATRA 244

Query: 244  SELSDD-GKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDLAR 302
          SE + GK+DN+ ++ L ++ AKLLGF Y ELSLATKMA+ P+QVL+FL LA
Sbjct: 245  SEQGPNAGKWDNSKVMEEILTLRVELAKLLGFNTYTELSLATKMAENPQQVLDFLDHLAE 304

Query: 303  RAKPYAEKDLAEVKAFARESLGLADLQPWDLGYAGEKLREAKYAFSETEVKKYFPVGVKVL 362
          RAKP EK+L E+K + + G+ +L PWD+G+ EK ++ YA ++ E++ YFP +V+
Sbjct: 305  RAKPQGEKELQELKGYCEKEFGVTELPWDIGFYSEKQKQHLAYAINDEELRPYPENRVI 364

```

Query: 363 NGLFAQIKKLYGIGFTE-KTVPVWHKDVRYFEL-QQNGETIGGVYMDLYAREGKRGGAWM 420
 +GLF IK+++ I E K V WHKDVR+F+L +N + G Y+DLYARE KRGGAWM
 Sbjct: 365 SGLFELIKRIFNIRAVRKGVDTHWKDVRFFDLIDENDQLRGSFYLDLYAREHKRGGAWM 424

Query: 421 NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEIXXXXXXXXXXXXXXXXXXQVD 480
 +D GR+R DG+++ P AYL CNF P+G K A +H+E+ Q+D
 Sbjct: 425 DDCIGRKRKLDGSIETPVAYLTCNFNAPIGNKPALFTHNEVTTLFHEFGHGIHMLTQID 484

Query: 481 ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ 540
 V+GINGV WDAVELPSQFMEN+ WE LA +S H ETG PLPKE ++L AKNFQ
 Sbjct: 485 VSDVAGINGVPPWDAVELPSQFMENWCWEEALAFISGHYETGEPLPKEKLTQLLAKNFQ 544

Query: 541 RGMFLVRQMEFALFDMMIYSEDDEGR LKNWQQVLDVSRKEVAVVRPEYNRFANSFGHIF 600
 MF++RQ+EF +FD ++ D + L SV+ +VAV++ ++ R +SF HIF
 Sbjct: 545 AAMFILRQLEFGIFDFRLHHTFDAEKTNQILD LKSVKSVQVAVIKGVVDWARAPHSHIF 604

Query: 601 XXXXXXXXXXXXXWAEVLSADAYAAFEESDDV-AATGKRFWQEILAVGGSRSAAESFKA FR 659
 WAEVLSADAY+ FEE TKG F EIL GGS E FK FR
 Sbjct: 605 AGGYAAGYYSYLWAEVLSADAYS RFEEGIFNPITGKSFLDEILTRGGSSEEPME LFKRFR 664

Query: 660 GREPSIDALLRHSGFDN 676
 GREP +DALLRH G N
 Sbjct: 665 GREPQLDALLRHKGIMN 681

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 493>:

g129.seq

```

1  ATGCTTTCAC CTCCTCGGCG TAAAACGGCG GCACATCAAT CAAGCCGTCT
51  TTCATTTGCG TGCAGAAAAA ATGCGGCGTG TTGCCGTGAT CAAAATCAAT
101 ATCGTG CAGC ATCCAGCCCA AATCGCGGTT TGCCTCGCTT TCCGATAACG
151 CCCACGGCGG CAGCGGTTCA CCCTTATCCG CGCTTTCGCC ATTTGCCCTT
201 TCAGGCTGCG GGCATAGGGG CGGAACAGGC GCGGTCGAA TCCTGTTTCA
251 TCCGGACAAA CGCGTTGGCA GTCGGAAT CCGGCCGCC GTGTCAAATA
301 ATGCGTTACT TTGGCCGGGT CTGTCTCTT GTAAGCGGCG GTCTTTTTTT
351 GCGCGCCATC CGCATCTGTT TGGGCGCATG GCAAACGGCG GCTGCCGTAC
401 AATCAAAATG TTTGGCGATT TCATGCAGAC AGGCATCCGG ATGCCGCCCG
451 ACATATCGAG CCGGTTTTTG CCTATCCGAT TTGGCGGCAT TTAGGCCGGT
501 AACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 494; ORF 129.ng>:

g129.pep

```

1  MLSPPRRKA AHQSSRLSFA CGKNAACCRD QNQYRAASSP NRGLPRFPIT
51  PTAAAVHPYP RFRHLFPQAA GIGAEQAAVE SCFIRTNALA VGKSGRPCQI
101 MRYFGRVLSF VSGGLFLRAI RICLGAWQTA AAVQSKCLAI SCRQASGCRP
151 TYRAGFCLSD LAAFRPVT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 495>:

m129.seq (partial)

```

1  ..TATCTGCGCT TTCACTATTT GCCCTTTCAG GCTGCGGGCA TAGGGACGGA
51  ACAGGTAGCG GTCAAATCCT GTTTCATCCA AATAAACACG TTGGTAGTCG
101 GAAAATTCGG CCGGCTGTGT CAAATAATGC GTTACTTTGG CCGGGTCTTG
151 TTCTTTGTAA GTGGTGGTCT TTTTTCGCGC GTTATCCCCA TCTGTTTGAG
201 TGCATAGCAA ATGGTGGCTG CCGTACAATC AAAATGTTTG GCGATTTCAT
251 GCAGATAGGC ATCCGGGTGT TGCCCAACAT ATTGAGCCGG TTTTTCCTA
301 TCCGATTGA CCGCATTTAG ACCGGTAACT TGA

```

This corresponds to the amino acid sequence <SEQ ID 496; ORF 129>:

m129.pep (partial)

```

1  ..YLRFHYPFQ AAGIGTEQVA VKSCFIQINT LVVGKFGRLC QIMRYFGRVL
51  FFVSGGLFLR VIPICLSAXQ MVAAVQSKCL AISCRXASGC CPTYXAGFCL
101 SDLTAFRPVT *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 129 shows 79.1% identity over a 110 aa overlap with a predicted ORF (ORF 129.ng) from *N. gonorrhoeae*:

m129/g129

```

                                10      20      30
m129.pep                      YLRFHYLPFQAAGIGTEQVAVKSCFIQINT
                                | |::| | | | | | | | | | | | | | | | | | | | | |
g129      RDQNQYRAASSPNRGLPRFPITPTAAAVHPYPRFRHLPFQAAGIGAEQAAVESCFIRTNA
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m129.pep      LVVGKFGRLCQIMRYFGRVLFVVS GGLFLRVIPICLSAXQMVA AVQSKCLAISCRXASGC
                |::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g129      LAVGKSGRPCQIMRYFGRVLSFVS GGLFLRAIRICLGAWQTAA AVQSKCLAISCRQASGC
                90      100     110     120     130     140

                                100     110
m129.pep      CPTYXAGFCLSDLTAFRPVTX
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g129      RPTYRAGFCLSDLA AFRPVTX
                150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 497>:

```

a129.seq (partial)
1   TATCTGCGCT TTCACTATTT GCCCTTTCAG GCTGCGGGCA TAGGGACGGA
51  ACAGGTAGCG GTCAAATCCT GTTTCATCCA AATAAACACG TTGGTAGTCG
101 GAAATTCGG CCAGCTGTGT CAAATAATGC GTTACTTTGG CCGGGTCTTG
151 TTCTTTGTAA GTGGTGGTCT TTTTTTGCGC GTTATCCCA TCTGTTTGAG
201 TGCATAGCAA ATGGTGGCTG CCGTACAATC AAAATGTTG GCGATTTTCA
251 GCAGATAGGC ATCCTGGTGT TGCCCAACAT ATTGAGCCGG TTTTGCCTA
301 TCCGATTGTA CGGCATTTAG ACCGTAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 498; ORF 129.a>:

```

a129.pep (partial)
1   YLRFHYLPFQ AAGIGTEQVA VKSCFIQINT LVVGKFGQLC QIMRYFGRVL
51  FFVSGGLEFLR VIPICLSA*Q MVA AVQSKCL AISCR*ASWC CPTY*AGFCL
101 SDLTAFRPVT *

```

m129/a129 98.2% identity in 110 aa overlap

```

                                10      20      30      40      50      60
m129.pep      YLRFHYLPFQAAGIGTEQVAVKSCFIQINTLVVGKFGRLCQIMRYFGRVLFVVS GGLFLR
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a129      YLRFHYLPFQAAGIGTEQVAVKSCFIQINTLVVGKFGQLCQIMRYFGRVLFVVS GGLFLR
                10      20      30      40      50      60

                                70      80      90      100     110
m129.pep      VIPICLSAXQMVA AVQSKCLAISCRXASGCCPTYXAGFCLSDLTAFRPVTX
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a129      VIPICLSAXQMVA AVQSKCLAISCRXASWCCPTYXAGFCLSDLTAFRPVTX
                70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 499>:

```

g130.seq
1   ATGAAACAAC TCCGCGACAA CAAAGCCCAA GGCTCTGCAC TGTTTACCCT
51  TGTGAGCGGT ATCGTTATTG TTATTGCAGT CCTTTATTTC CTGATTAAGC
101 TGGCGGGCAG TGGATCGTTC GCGATGTCG ATGCCACTAC GGAAGCGGCA
151 ACGCAGACCC GCATCCAGCC TGTCGGACAA TTGACGATGG GTGACGGCAT
201 CCCCCTCGGC GAACGCCAAG GCGAACAGAT TTTCGGCAA ATCTGTATCC

```



```

251 AATGCCACGC GCGGACAGC AATGTGCCGA ACGCTCCGAA ACTGGAACAC
301 AACGGCGACT GGGCGCCGCG TATCGCGCAA GGCTTCGATA CCTTGTTCCA
351 ACACGCGCTG AACGGCTTTA ACGCCATGCC TGCCAAAGGC GGTGCGGCAG
401 ACCTGACCGA TCAGGAACTC AAACGGGCGA TTACCTACAT GGCGAATAAA
451 AGCGGCGGTT CTTTCCCAGG TCCTGATGAG GCTGCGCCTG CCGACAATGC
501 CGCTTCAGGA ACAGCTTCTG CTCCTGCCGA TAGTGCAGCT CCGGCAGAAG
551 CGAAGGCAGA AGACAAGGGT GCGGCAGCCC CTGCGGTCGG CGTTGACGGT
601 AAAAAAGTCT TCGAAGCAAC CTGTCAGGTG TGCCACGGCG GTTCGATTCC
651 CCGTATTCCC GGCATAGGCA AAAAAGACGA TTGGGCACCG CGTATCAAAA
701 AAGGCAAAGA AACCTTGCAC AAACATGCCC TTGAAGGCTT TAACGCGATG
751 CCGGCCAAAG GCGGCAATGC AGGTTTGAGC GATGACGAA TCAAAGCGGC
801 TGTGACTAT ATGGCAAACC AATCCGGTGC AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 500; ORF 130.ng>:

```

g130.pep
  1 MKQLRDNKAQ GSALFTLVSG IVIVIAVLYF LIKLAGSGSF GDVDATTEAA
 51 TQTRIQPVGQ LTMGDGIPVG ERQGEQIFGK ICIQCHAADS NVPNAPKLEH
101 NGDWAPRIAQ GFDTLFQHAL NGFNAMPAKG GAADLTQDEL KRAITYMANK
151 SGGSFNPDE AAPADNAASG TASAPADSAA PAEAKAEDKG AAPAVGVVDG
201 KKVFEATCQV CHGGSIPGIP GIGKKDDWAP RIKKGKETLH KHALEGFNAM
251 PAKGGNAGLS DDEVKAAVDY MANQSGAKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 501>:

```

m130.seq (partial)
  1 ..GGCGAACAGA TTTTCGGCAA AATCTGTATC CAATGCCACG CCGCGGACAG
 51 CAATGTGCCG AACGCTCCGA AACTGGAACA CAACGGCGAT TrGGCACC GC
101 GTATCGgCAA GGCTTCGATA CCTTGTTCCA ACACGCGCTG AACGGCTTTA
151 ACGCCATGCC TGCAAAAGGC GGTGCGGCAG ACCTGACCGA TCAGGAACTT
201 AAACGGGCGA TTACTTACAT GGCGAACAAA AGCGGCGGTT CTTTCCCAGG
251 TCCTGATGAG GCTGCGCCTG CCGACAATGC CGCTTCAGGA ACAGCTTCTG
301 CTCCTGCCGA TAGTGCAGCT CCGGCAGAAG CGAAGGCAGA AGACAAGGGT
351 GCGGCACcCC TGCGGTCTGC GTTGACGGTA AAAAAAGTCTT CGAAGCAACC
401 TGTCAGGTGT GCCACGGCGG TTCGATTCCC GGTATTCCCG GCATAGGCAA
451 AAAAGACGAT TGGGCACCGC GTATCAAAAA AGGCAAAGAA ACCTTGACA
501 AACACGCCCT TGAAGGCTTT AACGCGATGC CTGCCAAaG CGgCAATGCA
551 GGTTTGAGCG ATGACGAaGT CAAAGCGGCT GTTGACTATA TGGCAAACCA
601 ATCCGGTGCA AAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 502; ORF 130>:

```

m130.pep (partial)
  1 ..GEQIFGKICI QCHAADSNVP NAPKLEHNGD XAPRIQGFDT LFQHALNGFN
 51 AMPAKGGAAD LTDQELKRAI TYMANKSGGS FPNPDEAAPA DNAASGTASA
101 PADSAPAEA KAEDKGAAPA VGVDGKKVFE ATCQVCHGGS IPGIPGIGKK
151 DDWAPRIKKG KETLHKHALE GFNAMPAKXG NAGLSDEVK AAVDYMANKS
201 GAKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 130 shows 98.1% identity over a 206 aa overlap with a predicted ORF (ORF 130.ng) from *N. gonorrhoeae*:

```

m130/g130
m130.pep
                                     10      20      30
                                     GEQIFGKICIQCHAADSNVPNAPKLEHNGD
                                     |||
g130      DATTEAATQTRIQPVGQLTMGDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD
                                     50      60      70      80      90     100

                                     40      50      60      70      80      89
m130.pep      XAPRI-QGFDTLFQHALNGFNAMPAKGGAADLTQDELKRAITYMANKSGGSFPNPDEAAP
                                     |||
g130      WAPRIAQGFDTLFQHALNGFNAMPAKGGAADLTQDELKRAITYMANKSGGSFPNPDEAAP
                                     110     120     130     140     150     160

```

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```

          90      100      110      120      130      140
m130.pep  ADNAASGTASAPADSAAPEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          |||||
g130      ADNAASGTASAPADSAAPEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          170      180      190      200      210      220

          150      160      170      180      190      200
m130.pep  KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDDEVKAAVDYMANQSGAKFX
          |||||
g130      KKDDWAPRIKKGKETLHKHALEGFNAMPKGGNAGLSDDEVKAAVDYMANQSGAKFX
          230      240      250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 503>:

```

a130.seq
1  ATGAAACAAC TCCGCGACAA CAAAGCCCAA GGCTCTGCAC TGTTTACCCT
51  TGTGAGCGGT ATCGTTATTG TTATTGCAGT CCTTTATTTT CTGATTAAGC
101 TGGCGGGCAG CGGCTCGTTC GGCGATGTCG ATGCCACTAC GGAAGCAGCA
151 ACGCAGACCC GTATCCAGCC TGTCGGACAA TTGACGATGG GCGACGGCAT
201 CCCCCTCGGC GAACGCCAAG GCGAACAGAT TTTCCGCAAA ATCTGTATCC
251 AATGCCACGC GCGGCACAGC AATGTGCCGA ACGCTCCGAA ACTGGAACAC
301 AACGGCGATT GGGCGCCGCG TATCGCGCAA GGCTTCGATA CCTTGTTCCT
351 ACACGCGCTG AACGGCTTTA ACGCCATGCC TGCCAAAGGC GGTGCGGTAG
401 ACCTGACCGA TCAGGAATC AAACGGGCGA TTACTTACAT GGCGAACAAA
451 AGCGGCGGTT CTTTCCCGAA TCCTGATGAG GCTGCGCCTG CCGACAATGC
501 CGCTTCAGGA ACAGCTTCTG CTCCTGCCGA TAGTGCAGCT CCGGCAGAAG
551 CGAAGGCAGA AGACAAGGGT GCGGCAGCCC CTGCGGTCGG CGTTGACGGT
601 AAAAAAGTCT TCGAAGCAAC CTGTCAAGTG TGCCACGGCG GTTCGATTCC
651 CGGTATTCCC GGCATAGGCA AAAAAGACGA TTGGGCACCG CGTATCAAAA
701 AAGGCAAAGA AACCTTGCAC AAACACGCCC TTGAAGGCTT TAACGCGATG
751 CCTGCCAAAG GCGGCAATGC AGGTTTGAGC GATGACGAAG TCAAAGCGGC
801 TGTGACTAT ATGGCAAACC AATCCGGTGC AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 504; ORF 130.a>:

```

a130.pep
1  MKQLRDNKAQ GSALFTLVSG IVIVIAVLYF LIKLAGSGSF GDVDATTEAA
51  TQTRIQPVGQ LTMGDGIPVG ERQGEQIFGK ICIQCHAADS NVNPAPKLEH
101 NGDWAPRIAQ GFDTLFQHAL NGFNAMPAKG GAVDLTDQEL KRAITYMANK
151 SGGSFNPDE AAPADNAASG TASAPADSAA PAEAKAEDKG AAPAVGVDG
201 KKVFEATCQV CHGGSIPGIP GIGKKDDWAP RIKKGKETLH KHALEGFNAM
251 PAKGGNAGLS DDEVKAAVDY MANQSGAKF*

```

m130/a130 97.6% identity in 206 aa overlap

```

          10      20      30
m130.pep  GEQIFGKICIQCHAADSNVPNAPKLEHNGD
          |||||
a130      DATTEAATQTRIQPVGQLTMGDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD
          50      60      70      80      90      100

          40      50      60      70      80      89
m130.pep  XAPRI-QGFDTLFQHALNGFNAMPAKGGAADLTDQELKRAITYMANKSGGSFNPDEAAP
          ||| |||||
a130      WAPRIAQGFDTLFQHALNGFNAMPAKGGAADLTDQELKRAITYMANKSGGSFNPDEAAP
          110      120      130      140      150      160

          90      100      110      120      130      140
m130.pep  ADNAASGTASAPADSAAPEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          |||||
a130      ADNAASGTASAPADSAAPEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          170      180      190      200      210      220

          150      160      170      180      190      200
m130.pep  KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDDEVKAAVDYMANQSGAKFX

```

```

a130      |||||
          KKDDWAPRIKKGKETLHKHLEGFNAMPAGGNAGLSDDDEVKAAVDYMANQSGAKFX
          230      240      250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 505>:

```

g132.seq
1  ATGGAAGCCT  TCAAAACCTT  AATTTGGATT  ATTAATATTA  TTTCCGCTTT
51  GGCCGTCATC  GTGTTAGTAT  TGCTCCAACA  CGGCAAAGGC  GCGGATGCCG
101 GCGCGACCTT  CGGATCGGGA  AGCGGCAGCG  CGCAAGGCGT  ATTCGGCTCT
151 GCCGGCAACG  CCAACTTcct  CAgccGCTCG  AccGccGTTG  CAGCAACAtt
201 tttcttTGca  acctgcAtgg  gctatggTgt  atattcacac  CCACACGACA
251 AAACACGGTT  TGGACTtcag  caacataCGA  CAGACTCAGC  AagcACCCAA
301 ACCcgtAAGC  AATACCGAAC  CTTCTGCCCC  TGTTCCTCAG  CAGCAGAAAT
351 AACagtTTTT  CAAATgccga  catGgtga

```

This corresponds to the amino acid sequence <SEQ ID 506; ORF 132.ng>:

```

g132.pep
1  MEAFKTLIWI  INIISALAVI  VLVLLQHGKG  ADAGATFGSG  SGSAQGVFGS
51  AGNANFLSRS  TAVAATFFFA  TCMGYGVYSH  PHDKTRFGLQ  QHTTDSASTQ
101 TRKQYRTFCP  CSSAAEITVF  QMPTW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 507>:

```

m132.seq (partial)
1  ATGGAACCTT  TCAAAACCTT  AATTTGGATT  GTTAATTTAA  TTTCCGCTTT
51  GGCCGTCTTC  GTGTTAGTAT  TGCTCCAACA  CGGCAAAGGC  GCGGATGCCG
101 GCGCGACTTT  CGGA...

```

This corresponds to the amino acid sequence <SEQ ID 508; ORF 132>:

```

m132.pep (partial)
1  MEPFKTLIWI  VNLISALAVF  VLVLLQHGKG  ADAGATFG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 132 shows 89.5% identity over a 38 aa overlap with a predicted ORF (ORF 132.ng) from *N. gonorrhoeae*:

```

m132/g132
          10      20      30
m132.pep  MEPFKTLIWI  VNLISALAVF  VLVLLQHGKG  ADAGATFG
          || ||||| ||: |||||: ||||| ||||| |||||
g132      MEAFKTLIWI  INIISALAVI  VLVLLQHGKG  ADAGATFGSGSGSAQGVFGSAGNANFLSRS
          10      20      30      40      50      60

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 509>:

```

a132.seq
1  ATGGAAGCCT  TCAAAACCTT  AATTTGGATT  GTTAATATAA  TTTCCGCTTT
51  GGCCGTCATC  GTGTTAGTAT  TGCTCCAACA  CGGCAAAGGC  GCGGATGCCG
101 GCGCGACTTT  CGGATCGGGA  AGCGGCAGCG  CGCAAGGCGT  ATTCGGCTCT
151 GCCGGCAACG  CTAACCTCCT  CAGCCGCTCG  ACCGCCGTTG  CAGCAACATT
201 TTTCTTTGCA  ACCTGCATGg  GCTATGGTGT  ATATTCACAC  CCACACGACA
251 AAACACGGTT  TGGACTTCAG  CAACGTACAA  CAAACTCAGC  AAGCACCCAA
301 ACCCGTAAGC  AATACCGAAC  CTTCTGCCCC  TGTTCCTCAG  CAGCAGAAAT
351 AACAGTTTTT  CAAATGCCGA  CATGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 510; ORF 132.a>:

```

a132.pep
1  MEAFKTLIWI  VNIISALAVI  VLVLLQHGKG  ADAGATFGSG  SGSAQGVFGS
51  AGNANFLSRS  TAVAATFFFA  TCMGYGVYSH  PHDKTRFGLQ  QRTTNSASTQ
101 TRKQYRTFCP  CSSAAEITVF  QMPTW*

```

m132/a132 92.1% identity in 38 aa overlap

378

	10	20	30	
m132.pep	MEPFKTLIWIIVNLISALAVFVLVLLQHGKGADAGATFG			
	: :			
a132	MEAFKTLIWIIVNIISALAVIVLVLLQHGKGADAGATFGSGSGSAQGVFGSAGNANFLSRS			
	10	20	30	40 50 60

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 511>:

g134.seq

1	ATGTCCCAAG	AAATCCTCGA	CCAAGTGCGC	CGCCGCCGCA	CGTTTGCCAT
51	CATCTCCAC	CCCGATGCGG	GTAAAACCAC	GCTGACCGAA	AAACTGCTGC
101	TGTTTTTCGGG	CGCGATTCAA	AGCGCAGGCA	CGGTGAAAGG	TAAGAAAACC
151	GGCAAATTCG	CCACCTCCGA	CTGGATGGAC	ATCGAGAAGC	AGCGCGGCAT
201	TTCCGTGGCA	TCAAGCGTGA	TGCAGTTCGA	CTACAAAGAC	CACACCGTCA
251	ACCTCTTGGA	CACGCCGGGA	CACCAAGACT	TCTCCGAAGA	CACCTACCGC
301	GTTTTAACCG	CAGTGGACAG	CGCCTTGATG	GTCATCGACG	CGGCAAAAGG
351	CGTGAAGCG	CAAACCATCA	AACTCTTGAA	CGTCTGCCGC	CTGCGCGATA
401	CGCCGATTGT	TACCTTCATG	AACAAATACG	ACCGCGAAGT	GCGCGATTCT
451	TTGGAATCT	TGGACGAAGT	GGAAGACATC	CTGCAAATCC	GCTGCGCGCC
501	CGTTACCTGG	CCGATCGGTA	TGGGCAAAAA	CTTCAAGGGC	GTGTACCACA
551	TCCTGAACGA	CGAAATCTAT	CTCTTTGAAG	CGGGCGGCGA	ACGCCTGCCG
601	CACGAGTTCG	ACATCATCAA	AGGCATAAAC	AATCCCGAAT	TGGAACAACG
651	CTTTCCGTTG	GAAATCCAGC	AGTTGCGCGA	CGAAATCGAA	TTGGTGCAGG
701	CGGCTTCCAA	CGAATTTAAT	CTCGacgaAT	TTCTCGccgG	CGAACTCACG
751	CCAGTGTTC	TCGGCTCTGC	GATTAACAAC	TTCGGCATTC	AGGAAATCCT
801	CAATTCATG	ATTGACTGGG	CACCCGCACC	GAAACCGCGC	GACGCGACCA
851	TCGCGATGGT	CGGGCCGGAC	GAGCCGAAAT	TTTCCGGATT	TATCTTTAAA
901	ATCCAAGCCA	ATATGGACCC	GAAACACCGC	GACCGTATCG	CCTTCTTGCG
951	CGTCTGCTCC	GGTAAATTCG	AGCGCGGCAT	GAAGATGAAA	CACCTGCGTA
1001	TCAACCGCGA	AATCGCCGCC	TCCAGCGTAG	TAACCTTCAT	GTCGCACGAC
1051	CGCGAACTGG	CGGAAGAAGC	CTACGCCGGC	GACATCATCG	GCATCCCGAA
1101	CCACGGCAAC	ATCCAATTCG	GCGACAGCTT	CTCCGAAGGC	GAACAACTGG
1151	CGTTTACCGG	CATCCCATTC	TTGCGGCCCG	AACTGTTC	CAGCGTCCGC
1201	ATCAAAAACC	CGCTGAAAAT	CAAACAAC	CAAAAAGGTT	TGCAACAACT
1251	CGGCGAAGAA	GGTGCGGTT	AAGTATTCAA	ACCGATGAGC	GGCGCGGATT
1301	TGATTTTGGG	TGCGGTCGGC	GTGTTGCAGT	TTGAAGTCGT	AACCTCACGC
1351	CTCGCCAACG	AATACGGCGT	GGAAGCCGTG	TTGACAGCG	CATCCATCTG
1401	GTCGGCGCGC	TGGGTATCGT	GCGACGACAA	GAAAAA	CTGCGGAATTTG
1451	AAAAAGCCAA	CGCAGGCAAC	CTCGCCATCG	ACGCAGGCGG	CAACCTCGCC
1501	TACCTCGCCC	CCAACCGCGT	GAATTTGGGG	TTGACGCAAG	AACGCTGGCC
1551	GGACATCGTG	TTCCACGAAA	CGCGCGAACA	TTCGGTCAAA	CTCTAA

This corresponds to the amino acid sequence <SEQ ID 512; ORF 134.ng>:

g134.pep

1	MSQEILDQVR	RRRTFAIISH	PDAGKTLTE	KLLLFSGAIQ	SAGTVKGKKT
51	GKFATSDWMD	IEKQRGISVA	SSVMQFDYKD	HTVNLLDTPG	HQDFSEDYR
101	VLTAVDSALM	VIDAAKVEA	QTIKLLNVCR	LRDTPIVTFM	NKYDREVRDS
151	LELLDEVEDI	LQIRCAPVTW	PIGMGKNFKG	VYHILNDEIY	LFEAGGERLP
201	HEFDIIKGIN	NPELEQRFPL	EIQQLRDEIE	LVQAASNEFN	LDEFLLAGELT
251	PVFFGSAINN	FGIQEILNSL	IDWAPAPKPR	DATMRMVGPD	EPKFSGFIFK
301	IQANMDPKHR	DRIAFRLVCS	GKFERGMKMK	HLRINREIAA	SSVVTFSMD
351	RELAEEAYAG	DIIGIPNHGN	IQIGDSFSEG	EQLAFTGIPF	FAPELFRSVR
401	IKNPLKIKQL	QKGLQQLGEE	GAVQVFKPMS	GADLILGAVG	VLQFEVVTSR
451	LANEYVEAV	FDSASIWSAR	WVSCDDKKKL	AEFEKANAGN	LATDAGGNLA
501	YLAPNRVNLG	LTQERWPDIV	FHETREHSVK	L*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 513>:

m134.seq

1	ATGTCCCAAG	AAATCCTCGA	CCAAGTGCGC	CGCCGCCGCA	CGTTTGCCAT
51	CATCTCCAC	CCTGACGCAG	GTAAAACCAC	GTTGACTGAA	AAACTCTTGC
101	TGTTTTTCGGG	CGCGATTGAG	AGCGCGGGTA	CGGTAAAAGG	CAAGAAAACC
151	GGCAAATTCG	CCACTTCCGA	CTGGATGGAA	ATCGAGAAGC	AGCGCGGCAT

```

201 TTCCGTGGCA TCAAGTGTGA TGCAGTTCGA TTACAAAGAC CACACCGTCA
251 ACCTCTTGA CACGCCGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTAACCG CCGTGGACAG CGCATTAATG GTCATCGACG CGGCAAAAGG
351 CGTGAAGCG CAAACCATCA AGCTCTTAAA CGTCTGCCGC CTGCGCGATA
401 CACCGATTGT TACGTTTATG AACAAATACG ACCGCGAAGT GCGCGATTCC
451 CTGGAACCTT TGGACGAAGT GGAAAACATT TAAAAAATCC GCTGCGCGCC
501 CGTTACCTGG CCGATCGGTA TGGGCAAAAA CTTCAAGGGC GTGTACCACA
551 TCCTGAACGA TGAATTTTAT CTCTTTGAAG CTGGCGGCGA ACGCCTGCCG
601 CACGAGTTCG ACATCATCAA AGGCATCGAT AATCCTGAAT TGGAAACAACG
651 CTTTCCGTTG GAAATCCAGC AGTTGCGCGA CGAAATCGAA TTGGTGACAG
701 CGGCTTCCAA CGAGTTTAAT CTCGACGAAT TCCTCGCCGG CGAACTCACG
751 CCCGTATTCT TCGGCTCTGC GATTAACAAC TTCGGTATTC AGGAAATCCT
801 CAATTCATTG ATTGACTGGG CGCCCGCGCC GAAACCGCGC GACGCGACCG
851 TACGTATGGT CGAGCCGAC GAGCCGAAGT TTTCCGGATT TATCTTCAAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATTG CCTTCTTGCG
951 CGTCTGCTCC GGCAAATTCG AGCGCGGCAT GAAGATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TTACCTTCAT GTCGCACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGGC GACATTATCG GCATCCCGAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACTGG
1151 CGTTTACCAG CATCCCATTC TTCGCACCCG AACTGTTCCG CAGCGTACGC
1201 ATCAAAAACC CGCTGAAAAT CAAACAACCTG CAAAAAGGCT TGCAACAGCT
1251 CGGCGAAGAA GCGCGGTGTC AGGTGTTCAA ACCGATGAGC GCGCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTTGCAGT TTGAAGTCGT TACCTCGCGC
1351 CTCGCCAACG AATACGGCGT AGAAGCCGTG TTCGACAGCG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAAGT GCTGAATTTG
1451 AAAAAGCCAA CGCGGGCAAC CTCGCCATCG ACGCAGCGCG CAACCTCGCC
1501 TACCTCGCCC CCAACCGCGT GAATTTGGGA CTCACGCAAG AACGTTGGCC
1551 GGACATCGTG TTCCACGAAA CACGCGAACA TTCGGTCAAA CTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 514; ORF 134>:

```

m134 . pep
  1 MSQEILDQVR RRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
 51 GKFATSDWME IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRDTPIVTFM NKYDREVRDS
151 LELLDEVENI LKIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKID NPELEQRFPL EIQQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IDWAPAPKPR DATVRMVEPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELVEEAYAG DIIGIPNHGN IQIGDSFSEG EQLAFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYGVEAV FDSASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 134 shows 98.7% identity over a 531 aa overlap with a predicted ORF (ORF 134.ng) from *N. gonorrhoeae*:

```

m134/g134
      10      20      30      40      50      60
m134 . pep MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWME
          |||
g134      MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWMD
          |||
      10      20      30      40      50      60

      70      80      90     100     110     120
m134 . pep IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDLSALMVIDAAGVEA
          |||
g134      IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDLSALMVIDAAGVEA
          |||
      70      80      90     100     110     120

      130     140     150     160     170     180

```

380

m134 . pep	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLLDEVENILKIRCAPVTWPIGMGKNFKG
g134	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLLDEVEDILQIRCAPVTWPIGMGKNFKG
	130 140 150 160 170 180
m134 . pep	190 200 210 220 230 240
	VYHILNDEIYLF EAGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN
g134	VYHILNDEIYLF EAGGERLPHEFDIIKGINNPELEQRFPLEIQQLRDEIELVQAASNEFN
	190 200 210 220 230 240
m134 . pep	250 260 270 280 290 300
	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATVRMVEPDEPKFSGFIFK
g134	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATMRMVGPDPEPKFSGFIFK
	250 260 270 280 290 300
m134 . pep	310 320 330 340 350 360
	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFMSHDRELVEEAYAG
g134	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFMSHDRELAEEAYAG
	310 320 330 340 350 360
m134 . pep	370 380 390 400 410 420
	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE
g134	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE
	370 380 390 400 410 420
m134 . pep	430 440 450 460 470 480
	GAVQVFKPMSGADLILGAVGVQLQFEVVTSRLANEYGVEAVFDSASIWSARWVSCDDKKKL
g134	GAVQVFKPMSGADLILGAVGVQLQFEVVTSRLANEYGVEAVFDSASIWSARWVSCDDKKKL
	430 440 450 460 470 480
m134 . pep	490 500 510 520 530
	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
g134	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
	490 500 510 520 530

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 515>:

a134 . seq

1	ATGTCCCAAG	AAATCCTCGA	CCAAGTGCGC	CGCCGCCGCA	CGTTTGCCAT
51	CATCTCCAC	CCTGACGCAG	GTAAAACCAC	GTTGACTGAA	AAACTCTTGC
101	TGTTTTCAGG	TGCGATTCAA	AGCGCGGGTA	CGGTAAAAGG	CAAGAAAACC
151	GGCAAATTCG	CCACCTCCGA	CTGGATGGAC	ATCGAGAAGC	AGCGCGGCAT
201	TTCCGTGGCA	TCAAGCGTGA	TGCAGTTCGA	CTATAAGAC	CACACCGTCA
251	ACCTTTTGGA	CACGCCGGGA	CACCAAGACT	TCTCCGAAGA	CACCTACCGC
301	GTTTTGACCG	CCGTCGATAG	TGCCTTGATG	GTATCGACG	CGGCAAAAGG
351	CGTGAAGCG	CAAACCATCA	AACTCTTGAA	CGTCTGCCGC	CTGCGCAATA
401	CGCGGATTGT	TACGTTTCATG	AACAAATACG	ACCGCGAAGT	GCGCGATTCC
451	CTGGAATTGC	TGGACGAAGT	GGAAAACATC	CTGCAAATCC	GCTGCGCGCC
501	CGTAACCTGG	CCGATCGGCA	TGGGCAAAAA	CTTCAAAGGC	GTGTACCACA
551	TCCTGAACGA	CGAAATCTAT	CTCTTTGAAG	CGGGCGGCGA	ACGCTTGCCG
601	CACGAGTTCG	ACATCATCAA	AGGCATCGAT	AATCCCGAAT	TGGAACAACG
651	CTTTCCGTTA	GAAATACAGC	AGTTGCGCGA	CGAAATCGAA	TTGGTGCAGG
701	CGGCTTCCAA	CGAGTTCAAT	CTCGACGAAT	TCCTCGCCGG	CGAACTCAGG
751	CCCGTATTCT	TCGGCTCTGC	GATTAACAAC	TTCCGTATTC	AGGAAATCCT
801	CAATTTCATTG	ATTGAATGGG	CGCCCGCGCC	GAAACCACGC	GATGCGACCG
851	TGCGTATGGT	CGAGCCGGAC	GAGCCGAAGT	TTTCCGGATT	TATCTTCAAA
901	ATCCAAGCCA	ATATGGACCC	GAAACACCGC	GACCGTATTG	CCTTCTTGCG

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951 CGTCTGCTCC GGCAAATTCG AGCGCGGCAT GAAAATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TAACCTTCAT GTCCCACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGGC GACATTATCG GTATCCCAAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACCTGA
1151 CGTTTACCGG CATCCCATTC TTCGCGCCCG AACTGTTCCG CAGCGTTCCG
1201 ATCAAAAACC CGCTGAAAAT CAAGCAACTG CAAAAGGTT TGCAACAGCT
1251 TGGCGAAGAA GGTGCGGTGC AGGTGTTCAA ACCAATGAGC GGCGCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTTGCAGT TTGAAGTCGT TACCTCGCGC
1351 CTTGCCAACG AATACGGCGT GGAAGCCGTG TTCGACAACG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAATG GCGGAATTTG
1451 AAAAAGCCAA CGCGGGCAAC CTCGCCATCG ACGCGGGCGG CAACCTCGCC
1501 TACCTCGCCC CTAACGCGCT GAATCTGGGA CTCACGCAAG AACGCTGGCC
1551 GGACATCGTG TTCCACGAAA CGCGCGAGCA TTCGGTCAAA CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 516; ORF 134.a>:

```

a134.pep
1 MSQEILDQVR RRRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
51 GKFATSDWMD IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRNTPIVTFM NKYDREVRDS
151 LELLDEVENI LQIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKID NPELEQRFPL EIQQLRDEIE LVQAASNEFN LDEFELAGLT
251 PVFFGSAINN FGIQEILNSL IEWAPAPKPR DATVRMVEPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELVEEAYAG DIIGIPNHGN IQIGDSFSEG EQLTFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYGVEAV FDNASIWSAR WVSCDDKKKL AEFEKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

m134/a134 98.9% identity in 531 aa overlap

m134.pep	10	20	30	40	50	60
a134	10	20	30	40	50	60
m134.pep	70	80	90	100	110	120
a134	70	80	90	100	110	120
m134.pep	130	140	150	160	170	180
a134	130	140	150	160	170	180
m134.pep	190	200	210	220	230	240
a134	190	200	210	220	230	240
m134.pep	250	260	270	280	290	300
a134	250	260	270	280	290	300
m134.pep	310	320	330	340	350	360
a134	310	320	330	340	350	360

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	370	380	390	400	410	420
m134.pep	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
a134	DIIGIPNHGNIQIGDSFSEGEQLTFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m134.pep	GAVQVFKPMSGADLILGAVGVQLQFEVVT SRLANEYGV EAVFDSASIWSARWVSCDDKKKL					
a134	GAVQVFKPMSGADLILGAVGVQLQFEVVT SRLANEYGV EAVFDNASIWSARWVSCDDKKKL					
	430	440	450	460	470	480
	490	500	510	520	530	
m134.pep	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
a134	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 517>:

g135.seq

```

1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCG
51  TTCGGAcgGC AGCCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCTG CAGGGTTCGG CGCGCTGGGT TTCAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GTGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCGATTCCC ATCATCAATG
401 AAAACGACAC GGTTCGGTT GAGGAGTTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTTCGGC AAACGGCAGC GGCGGTATGC TGACCAAAAT
651 CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701 CCTCACTCAA ACCCGATTCA TTGGCCGAAG CCGCCGAACA TCAGGCGGAC
751 GGCTCGTTTT TCGTcccCcg tgCCAAAGGT TTGCGGACAC AGAAGCAATG
801 GctggCGTTC TATTcGaaa gcggGGgcag cgttTAtgtg gacgaaagtg
851 cggaacacgc tTgtccgaa caagggaaag cctgCTGA

```

This corresponds to the amino acid sequence <SEQ ID 518; ORF 135.ng>:

g135.pep

```

1  MKYKRIVFKV GTSSITRSDG SLRSGKIQTI TRQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQORRAIP IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHNHEIIEM
201 AGGSGSANGT GGMLTKIKAA TIAESGVPV YICSSLKPDS LAEAAEHQAD
251 GSFFVPRAKG LRTQKQWLAF YSESGGSVYV DESAEHALSE QGKAC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 519>:

m135.seq

```

1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCTGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCGG CAGGGTTCGG TGCGCTGGGT TTCAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCGCAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGGTT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT

```



```

501. GACCGACATA GACGGTCTTT ACACGGGCAA CCCGAACAGC AATCCCAGATG
551. CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601. GCGGGCGGCT CGGGTTCGGC AAACGGCACG GCGGGTATGC TGACCAAAAT
651. CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701. CCTCGCTCAA ACCCGATGCA CTGCCCAGG CTGCCGAACA TCAGGCGGAC
751. GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801. GCTGGCGTTC TATTCCGAAA GCCGGGGCAG CGTTTATGTG GACGAAGGTG
851. CGGAACACGC TTTGTCCGAA CAGGGGAAAA GCCTGCTGAT GTCGGGCATT
901. GCCGGAATCG AAGGGCATT TCCCGTATG GACACCGTAA CCGTGTACAG
951. CAAGGCAACC AAACAGCCCC TGGGCAAAGG GCGCGTCCTG TTCGGCTCTG
1001. CCGCCGCCGA AGACCTGCTC AAATCGCGTA AGGCGAAAGG CGTGTTTCATC
1051. CATCGGGACG ACTGGATTTC CATCACGCC GAAATACGCC TGCTTCTGAC
1101. CGAATTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 520; ORF 135>:

```

m135.pep
  1 MKYKRIVFKV GTSSITHSDG SLSRGKIQTI TCQLAALHHA GHLELVSSG
 51 AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRAPV IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGlyTGNPNS NPDAVRLDKI EhinHEIEM
201 AGGSGSANGT GGMLTKIKAA TIAESGVPV YICSSLKPDA LAEAAEHQAD
251 GSFFVPRAKG LRTQKQWLAF YSESRGSVYV DEGAEHALSE QGKSLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAEDLL KSRKAKGVFI
351 HRDDWISITP EIRLLTEF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 135 shows 97.6% identity over a 294 aa overlap with a predicted ORF (ORF 135.ng) from *N. gonorrhoeae*:

m135/g135

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLSRGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG					
g135	MKYKRIVFKVGTSSITRSDGSLSRGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
m135.pep	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
g135	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
m135.pep	SVLLQRRAPVPIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGNPNS					
g135	SVLLQRRAPVPIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGNPNS					
	130	140	150	160	170	180
m135.pep	NPDAVRLDKIEHINHEIEMAGGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPDA					
g135	NPDAVRLDKIEHINHEIEMAGGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPD					
	190	200	210	220	230	240
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESRGSVYVDEGAEHALSEQGKSLMSGI					
g135	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESGGSVYVDESAEHALSEQGKACX					
	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESRGSVYVDEGAEHALSEQGKSLMSGI					
g135	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESGGSVYVDESAEHALSEQGKACX					
	310	320	330	340	350	360

m135.pep AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFSGSAAEDLLKSRKAKGVFIHRDDWISITP

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 521>:

```
a135.seq
1   ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCGG CAGGGTTTCGG TGCCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CCGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCGCG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGCTT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCGGC AAACGGCACA GCGGTATGC TGACTAAAT
651 CAAAGCGGCG ACGATTGCGA CCGAGTCCGG CGTACCGGTC TATATCTGTT
701 CCTCGTCAA ACCCGATGCA CTTGCCGAAG CGGCAGATAA TCAGGCGGAC
751 GGCTCGTTT TCGTCCCGG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801 GCTGGCGTTC TATTCGAAA GCAGGGCGCG CGTTTATGTG GACGAAGGTG
851 CGGAACACGC TTTGTCCGAA CAGGGAAAAA GCCTGCTGAT GTCGGGCATT
901 GCCGGAATCG AAGGGCATTT TTCCCGTATG GACACCGTAA CCGTGACAG
951 CAAGGCAACC AAACAGCCTT TGGGCAAAAG GCGAGTCTG TTCGGCTCTG
1001 CCGCCGCCGA AGACCTGCTC AAATTGCGTA AGGCGAAAGG CGTGTTTCATC
1051 CATCGGACG ACTGGATTTC CATCACGCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTAG
```

This corresponds to the amino acid sequence <SEQ ID 522; ORF 135.a>:

```
a135.pep
1   MKYKRIVFKV GTSSITHSDG SLRSGKIQTI TRQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGQG LMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRVAV IINENDTVSV EELKIGNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHNHEIEM
201 AGGSGSANGT GGMLTKIKAA TIATESGVPV YICSSLKPKA LAEADNQAD
251 GSFFVPRAKG LRTQKQWLAF YSESRGGVYV DEGAEHALSE QGKSLLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAEDLL KLRKAKGVFI
351 HRDDWISITP EIRLLLTEF*
```

m135/a135 98.4% identity in 369 aa overlap

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLRSGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG					
a135	MKYKRIVFKVGTSSITHSDGSLRSGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
m135.pep	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLSRADFADKRRYQNAGGAL					
a135	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLSRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
m135.pep	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLSRADFADKRRYQNAGGAL					
a135	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLSRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
m135.pep	SVLLQRRVPIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGNPNS					
a135	SVLLQRRVPIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGNPNS					
	130	140	150	160	170	180
m135.pep	SVLLQRRVPIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGNPNS					
a135	SVLLQRRVPIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGNPNS					
	130	140	150	160	170	180
m135.pep	NPDAVRLDKIEHNHEIEMAGGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPKA					
a135	NPDAVRLDKIEHNHEIEMAGGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPKA					
	190	200	210	220	230	240
m135.pep	NPDAVRLDKIEHNHEIEMAGGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPKA					
a135	NPDAVRLDKIEHNHEIEMAGGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPKA					
	190	200	210	220	230	240

	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSES	SRGSVYVDEGA	EHALSEQGKSL	LMSGI		
	::					
a135	LAEAADNQADGSFFVPRAKGLRTQKQWLAFYSES	RGGVYVDEGA	EHALSEQGKSL	LMSGI		
	250	260	270	280	290	300
	310	320	330	340	350	360
m135.pep	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLF	GSAAEDLLKSR	KAKGVFIHR	DDWISITP		
a135	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLF	GSAAEDLLKLR	KAKGVFIHR	DDWISITP		
	310	320	330	340	350	360
	370					
m135.pep	EIRLLLLTEFX					
a135	EIRLLLLTEFX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 523>:

g136.seq

1	ATGGAATCC	GGTTTCAGAC	AGCATTTTTA	CGTTTGGTTC	AGatgaAAAC
51	AAACGCTtca	aTCTTaccg	caACACGCCT	TGTATTTCCT	GccgCTGCCG
101	CACGGACAGG	GATCGTTCCT	GCCGgtTTT	TCCCTTCCC	TGCGGACGGT
151	TTGCGGTTTG	TTGATGACCG	CCTGCCAGTA	GCGGTAGATG	TCtgccagcg
201	cgTAAGGcag	tTCGGACgca	agttccgcga	gctcgccctc	ggTGAATTGC
251	Aagcggataa	cgccgthtTC	CTCTTCGTGc	taaatgccgc	ccactgccat
301	cacgGGGTAA	AACAGCTCTT	CAAACGCCTC	ATCATCGCGC	GCTTCAAAACC
351	AATCGGTCGG	CACAATGTCC	AAACCGTAAA	GATAGGCGTT	GCACCAAGTG
401	TAAAAATCGC	TGCCGCCCTC	GCCGTCGTCG	TAGAGCCACA	AATCGGGCAG
451	CTTTTTATCC	GACATCGCGG	CGGTTGT TTC	CATGCCATT	GCCAAAACCA
501	GCCGTTTCGAT	TCGGAACGT	TCGGCGGCGG	TAAATTGCGA	TTCGTCGCCC
551	AAACACTTCGG	GAGCCAGTC	GAGCGGTGCC	AATTTGTCCG	GCCCCGTCAA
601	CAGCGCGGTC	ATAAAAACCTT	GAACTCGTC	GCAACGCATC	GTGTTGCCTT
651	GTTTCGCTTTT	GGCATCCAAT	AA		

This corresponds to the amino acid sequence <SEQ ID 524; ORF 136.ng>:

g136.pep

1	MEIRFQTAFL	RLVQMKTNAS	ILTATRLVFP	AAAARTGIVP	AGFFPPPADG
51	LRFVDDRLPV	AVDVCQVRVQ	FGRKFRQLAF	GELQADNAVF	LFVVNAAHCH
101	HGVKQLFKRF	IIGGFKPIGR	HNVTQVKIGV	<u>APSVKIAAAL</u>	<u>AVVVEPQIGQ</u>
151	LFIRHRGGCF	HRHCQNQFDF	FGTFGGGKLR	FVAQHFGQPV	ERCQFVRPAQ
201	QRRHKTLNLV	ATHRVALFAF	GIQ*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 525>:

```

m136.seq
1  ATGGAACAA ACGCTTCAAT TCTTACCGCA ACACGCCTTG TATTTTCTGC
51  CGCTGCCGCA CGGACAGGGA TCGTTCCTGC CTGTTTTTTC GCCTTCCCTG
101 CGGACGGTTT GCGGTTTGTT GATGACTGCC TGCCAGTAGC GGTAGATATC
151 CGCCAATGCA TAAGGCAACT CGGATTCCAG TTCCGCCAGC TCGCCTTCTG
201 TGAATTGCAG ACGGATAGCG CCGTTTTCTT CTTCGTCTGA AATACCGCCC
251 AATGCCATGA TGGGATAAAA CAACTCTTCA AACGCTTCAT CATCGACGGC
301 TTCAAACCAA TCGGTCGGCA CAATATCCAA ACCGTAAAGA TAAGCATTGC
351 ACCATGTGTA AAAATCGCTG CCGCCGCTTT CGTTTTCATA CAGCCACAAA
401 TCGGGCAGTT TTTTATCCGA CATCGCGGCG GTTGTTTCCA TCGCCATTGC
451 CAAAACCAGC CGTTCGATTT CGGAACGTTT GCGGCGGTA AATTGCGATT
501 CGTCGCCCAA CACTTCGGGC AGCCAGTCGA GCGGTGTCAA TTGTCCGGC
551 CCGTCAACA TCGCCGTCAT AAAACCTTGA ACCTCGTCGC AACGCATCGT
601 GTTGCCCTTG TCGCTTTTGG CATCCAACAA TTCGCTCAAC CGCCGTTTGG
651 ATGCTTCGGT AAATTTTCGG GAATCCATCA TTTCCCTTTT CAAATGGGTT
701 TTGCGCCCTA TTATCGCCGC AATGCCGTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 526; ORF 136>:

386

m136.pep
 1 METNASILTA TRLVFSAAAA RTGIVPACFF AFPADGLRFV DDCLPVAVDI
 51 RQCIRQLGFQ FRQLAFCELQ TDSAVFLFVV NTAQCHDGIK QLFKRFIIDG
 101 FKPIGRHNIQ TVKISIAPCV KIAAAVFVFI QPQIGQFFIR HRGGCFHRHC
 151 QNQPFDFGTF GGGKLRFVAQ HFGQPVERCQ FVRPAQRRH KTLNLVATHR
 201 VALFAFGIQQ FAQPPFGCFG KFSGIHHFPF QMGFAPYYRR NAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 136 shows 85.6% identity over a 209 aa overlap with a predicted ORF (ORF 136.ng) from *N. gonorrhoeae*:

m136/g136

m136.pep	10	20	30	40
	METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRFVDDCLPV			
g136	10	20	30	40
	MEIRFQTAFLRLVQMKTNASILTATRLVFPA AAAARTGIVPAGFFFPADGLRFVDDRLPV			
m136.pep	50	60	70	80
	AVDIRQCIRQLGFQFRQLAFCELQ TDSAVFLFVVNTAQCHDGIKQLFKRFIIDGFKPIGR			
g136	50	60	70	80
	AVDVCQVRVRFGRKFRQLAFGELQADNAVFLFVNAAHCHHGKQLFKRFIIGGFKPIGR			
m136.pep	110	120	130	140
	HNIQTVKISIAPCVKIAAAVFVFIQPQIGQFFIRHRGGCFHRHCQNQPFDFGTFGGGKLR			
g136	110	120	130	140
	HNVQTVKIGVAPSVKIAAALAVVVEPQIGQLFIRHRGGCFHRHCQNQPFDFGTFGGGKLR			
m136.pep	170	180	190	200
	FVAQHFGQPVERCQFVRPAQRRHKTLNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIH			
g136	170	180	190	200
	FVAQHFGQPVERCQFVRPAQRRHKTLNLVATHRVALFAFGIQX			
m136.pep	230	240		
	HFPFQMGFAPYYRRNAVX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 527>:

a136.seq
 1 ATGGAAACAA ACGCTTCAAT TCTTACCGCA ACACGCCTTG TATTTTCTGC
 51 CGCTGCCGCA CGGACAGGGA TCGTTCCTGC CTGTTTTTTC GCCTTCCCTG
 101 CGGACGGTTT GCGGCTTGTT GATGACCGCC TGCCAGTAGC GG TAGATATC
 151 CGCCAATGCA TAAGGCAACT CGGATTCCAG TTCCGCCAGC TCGCCTTCTG
 201 TGAATTGCAG ACGGATAGTG CCGTTGTCCT CTTCGTCGTA AATACCGCCC
 251 AATGCCATGA TGGGATAAAA CAACTCTTCA AACGCTTCAT CATCGACGGC
 301 TTCAAACCAA TCGGTCGGCA CAATATCCAA ACCGTAAAGA TAAGCATTCG
 351 ACCATGTGTA AAAATCGCTG CCGCCGTCTT CGTTTTTATA CAGCCACAAA
 401 TCGGGCAGTT TTTTATCCGA CATCGCGGCG GTTGTTCCTA TCGCCATTGC
 451 CAAAACCAGC CGTTCGATTT CGGAACGTTT GCGCGCGGTA AATTGCGATT
 501 CGTCGCCCAA CACTTCGGGC AGCCAGTCGA GCGGTGTCAA TTTGTCCGGC
 551 CCGCTCAACA GCGCCGTCAT AAAACCTTGA ACCTCGTCGC AACGCATCGT
 601 GTTGCTTGT TCGCTTTTGG CATCCAACAA TTCGCTCAAC CGCCGTTTGG
 651 ATGCTTCGGT AAATTTTCGG GAATCCATCA TTTTCCTTTT CCAATGGGTT
 701 TTGCGCCCTA TTATAGTGGA TTAAATTAA ATCAGGACAA GGCGACGAAG
 751 CCGCAGACAG TACAAATAGT ACGGCAAGGC GAGGCAACGC CGTACTGGTT
 801 TAAATTTAAT CCACTATATC GCCGCAATGC CGTCTGA

This corresponds to the amino acid sequence <SEQ ID 528; ORF 136.a>:

a136.pep

387

```

1  METNASILTA  TRLVFSAAAA  RTGIVPACFF  AFPADGLRLV  DDRLPVAVDI
51  RQCIRQLGFQ  FRQLAFCELO  TDSAVVLFVV  NTAQCHDGIK  QLFKRFIIDG
101 FKPIGRHNIQ  TVKISIAPCV  KIAAAVFVFI  QPQIGQFFIR  HRGGCFHRHC
151 QNQPFDFGTF  GGGKLRFVAQ  HFGQPVERCQ  FVRPAQQRH  KTLNLVATHR
201 VALFAFGIQQ  FAQPPFGCFG  KFSGIHHFPP  PMGFAPYYS  LNLNQDKATK
251 PQTQIVRQG  EATPYWFKFN  PLYRRNAV*

```

m136/a136 98.3% identity in 238 aa overlap

```

10      20      30      40      50      60
m136.pep  METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRFVDDCLPVAVDIRQCIRQLGFQ
|||||:|||||
a136      METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRLVDDRLPVAVDIRQCIRQLGFQ
10      20      30      40      50      60

70      80      90      100     110     120
m136.pep  FRQLAFCELOTD SAVVLFVVNTAQCHDGIKQLFKRFIDGFKPIGRHNIQTVKISIAPCV
|||||:|||||
a136      FRQLAFCELOTD SAVVLFVVNTAQCHDGIKQLFKRFIDGFKPIGRHNIQTVKISIAPCV
70      80      90      100     110     120

130     140     150     160     170     180
m136.pep  KIAAAVFVFIQPQIGQFFIRHRGGCFHRHCQNQPFDFGTGGGKLRFVAQHFGQPVERCQ
|||||:|||||
a136      KIAAAVFVFIQPQIGQFFIRHRGGCFHRHCQNQPFDFGTGGGKLRFVAQHFGQPVERCQ
130     140     150     160     170     180

190     200     210     220     230     240
m136.pep  FVRPAQQRHKT LNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFPPQMGFAPYYR
|||||:|||||
a136      FVRPAQQRHKT LNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFPPQMGFAPYYSG
190     200     210     220     230     240

m136.pep  NAVX
a136      LNLNQDKATKPQTQIVRQGEATPYWFKFNPLYRRNAVX
250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 529>:

```

g137.seq
1  ATGATTATCC ATCACcaaTT CGATCCCGTC CTCATCAGTA TCGGCCCGCT
51  TGCCGTCCGC TGGTATGCCT TAAGTACAT CCTCGGATTT ATTCTTTTAA
101 CCTTTCTCGG CAGAAGCGGC ATCGCGCAAG GCTTGTCCGT TTTTACCAAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC ATTTTGGGCG TGATTTTGGG
201 CGGACGCTTG GGCTATGTCC TGTTTTACAA ATTCTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTTCCACGGC
301 GGCTTTTGGG GTGTAGTTAT TGCCATATGG TTGTTAGACC GCAAGCACGG
351 CATCGGCTTC CTCAACTGA TGGACACGGT CGCGCCGCTC GTTCCGCTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTTA TCAACGGCGA ACTTTGGGGA
451 CGCATTACCG ACATTAACGC ATTTTGGGCA ATGGGCTTCC CGCAAGCGCA
501 TTACGAAGAT GCCGAAGCCG CCGCGCACAA TCCGCTTTGG GCAGAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGCT TTATCAGTTT
601 GCCCTTGAAG GCATCTGCCT GTTCGCCGTC GTTTGGCTGT TTTCCAAAAA
651 ACCGCGCCCG ACCGGGCAGA CTGCCGCGCT TTTTCTCGGC GGCTACGGCG
701 TGTTCGCTT TATTGCCGAA TTTGCGCGCC AACCCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGGTTGAGCG TCCCGATGAT
801 TGTTTGGGT ATCGTCGGCT TTGTCCGGTT CGGCATGAAA AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 530; ORF 137.ng>:

g137.pep

```
m137.seq
1  ATGATTACCC ATCCCCAATT CGATCCCGTC CTTATCAGTA TCGGCCCGCT
51  TGCCGTCCGC TGGTATGCCG TAAGCTACAT CCTCGATTT ATTCTTTTTA
101 CCTTCTCGG CAGAAGGCGC ATCGCGCAAG GCTTGTCGGT TTTTACCAAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC ATTTTGGGCG TAATTTTGGG
201 CGGGCGTTTG GGTTACGTCG TGTTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTTG TATTTTCAAG GTATGGGAAG CGGGAATGTC GTTCCACGGC
301 GGCTTTTTTG GTGTAGTTAT TGCCATACGG TTGTTTCGGC GCAAACACGG
351 CATCGGCTTC CTCAAACCTG TGGATACGGT CGCACCGCTC GTTCCGCTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTCA TCAACGGCGA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGGCGCG
501 TTACGAAGAT GCCGAAGCCG CCGCGCACAA TCCGCTTTGG GCAGAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGAGCT TTTATCAGTTT
601 GCACTTGAAG GCATCTGCCT GTTCACCGTC ATTTGGCTGT TCTCTAAAAA
651 ACAGCGGTCG ACCGGACAAG TCGCCTCGCT CTTCCTCGGC GGCTACGGCA
701 TATTCCGCTT CATTGCCGAA TTCGCACGCC AACCCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGTTGAGCG TCCCAGATGAT
801 TGTTTTGGGT ATCGTCGGCT TTGTCCGGTT CGGCATGAAA AAACAGCACT
851  GA
```

```
m137.pep
  1  MITHPQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGRL GYVLFYKFS D YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIR LFGRKHGIGF LKLMDTVAPL VPLGLASGRI GNFIGELWG
151 RVTDINAFWA MGFPQARYD AEAAAHNPLW AEWLQQYGML PRHPSQLYQF
201 ALEGICLFTV IWLSFKKQRS TGQVASLFLG GYGIFRFAE FARQPDDYLG
251 LLTGLGLSMGO WLSVPMIVLG IVGFVRFGMK KOH*
```

[illegible]

389

```

|||||
g137  AEWLQQYGMLPRHPSQLYQFALEGICLFAVVWLFSSKKPRPTGQTAALFLGGYGVRFRFAE
      190      200      210      220      230      240

      250      260      270      280
m137.pep FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFMGKKQHX
|||||
g137  FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFMGKKQHX
      250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 533>:

```

a137.seq
1  ATGATTACCC ATCCCCAATT CGACCCCGTC CTTATCAGTA TCGGCCCCGT
51  TGCCGTCCGC TGGTATGCCC TAAGCTACAT CCTCGGATTT ATTCTTTTAA
101 CCTTTCTCGG CAGAAGGCGC ATCGCGCAAG GCTTGTCCGT TTTTACCAA
151 GAATCGCTCG ACGACTTCCT GACATGGGCG ATTTTGGGCG TAATTTTGGG
201 CGGGCGTTTG GGTACGTCC TGTTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTTCCACGGC
301 GGCTTTTGGG GTGTAGTTAT TGCCATATGG TTGTCGGTC GCAAACACGG
351 CATCGGCTTC CTCAAACCTGA TGGACACGGT CGCACCGCTC GTTCCACTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTCA TCAACGGCGA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGGCGCG
501 TTACGAAGAC CTCGAAGCCG CCGCGCACAA TCCGCTTTGG GCAGAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGCT TTATCAGTTT
601 GCACTTGAAG GCATCTGCCT GTTCGCCGTC GTTGGCTGT TCTCTAAAAA
651 ACAGCGGCCG ACCGGACAAG TCGCCTCACT CTTCTCGGC GGCTACGGCA
701 TATTCGCTT CATTGCCGAA TTTGCACGCC AACCCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGGTTGAGCG TCCCGATGAT
801 TGTTTTGGGT ATCGTCGGCT TTGTCCGTT CGGCATGAAA AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 534; ORF 137.a>:

```

a137.pep
1  MITHPQFDPV LISIGPLAVR WYALSILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTWG ILGVILGGRL GYVLFYKFS YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIW LFGRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINGELWG
151 RVTDINAFWA MGFPQARYED LEAAAHNPLW AEWLQQYGML PRHPSQLYQF
201 ALEGICLFAV VWLFSSKKQRP TGQVASLFLG GYGIFRFIAE FARQPDDYL
251 LTLGLSMGQ WLSVPMIVLG IVGFVRFMGK KQH*

```

m137/a137 98.2% identity in 283 aa overlap

```

      10      20      30      40      50      60
m137.pep MITHPQFDPVLISIGPLAVRWYALSILGFILFTFLGRRRIAQGLSVFTKESLDDFLTWG
|||||
a137  MITHPQFDPVLISIGPLAVRWYALSILGFILFTFLGRRRIAQGLSVFTKESLDDFLTWG
      10      20      30      40      50      60

      70      80      90      100     110     120
m137.pep ILGVILGGRLGYVLFYKFSYLAHPLDIFKVVWEGGMSFHGGFLGVVIAIRLFGGRKHGIGF
|||||
a137  ILGVILGGRLGYVLFYKFSYLAHPLDIFKVVWEGGMSFHGGFLGVVIAIWLFGRKHGIGF
      70      80      90      100     110     120

      130     140     150     160     170     180
m137.pep LKLMDTVAPLVPLGLASGRIGNFINGELWGRVTDINAFWAMGFPQARYEDAEAAAHNPLW
|||||
a137  LKLMDTVAPLVPLGLASGRIGNFINGELWGRVTDINAFWAMGFPQARYEDLEAAAHNPLW
      130     140     150     160     170     180

      190     200     210     220     230     240
m137.pep AEWLQQYGMLPRHPSQLYQFALEGICLFTVIWLFSSKKQRPSTGQVASLFLGGYGIFRFIAE
|||||
a137  AEWLQQYGMLPRHPSQLYQFALEGICLFAVVWLFSSKKQRPSTGQVASLFLGGYGIFRFIAE

```

390

	190	200	210	220	230	240
	250	260	270	280		
m137 . pep	FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQHX					
a137	FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQHX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 535>:

g138 . seq

```

1  ATGGAGTTTG AAAACATTAT TTCCGCCGCC gaCAAGGCGC GTATCCTTGC
51  CGAAGCACTG CCTTACAtcc gccgGTTTTC CGGTTCCGTC GCCGTCATCA
101 AGTAGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GCGAATTTGT CCAAGGAATG CGCGTTACCG ACAAAGAGAC GATGGATATT
301 GTCGAAATGG TATTGGGCGG GCACGTCAAC AAGGAAATCG TGTCGATGAT
351 TAACACATAT GGAGGGCACG CGGTCGGCGT GAGCGGGCGC GACGACCATT
401 TCATTAAGGC GAAGAAACTT TTGGTCGATA CGCCCGAACA GAATAGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGCGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATT'TGGT GGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAAtatcgc
651 cgGTGTGATG GACAAAACGG GCAATCTGCT GACCAAACTC acgCCGAAAC
701 GGATTGATGG GCTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCcgccgtc aACGGTGTGA AAGCCACGCA
801 CATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGGTCGATG ATTTTAGGCA GAGGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 536; ORF 138.ng>:

g138 . pep

```

1  MEFENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
51  RDVLLKLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKETMDI
101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LVDTPEQNSV
151 DIGQVGTVES IDTGLVKGLI ERGCI PVVAP VGVGEKGEAF NINADLVAGK
201 LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDGLIA DGTLYGGMLP
251 KIASAVEAAV NGVKATHIID GRLPNALLE IFTDAGIGSM ILGRGEDA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 537>:

m138 . seq

```

1  ATGGAGTCTG AAAACATTAT TTCCGCCGCC GACAAGGCGC GTATCCTTGC
51  CGAAGCGCTG CCTTACATCC GCCGGTTTTC CGGTTCCGTC GCCGTCATCA
101 AATACGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GTGAGTTTGT CCAAGGAATG CGCGTTACCG ACAAAGAGGC GATGGATATT
301 GTCGAAATGG TGTTGGGCGG GCATGTCAAT AAAGAAATCG TGTCGATGAT
351 TAACACATAT GGCGGACACG CGGTCGGCGT AAGCGGACGC GACGACCATT
401 TCATTAAGGC GAAGAAACTT TTGATCGATA CGCCCGAACA GAATGGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGTGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATT'TGGT AGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAATATCGC
651 CCGTGTGATG GACAAAACGG GCAATCTGCT GACCAAACTC ACGCCGAAAC
701 GGATTGATGA ACTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCCGCCGTC AACGGTGTGA AAGCCACGCA
801 TATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGTTTCGATG ATTTTGGGCG GTGGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 538; ORF 138>:

m138 . pep

```

1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA

```


This corresponds to the amino acid sequence <SEQ ID 540; ORF 138.a>:

```
a138.pep
  1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGF
51  RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDEAMDI
101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV
151 DIGQVGTVES IDTGLVKGLI ERGCI PVVAP VGVGEKGEAF NINADLVAGK
201 LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA DGTLYGGMLP
251 KIASAVEAAV NGVKATHIID GRVPNALLE IFTDAGIGSM ILGGGEDA*
```

m138/a138 99.7% identity in 298 aa overlap

m138.pep	10	20	30	40	50	60
	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
a138	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
	10	20	30	40	50	60
m138.pep	70	80	90	100	110	120
	IHPVIVHGGGPQINAMLEKVGGKGEFVQGM RVTDEAMDIVEMVLGGHVNKEIVSMINTY					
a138	IHPVIVHGGGPQINAMLEKVGGKGEFVQGM RVTDEAMDIVEMVLGGHVNKEIVSMINTY					
	70	80	90	100	110	120
m138.pep	130	140	150	160	170	180
	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCI PVVAP					
a138	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCI PVVAP					
	130	140	150	160	170	180
m138.pep	190	200	210	220	230	240
	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
a138	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
	190	200	210	220	230	240
m138.pep	250	260	270	280	290	299
	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRLPNALLEIFTDAGIGSMILGGGEDAX					
a138	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRVPNALLEIFTDAGIGSMILGGGEDAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 541>:

```
g139.seq
  1  ATGCGAACCA CCTCAACCTT CCCTACAAAA ACTTTCAAAC CGGCTGCCAT
51  GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAagg ggcggcggag
101 gcGGCACTTC TGCTCCCGAC TTTAATGCAG GCGGCACCGG TATCGGCAGC
151 AACAGCAGGG CAACGATAGC GGAATCAGCA GCAGTATCTT ACGCCGGTAT
201 AAAAAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTCCGGGATG
251 ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAAAGCCCC CCGAATCTGC
301 ATACCGGAGA CTTTTCAAAC CCAAATGACC AATATTAAGA ATATGATCAA
351 CCTCAAACCT GCAATTGAAG CAGGCTATAC AGGACGCGGG GTAGAGGTAG
401 GTATCGTCGA TACAGGCGAA TCCGTCGGCA GCATATCCTT TCCCGAACTG
451 TATGGCAGAA AAGAACACGG CTATAACGAA AATTACAAA ACAAATTACA
501 AAAACTATAC GCGGTATATG CGGAAGGAAG CGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 542; ORF 138.ng>:

```
g139.pep
  1  MRTTSTFPTK TFKPAAMALA VATTLSACLG GGGGGTSAPD FNAGGTGIGS
51  NSRATIAESA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKIKAPRIC
101 IPETFQTQMT NIKNMINLKP AIEAGYTGRG VEVGIVDTGE SVGSISFPEL
151 YGRKEHGYNE NYKNKLQKLY GVYAEGSA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 543>:

```
m139.seq
  1  ATGCGAACGA CCCCAACCTT CCCTACAAAA ACTTTCAAAC CGACTGCCAT
51  GGC GTTAGCT GTTGCAACAA CACTTCTGCG CTGCTTAGCG GGCGGCGGAG
101 GCGGCACTTC TGCGCCCGAC TTCAATGCAG GCGGTACCGG TATCGGCAGC
151 AACAGCAGAG CAACAACAGC GAAATCAGCA GCAGTATCTT ACGCGCGTAT
201 CAAGAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTCGGGATG
251 ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAATGCCCC CCCC GAATC
301 TGCATACCGG AGACTTTC CAACCCAAATG ACGCATACA AGAATTTGAT
351 CAACCTCAAA CCTGCAATTG AAGCAGGCTA TACAGGACGC GGGGTAGAGG
401 TAGGTATCGT GCACACAGGC GAATCCGTCG GCAGCATATC CTTTCCCGAA
451 CTGTATGGCA GAAAAGAACA CGGCTATAAC GAAAATTACG AAAA ACTATA
501 CGGCGTATAT GCGGAAGGAA GCGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 544; ORF 138>:

```
m139.ppep
1  MRTTPTFTPTK  TFKPTAMALA  VATTLSACLG  GGGGGTSAPD  FNAGGTGIGS
51  NSRATTAKSA   AVSYAGIKNE  MCKDRSMLCA  GRDDVAVTDR  DAKINAPPRI
101 CIPETFTQTQM  THYKNLINLK  PAIEAGYTGR  GVEGVIVDGT  ESVGSISFPE
151 LYGRKEHGYN   ENYEKLYGVY  AESGA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 138 shows 92.2% identity over a 179 aa overlap with a predicted ORF (ORF 138.ng) from *N. gonorrhoeae*:

```

m139/g139

                10          20          30          40          50          60
m139.pep  MRTTPTFPTKTFKPTAMALAVATTLSACLGGGGGGTSAPDFNAGGTGIGSNSRATTAKSA
           |||| |||| |||| ||||:||||||| ||||| ||||| ||||| ||||| ||||| |||||
g139       MRTTSTFPTKTFKPAAMALAVATTLSACLGGGGGGTSAPDFNAGGTGIGSNSRATIAESA
           10          20          30          40          50          60

                70          80          90          100         110         120
m139.pep  AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKINAPPRICIPETFTQMTTHYNLNLK
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g139       AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKIP-RICIPETFTQMTNKNMINLK
           70          80          90          100         110

                130         140         150         160         170
m139.pep  PAIEAGYTGRGVEVGIVDTGESVGSISFPPELYGRKEHGYNENY----EKLYGVYAEGSAX
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g139       PAIEAGYTGRGVEVGIVDTGESVGSISFPPELYGRKEHGYNENYKNKLQKLYGVYAEGSAX
           120         130         140         150         160         170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 545>:

```

a139.seq
  1  ATGCGAACGA  CCCAACCTT  CCCTACAAAA  ACTTTCAAAC  CGGCTGCCAT
 51  GGCGTTAGCT  GTTGCAACAA  CACTTTCCTG  CTGCTTAGGC  GGCGCGGAG
101  GCGGCACTTC  TGCGCCCCAG  TTCAATGCAG  GCGGCACCGG  TATCGGCAGC
151  AACAGCAGGG  CAACACAGC  GAAATCAGCA  GCAATATCTT  AGCCCGGTAT
201  CAAGAACGAA  ATGTGCAAG  ACAGAAGCAT  GCTCTGTGCC  GGTGCGGATG
251  ACGTTGCGGT  TACAGACAGG  GATGCCAAAA  TCAATGCCCC  CCCCCGAATC
301  TGCATACCGG  AGACTTTACA  AACCCAAATG  ACGCAT.ACA  AGAATTTGAT
351  CAACCTCAAA  CCTGCAATTG  AAGCAGGCTA  TACAGGACGC  GGGGTAGAGG
401  TAGGTATCGT  CGACACAGGC  GAAATCCGTC  GCAGCATATC  CTTTCCCGAA
451  CTGTATGGCA  GAAAAGAA  CGGTATAAC  GAAAATTAC.  AAAAATAATA
501  CGGCGTATAT  GCGGAAGGAA  GCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 546; ORF 139.a>:

a139.pep
1 MRTTPTEPTK TFKPAAMALA VATTLSACLG GGGGGTSAPD ENAGGTGIGS

```

51 NSRATTAKSA AISYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI
101 CIPETLQTQM THXKNLINLK PAIEAGYTGR GVEVGIVDTG ES VGSI SFPE
151 LYGRKEHGYN ENYXKLYGVY AEGSA*

```

m139/a139 97.1% identity in 175 aa overlap

```

          10      20      30      40      50      60
m139.pep  MRTTPTFPTKTFKPTAMALAVATTL SACLGGGGGGTSAPDFNAGGTGIGSNSRATTAKSA
          |||||:|||||
a139      MRTTPTFPTKTFKPAAMALAVATTL SACLGGGGGGTSAPDFNAGGTGIGSNSRATTAKSA
          10      20      30      40      50      60

          70      80      90     100     110     120
m139.pep  AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKINAPPRICIPETFQTQMT HXKNLINLK
          |:|||||
a139      AISYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKINAPPRICIPETFQTQMT HXKNLINLK
          70      80      90     100     110     120

          130     140     150     160     170
m139.pep  PAIEAGYTGRGVEVGIVDTGESVGSISFP ELYGRKEHGYNENYKLYGVYAEGSAX
          |||||
a139      PAIEAGYTGRGVEVGIVDTGESVGSISFP ELYGRKEHGYNENYXKLYGVYAEGSAX
          130     140     150     160     170

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 547>:

```

g140.seq
1   Atgtcggcac gCGGCAAGGG GGCAGgctat ctAACAGTA CCGGACGACa
51  TGTTCCCTTC CTGAGTGCCG CCAAAATCGG GCAGGATTAT TCTTTCTTCA
101 AAAATATCAA AACCGACGGC GGTCTGCTGG CTTCCCTCGA CAGCGTCGAA
151 AAAACAGCGG GCAGTGAAGG CGACACGCCG TCCTATTATG TCCGTCGCGG
201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCCGGTC
251 TGA AACACGC CGTAGAACAG GCGGCAGCA ATCTGGA AAA CCTGATGGTC
301 GAGCTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
351 GGTCGCCGAC CGCACAGATA TGCCGGGCAT CCGCCTACGG CGCACA ACTT
401 TCCGCACAGC GGCAGCCGTA CAGCATGCGA ATACCGCCGA CGGCGTACGc
451 aTCTTcaaCA GTCTCGCCGC TAccgTCTAt GccgACAGTG CCGCCGCCCA
501 TGccgATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
551 ACAACGGTAC GGGTCTGCGC GTCATCGCGC AAACCCAACA GGACGGTGGA
601 ACGTGGGAAC AGGGCGGTGT CGAAGGCAAA ATGCGCGGCA GTACCCAAAC
651 TATCGGCATT GCCGCGAAAA CCGGCGAAAA TACGACAGCA GCCGCCACAC
701 TGGGCATAGG ACGCAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
751 GACAGCATTa GTCTGTTTGC AGGCATACGG CACGATGTGG GCGATATCGG
801 CTATCTCAAA GGCCTGTTCT CctaCGGACG CTACAAAAAC AGCATCAGCC
851 GCAGCACCGG TGCGGATGAA TATGCGGAAG GCAGCGTCAA CGGCACGCTG
901 ATGCAGCTGG GCGCACTGGG TGGTGTCAAC GTTCCGTTTG CCGCAACGGG
951 AGATTTGACG GTGAAGGCG GTCTGCGCCA CGACCTGCTC AAACAGGATG
1001 CATTCGCCGA AAAAGGCagt GCTTTGGGCT GGAGCGGCAA CAGCCTCACT
1051 GAAGGCACAC TGGTCGGACT CGCGGGTCTG AAAGTGTGCG AACCTTGAG
1101 CGATAAAGCC GTCCTGTCTG CGACGGCGGG CGTGGAACGC GACCTGAACG
1151 GACGCGACTA CGCGGTAACG GCGCGCTTTA CCGGCGCGGC TGCAGCAACC
1201 GGCAAGACGG GTGCACGCAA TATGCCGCAC ACCCGCCGGG TTGCCGTTCT
1251 GGGGGTGGAT GTCGAATTCG GCAACGGCTG GAACGGCTTG GCACGTTACA
1301 GCTACACCGG TTCCAAACAG TACGGCAACC ACAGCGGACA AATCGGCGTA
1351 GGCTACCGGT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 548; ORF 140.ng>:

```

g140.pep
1   MSARGKGAGY LNSTGRHVPF LSAAKIGQDY SFFKNIKTDG GLLASLDSVE
51  KTAGSEGDTP SYYVRRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
101 ELDAESSAT PETVETAVAD RTDMPGIRLR RTTFR TAAV QHANTADGVR
151 IFNSLAATVY ADSAAAHADM QGRR LKAVSD GLDHNGTGLR VIAQTQDGG
201 TWEQGGVEGK MRGSTQTIGI AAKTGENTTA AATLGIGRST WSENSANAKT

```

```

251 DSISLFAGIR HDVGDIGYLK GLFSYGRYKN SISRSTGADE YAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRHDLL KQDAFAEKGS ALGWSGNSLT
351 EGTLVGLAGL KLSQPLSDKA VLSATAGVER DLNGRDYAVT GGFTGAAAAT
401 GKTGARNMPH TRRVAGLGVD VEFNGWNGL ARYSYTGSKQ YGNHSGQIGV
451 GYRF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 549>:

```

m140.seq
1 ATGTCGGCAC GCGGCAAGGG GGCAGGCTAT CTCAACAGTA CCGGACGACG
51 TGTTCCTTC CTGAGTGCCG CCAAATCGG GCAGGATTAT TCTTCTTCA
101 CAAACATCGA AACCGACGGC GGCCTGCTGG CTCCCTCGA CAGCGTCGAA
151 AAAACAGCGG GCAGTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG
201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCCGGTC
251 TGAAACACGC CGTAGAACAG GCGGCAGCA ATCTGAAAAA CCTGATGGTC
301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
351 GGCAGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCCTAC GGCGCAACTT
401 TCCGCGCAGC GGCAGCCGTA CAGCATGCGA ATGCCGCCGA CGGTGTACGC
451 ATCTTCAACA GTCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA
501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
551 ACAACGGCAC GGGTCTGCGC GTCATCGCGC AAACCCAACA GGACGGTGA
601 ACGTGGGAAC AGGGCGGTGT TGAAGGCAAA ATGCGCGGCA GTACCCAAAC
651 CGTCGGCATT GCCGCGAAAA CCGCGGAAAA TACGACAGCA GCCGCCACAC
701 TGGGCATGGG ACGCAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
751 GACAGCATTG GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG
801 CTATCTCAAA GGCCTGTTCT CTTACGGACG CTACAAAAAC AGCATCAGCC
851 GCAGCACCGG TGCGGACGAA CATGCGGAAG GCAGCGTCAA CCGCACGCTG
901 ATGCAGCTGG GCGCACTGGG CGGTGTCAAC GTTCCGTTTG CCGCAACGGG
951 AGATTTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AAACAGGATG
1001 CATTCGCCGA AAAAGGCAGT GCTTTGGGCT GGAGCGGCAA CAGCCTCACT
1051 GAAGGCACGC TGGTCGGACT CGCGGGTCTG AAGCTGTCGC AACCTTGAG
1101 CGATAAAGCC GTCCTGTTTG CAACGGCGGG CGTGGAACGC GACCTGAACG
1151 GACGCGACTA CACGGTAACG GCGGCTTTA CCGGCGCGAC TGCAGCAACC
1201 GGCAAGACGG GGGCACGCAA TATGCCGCAC ACCCGTCTGG TTGCCGGCCT
1251 GGGCGCGGAT GTCGAATTCG GCAACGGCTG GAACGGCTTG GCACGTTACA
1301 GCTACGCCGG TTCAAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA
1351 GGCTACCGGT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 140>:

```

m140.pep
1 MSARGKGAGY LNSTGRRVPF LSAAKIGQDY SFFTNIETDG GLLASLDSVE
51 KTAGSEGDTL SYVVRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
101 ELDASESSAT PETVETAAAD RTDMPGIRPY GATFRAAAV QHANAADGVR
151 IFNSLAATVY ADSTAAHADM QGRRLLKAVSD GLDHNGTGLR VIAQTQDGG
201 TWEQGGVEGK MRGSTQTVGI AAKTGENTTA AATLGMGRST WSENSANAKT
251 DSISLFAGIR HDAGDIGYLK GLFSYGRYKN SISRSTGADE HAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSLT
351 EGTLVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGFTGATAAT
401 GKTGARNMPH TRLVAGLGAD VEFNGWNGL ARYSYAGSKQ YGNHSGRVGV
451 GYRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 140 shows 94.5% identity over a 454 aa overlap with a predicted ORF (ORF 140.ng) from *N. gonorrhoeae*:

```

m140/g140
10 20 30 40 50 60
m140.pep MSARGKGAGYLNSTGRRVPFLSAAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEGD
|||||
g140 MSARGKGAGYLNSTGRHVPFLSAAKIGQDYSFFKNIKTDGGLLASLDSVEKTAGSEGDTP
10 20 30 40 50 60
70 80 90 100 110 120

```

m140.pep	SYVVRGNAARTASAAAH SAPAGLK HAVEQQGSNLENLMVELDASESSATPETVETAAAD
g140	SYVVRGNAARTASAAAH SAPAGLK HAVEQQGSNLENLMVELDASESSATPETVETAVAD
	70 80 90 100 110 120
m140.pep	RTDMPGIRPYGATFRAAAVQHANAADGVRI FNSLAATVYADSTAAHADMQRRRLKAVSD
g140	RTDMPGIRLRRTTFR TAAVQHANTADGVRI FNSLAATVYADSAAAHADMQRRRLKAVSD
	130 140 150 160 170 180
m140.pep	GLDHNGTGLRVIAQTQQDGGTWEQGGVEGKMRGSTQTIGIAAKTGENTTAAATLGMGRST
g140	GLDHNGTGLRVIAQTQQDGGTWEQGGVEGKMRGSTQTIGIAAKTGENTTAAATLGIGRST
	190 200 210 220 230 240
m140.pep	WSENSANAKTDSISL FAGIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL
g140	WSENSANAKTDSISL FAGIRHDVGDIGYLKGLFSYGRYKNSISRSTGADEYAEGSVNGTL
	250 260 270 280 290 300
m140.pep	MQLGALGGVNPFAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSLTEGTLVGLAGL
g140	MQLGALGGVNPFAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSLTEGTLVGLAGL
	310 320 330 340 350 360
m140.pep	KLSQPLSDKAVLFATAGVERDLNGRDYVTGGFTGATAATGKTGARNMPHTRLVAGLGAD
g140	KLSQPLSDKAVLSATAGVERDLNGRDYAVTGGFTGAAAATGKTGARNMPHTRRVAGLGVD
	370 380 390 400 410 420
m140.pep	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYRFX
g140	VEFGNGWNLARYSYTGSKQYGNHSGQIGVGYRFX
	430 440 450

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 551>:

```

a140.seq
1  ATGTCGGCAG GCGGTAAGGG GGCAGGCTAT CTCAACCGTA CCGGACAACG
51  TGTTCCCTTC CTGAGTGCCG CCAAATCGG GCGGGATTAT TCTTCTTCA
101 CAAACATCGA AACCGACGGC GGTCTGCTGG CTTCCTCGA CAGCGTCGAA
151 AAAACAGCGG GTAGTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG
201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCCGGTC
251 TGAAACACGC CGTAGAACAG GCGGCGAGCA ATCTGGAAAA CCTGATGGTC
301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
351 GGCCGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCTAC GGCACAACCT
401 TCCGCGCAGC GGCAGCCGTA CAGCATGCGA ATGCCGCCGA CGGTGTACGC
451 ATCTTCAACA ATCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA
501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
551 ACAACGCTAC GGGTCTGCGC GTCATCGCGC AAACCAACA GGACGGTGGA
601 ACGTGGGAAC AGGGCGGTGT TGAAGGCAAA ATGCGCGGCA GTACCCAAAC
651 CGTCGGCATT GCCGCGAAAA CCGGCGAAAA TACGACAGCA GCCGCCACAC
701 TGGGCATGGG ACACAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
751 GACAGCATTA GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG
801 CTATCTCAAA GGCCTGTTCT CCTACGGACG CTACAAAAAC AGCATCAGCC
851 GCAGCACCGG TGCGGACGAA CATGCGGAAG GCAGCGTCAA CGGCACGCTG
901 ATGCAGCTGG GCGCACTGGG CGGTGTCAAC GTCCGTTTG CCGCAACGGG

```


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	370	380	390	400	410	420
	430	440	450			
m140.pep	VEFGNGWNG	LARYSYAGSKQYGNHSGRVGVGYRFX				
a140	VEFGNGWNG	LARYSYAGSKQYGNHSGRVGVGYRFX				
	430	440	450			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 553>:

g141.seq

```

1  atgagcttca aAAccgATGC CGAAACCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAGCTG
151 CCGCAAAAAC AAGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GGCGGGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TGCGCGAGCC TTCTTTGGGT
301 CCGGTGTTTC GCGTGAAAGG CGGCGCGGCA GGCGGCGGCT ACGCGCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGCGAC TTCCACGCCA
401 TCGGTGCGGC GAATAACCTC CTCGCCGCCA TGCTCGACAA CCATATCTAC
451 CAAGGTAACG AGTTGAACAT CGACCCCAAA CGCGTGCTGT GGCGGCGCGT
501 GGTCGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGTATGGGCA
551 AGCCTGTtga cggCGTGATG CGtcccGACG GCTTCGACAT CACCGTCGCC
601 TCCGAAGTga tggcgGTATT CTGCCTTGCC AAAGACATCA GCGATTTGAA
651 AGAGCGTttt gGCAATATTC TCGTCGCCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTTGAAG GCACACGGCG CGATGGCGGC ATTGCTAAAA
751 GATGCGATTA AGCCCAATTT GGTGCAAACC ATCGAAGGCA CTCCGGCCTT
801 TGTACACGGC GGCCCGTTCG CCAACATCGC CCACGGCTGC AACTCCGTTA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG TGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCAGT CGTCGTGGCG ACTGTCCGCG
1001 CCCTGAAATA CAACGGCGGC GTGGAACGCG CCAACCTTGG TGAAGAAAAC
1051 CTCGAAGCCT TGGCAAAAGG TTTGCCCAAC CTGTTGAAAC ACATTTCCAA
1101 CTTGAAAAAC GTATTGCGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GCGGCGCGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA TGCCATCGAC AACCACCTA
1301 ATAACCTCGG TTTGCGCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCCAAAAAGT GTACGCGCGG GAAGATGTCG ATTTCAGCGC
1401 GGAAGCGTCT GCCGAAATCG CCTCGCTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATATT CATTGAGCGA CAACGCCAAA
1501 CTCTTGGGCT GCCCGGAAGG CTTCGCGATC GCCGTACGCG GTATCACTGT
1551 TTCCGCCGGC GCGGGCTTCA TCGTTGCGTT GTGCGGCAAT ATGATGAAAA
1601 TGCCGGGCCT GCCGAAAGTT CCGGCTGCCG AGAAAATCGA TGTGGACGAA
1651 CACGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 554; ORF 141.ng>:

g141.pep

```

1  MSFKTDAETA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51  PQKQGRILIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFVGKGGAA GGGYAQVLPM EDINLHFTGD FHAIGAANNL LAAMLDNHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNIID GMGKPDVGM RPDGFDITVA
201 SEVMAVFCLA KDISDLKERF GNILVAYAKD GSPVYAKDLK AHGAMAALLK
251 DAIKENLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LEALAKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDSDAE LAMIEKACAE
401 HGVEVSLTEV WGKGAGGAD LARKVNAID NQPNMFGFAY DVELGIKDKI
451 RAIQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCPPEGFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDE
551 HGVHGLF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 555>:

m141.seq

```

1  ATGAGCTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTTGGTCT GAATGCCGAC AACATTGAGC
101 CTTACGGTCA TTACAAGGCG AAAATCAATC CTGCCGAAGC GTTCAAACCTG
151 CCGCAAAAAC AGGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GCGGGGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCGTTGC
251 GCCACATCGG CAAAGATGCC GTGATTGCCC TGCGCGAACC TTCTCTGGGG
301 CCGGTGTTTC GCGTGAAAGG CGGCGCGGCA GCGGCGGCT ATGCCCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTTGCCGCGA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAAA CGCGTGCTGT GGCGGCGCGT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGTA
551 AACCCGTTGA CCGCGTGATG CGTCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTTGAA
651 AGAGCGTTTG GGCAACATCC TTGTGCGCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAAAC ATCGAAGGCA CGCCCGCCTT
801 CGTACACGGC GGCCCGTTTC CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCAGACGA
901 GGCTTCGCGC CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCTGT TGTCGTGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGGCGGC GTGGAACGCG CCAACCTCGG CGAAGAAAAT
1051 TTAGACGCTT TGGAAAAAGG TTTGCCCAAC CTGTGAAAC ACATTTCCTAA
1101 CCTGAAAAAC GTATTCGGAC TGCCCGTCGT CGTTGCGCTC AACCCTTCG
1151 TGTCCGACGC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACCTTCG TTTCGCCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCCAAAAAGT GTACGCGCGC GAAGATGTTG ATTTCAGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCACTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCCCCGAAGA CTTCCGCATC GCCGTGCGCG GCATACCGT
1551 TTCCGCAGGC GCAGGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGGCCT GCCCAAAGTT CCGGCTGCCG AGAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 556; ORF 141>:

m141.pep

```

1  MSFKTDAEIA QSSTMRPIGE IAAKLGLNAD NIEPYGHYKA KINPAEAFKL
51  PQKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDA VIALREPSLG
101 PVFVGKGGAA GGGYAQVLPM EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNIID GMGKPDVDM RPDGFDITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDADAE LAMIEKACAE
401 HGVEVSLTEV WGKGAGGAD LARKVVNAIE SQTNNFGFAY DVELGIKDKI
451 RAIQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TOYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDA
551 EGVIHGLF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 141 shows 97.5% identity over a 558 aa overlap with a predicted ORF (ORF 141.ng) from *N. gonorrhoeae*:

m141/g141

	10	20	30	40	50	60
m141.pep	MSFKTDAEIAQSSTMRPIGEIAAKLGLNADNIEPYGHYKAKINPAEAFKL					
	:					
g141	MSFKTDAETAQSSTMRPIGEIAAKLGLNVDNIEPYGHYKAKINPAEAFKL					
	10	20	30	40	50	60

400

	70	80	90	100	110	120
m141.pep	TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFGVKGAAGGGYAQVLPM					
	:					
g141	TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFGVKGAAGGGYAQVLPM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m141.pep	EDINLHFTGDFHAIGAANNLLAAMLDNHIYQGNELNIDPKRVLWRRVVDMMNDRQLRNIID					
	:					
g141	EDINLHFTGDFHAIGAANNLLAAMLDNHIYQGNELNIDPKRVLWRRVVDMMNDRQLRNIID					
	130	140	150	160	170	180
	190	200	210	220	230	240
m141.pep	GMGKPVGDGVMRPDGFDTIVASEVMAVFLAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
	:					
g141	GMGKPVGDGVMRPDGFDTIVASEVMAVFLAKDISDLKERFGNILVAYAKDGSPVYAKDLK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m141.pep	ANGAMAALLKDAIKPNLVQTIIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	:					
g141	AHGAMAALLKDAIKPNLVQTIIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m141.pep	GFGADLGAEKFCDIKCRLAGLKPDAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
	:					
g141	GFGADLGAEKFCDIKCRLAGLKPDAVVVATVRALKYNGGVERANLGEENLEALAKGLPN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m141.pep	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAEHGVEVSLTEVWGKGGAGGAD					
	:					
g141	LLKHISNLKNVFGLPVVVALNRFVSDSDAELAMIEKACAEHGVEVSLTEVWGKGGAGGAD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m141.pep	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAIQKVYGAEDVDFSAEASAEIASLEKLG					
	: :					
g141	LARKVVNAIDNQPNNGFAYDVELGIKDKIRAIQKVYGAEDVDFSAEASAEIASLEKLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m141.pep	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
g141	LDKMPICMAKTQYSLSDNAKLLGCEPFGFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
	550	559				
m141.pep	PAAEKIDVDAEGVIHGLFX					
	:					
g141	PAAEKIDVDEHGVHGLFX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 557>:

a141.seq

```

1  ATGAGTTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAACCTG
151 CCGCAAAAAC AGGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC

```

```

201 GCGGGGCGAA GGTA AACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TGCGCGAGCC TTCTTTGGGT
301 CCGGTGTTTCG GCGTGAAAGG CGGCGCGGCA GCGCGCGGCT ATGCCCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTTGCCGCGA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAA CGCGTGCTGT GCGGCGCGCT
501 GGTGCATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGCA
551 AGCCTGTTGA CGGCGTGATG CGTCCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTAT CTGTCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTTTG GGCAACATCC TTGTGCGCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCACTT GGTGCAAACC ATCGAAGGCA CGCCGCGCTT
801 CGTACACGCG GCGCCGTTTCG CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCGCT AACCGAAGCA
901 GGCTTCGCGC CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGCTGT GTGCTGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGGCGGC GTGGAACGCG CCAACCTCGG CGAAGAAAAT
1051 TTAGACGCTT TGAAAAAGG TTTGCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTCGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAAC TTCGG TTTCCGCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCCAAAAAGT GTACGGCGCG GAAGATGTTG ATTTACGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCACTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCGCCGAAGA CTTCCGCATC GCGTGCGCG GCATCACCGT
1551 TTCCGCAGGC GCAGGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGCCT GCCCAAAGT CCGGCTGCCG AGAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 558; ORF 141.a>:

```

a141.pep
1 MSFKTDAEIA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51 PQKQGRILIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFVGKGGAA GGGYAQVLP EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVD NDRQLRNIID GMGKPDVGVM RPDGFDITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRVSDSDAE LAMIEKACAE
401 HGEVSLTEV WGKGAGGAD LARKVVNAIE SQTNNFGFAY DVELGIKDKI
451 RAIQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDA
551 EGVHGLF*

```

m141/a141 99.5% identity in 558 aa overlap

```

          10      20      30      40      50      60
m141.pep MSFKTDAEIAQSSTMRPIGEIAAKLGLNADNIEPYGHYKAKINPAEAFKL PQKQGRILIV
          |||||
a141      MSFKTDAEIAQSSTMRPIGEIAAKLGLNVDNIEPYGHYKAKINPAEAFKL PQKQGRILIV
          10      20      30      40      50      60

          70      80      90     100     110     120
m141.pep TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFGVKGGAGGGYAQVLP
          |||||
a141      TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFGVKGGAGGGYAQVLP
          70      80      90     100     110     120

          130     140     150     160     170     180
m141.pep EDINLHFTGDFHAIGAANLLAAMLNDHIYQGNELNIDPKRVLWRRVVDNDRQLRNIID
          |||||
a141      EDINLHFTGDFHAIGAANLLAAMLNDHIYQGNELNIDPKRVLWRRVVDNDRQLRNIID
          130     140     150     160     170     180

```

	190	200	210	220	230	240
m141.pep	GMGKPVGDGVMRPGFDITVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
a141	GMGKPVGDGVMRPGFDITVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m141.pep	ANGAMAALLKDAIKPNLVQTIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
a141	ANGAMAALLKDAIKPNLVQTIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m141.pep	GFGADLGAKEFCDIKCRLAGLKPDAAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
a141	GFGADLGAKEFCDIKCRLAGLKPDAAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m141.pep	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAEHGVESLTEVWGKGAGGAD					
a141	LLKHISNLKNVFGLPVVVALNRFVSDSDAELAMIEKACAEHGVESLTEVWGKGAGGAD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m141.pep	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAIQAQKVYGAEDVDFAEASAEIASLEKLG					
a141	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAIQAQKVYGAEDVDFAEASAEIASLEKLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m141.pep	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
a141	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
	550	559				
m141.pep	PAAEKIDVDAEGVIHGLFX					
a141	PAAEKIDVDAEGVIHGLFX					
	550					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 559>:

```

g142.seq
1  ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCCGTGC AGGTGCGCCA
51  ACGCGCCTTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAAATATGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTT
151 GGCAACATCC TGATGTTTCGT CCGCCAGCAT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATcggaATG AttcgCGCAC TCCGTTTAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCGGT AACCGGCGCA ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCAC
351 AGGATGCCAT CGCATCACGG AACGAAGTTT GAAAAGTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC CGTCCCCTAT ATAAGAATGC TGCACACAAG
451 GCATCCCCC ATGTGCAGCA GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 560; ORF 142.ng>:

```

g142.pep
1  MRADFMFADN MPVQVRQRAF YFKLSRFAAM PNMVGKPLFG RQAGQPGKMF
51  GNILMFVRQH IDAEAAVFRQ DRNDSRTPVY AQHHGRRLVG NRRNRHCNA
101 VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN RPLYKNAAHK
151 ASPHVQQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 561>:

```
m142.seq
  1 ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCCTGC AGGTGCGCCA
 51 ACGCGCCCTC TATTTCAGT  TGTCCCGTTT TGCCGCGATG CCAGATGTGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTC
151 GGCAACATCC TGATGTTTCG CCGCCAGCGT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATCGGAATG ATTCGCGCAC TCCGGTTGAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCGGT AACCGGCGCG ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCGC
351 AAGATGCCAT CGCATCACGG AACGAAGTTT GAAAATTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC TGTCCCTAT ATAAGAATGC TGCACACAAG
451 GCATCCCCcC ATGTGCAGCA GTTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 562; ORF 142>:

```
m142.pep
  1 MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF
 51 GNILMFVRQR IDAEAAVFRQ DRNDSRTPVD AQHHGRRLVG NRRDRRHCA
101 VTPCRTVCRD DMNACRARCH RITERSLKIF LQIRHFSPLN CPLYKNAAHK
151 ASPHVQQF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 142 shows 93.7% identity over a 158 aa overlap with a predicted ORF (ORF 142.ng) from *N. gonorrhoeae*:

```
m142/g142

      10      20      30      40      50      60
m142.pep MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMFNILMFVRQR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g142      MRADFMFADNMPVQVRQAFYFKLSRFAAMPNMVVGKPLFGRQAGQPGKMFNILMFVRQH
          10      20      30      40      50      60

      70      80      90      100     110     120
m142.pep IDAEAAVFRQDRNDSRTPVDAQHHGRRLVGNRRDRRHCAVTPCRTVCRDDMNACRARCH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:
g142      IDAEAAVFRQDRNDSRTPVYAQHHGRRLVGNRRNRHCAVTPCRTVCRDDMNACRTGCH
          70      80      90      100     110     120

      130     140     150     159
m142.pep RITERSLKIFLQIRHFSPLNCPPLYKNAAHKASPHVQQFX
          |||||:|||||:|||||:|||||:|||||:
g142      RITERSLKSFLLQIRHFSPLNRPPLYKNAAHKASPHVQQFX
          130     140     150
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 563>:

```
a142.seq
  1 ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCCTGC AGGTGCGCCA
 51 ACGCGCCCTC TATTTCAGT  TGTCCCGTTT TGCCGCGATG CCAGATGTGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTC
151 GGCAACATCC TGATGTTTCG CCGCCAGCGT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATCGGAATG ATTCGCGCAC TCCGGTTGAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCCGT AACCGGCGCA ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCGC
351 AGGATGCCAT CGCATCACGG AACGAAGTTT GAAAAGTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC TGTCCCTAT ATAAGAATGC TGCACACAAG
451 GCACCCCCCA TGTGCAGCAG TTCTGATTCA AAAAGCCGTC GGTCCGACAT
501 TTCCGCGCGT TACGGCGTAT TACGAGTTCA ACGCATCCTC GATTTTGGCA
551 AGTTCTGCCA ACAGGTCTTT AAGCAGCAGC ATTTTCTCGC GGCCAGCAC
601 TTCCTCGATA GCGTCGTAAC GTCGTCCAC TTCTTCGCCG ATTTCTCAT
651 ACAGCTTCTC GCCCTCGGCA GTCAGCTTCA GAAAAACACG TCGTTGGTCG
701 TTGGAAGGTT TCAGGCGGAC AACCAAACCC GCTTTTTCAA GGCGGGTCAG
751 GATACCGGTC AGGCTGGGCG GCAAAATGCA CGCCTGATTC GCCAAATCTT
```

801 GAAAGTCCAG CGTGCCGTTT TCCGCCAAAA GACGGATAAT CCGCCATTGC
 851 TGATCGGTAA TATTCGCCTG ATTCAGAATA GGCCTGAATT GGGTCATCAG
 901 GGCTTCCCTT GCCTGTATCA GACCGATATT GATAGACGCA TGTTTTGA

This corresponds to the amino acid sequence <SEQ ID 564; ORF 142.a>:

a142.pep
 1 MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF
 51 GNILMFVRQR IDAEAAVFRQ DRNDSRTPVD AQHHGRRLVR NRRNRRHCNA
 101 VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN CPLYKNAAHK
 151 APPMCSSSDS KSRRSDISAR YGVLVRQIRL DFGKFCQOVF KQQHFLAAQH
 201 FLDSVVTLVH FFADFLIQLL ALGSQLQKNT SLVVGRFQAD NQTRFFKAGO
 251 DTGQAGAONA RLIRQILKVQ RAVFRQKTDN PLLIGNIRL IQNRPELGHQ
 301 GFPCLYQTDI DRRMF*

m142/a142 96.1% identity in 153 aa overlap

m142.pep	10	20	30	40	50	60
	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMF					
a142	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMF					
	10	20	30	40	50	60
m142.pep	70	80	90	100	110	120
	IDAEAAVFRQDRNDSRTPVDAQHHGRRLVGNRRDRRHCAVTPCRTVCRDDMNACRARCH					
a142	IDAEAAVFRQDRNDSRTPVDAQHHGRRLVNRNRRRHCAVTPCRTVCRDDMNACRTGCH					
	70	80	90	100	110	120
m142.pep	130	140	150	159		
	RITERSLKIFLQIRHFSPLNCPPLYKNAAHKASPHVQQQFX					
a142	RITERSLKSFQIRHFSPLNCPPLYKNAAHKAPPMCSSSDSKSRRSDISARYGVLVRQIRL					
	130	140	150	160	170	180
a142	DFGKFCQOVFKQQHFLAAQHFLDSVVTLVHFFADFLIQLLALGSQLQKNTSLVVGRFQAD					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 565>:

g143.seq
 1 ATGTTGAGCT TCGGCTATCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAAG
 51 CTCGCAGATG AGCCGCATTT TTCAAACGCT AGGCGCAGAC CCGCACAAAT
 101 TGGGCTGGTT TTTCATCCTG CCGCCGCTGG CCGGGATGCT GGTTCAGCCG
 151 ATAGTGgGCT ACTACTCAGA CCGCACTTGG AAGCCGCGCT TGGGCGGCCG
 201 CCGCCTGCCG TATCTGCTTT ACGGCACGCT GATTGCGGTC ATCGTGATGA
 251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG
 301 GCCTTGTCGT TCGGCGCGCT GATGATTGCG CTGTTGGACG TGTCTGCGAA
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CCGCGATATG GTCAACGAGG
 401 AGCAGAAAAG CTACGCCTAC GGGATTCAA GTTTCTTAGC GAATACGGAC
 451 GCGGTTGTGG CAGCGATTCT GCCGTTTGTG TTcgcgata TCGGTTTGGC
 501 GAACACTGCC GAGAAAGGCG TTGTGCCACA AACCGTGGTC GTAGCATTCT
 551 ATGTGGGTGC GCGGTTACTG ATTATTACCA GTGCGTTCAC AATCTCCAAA
 601 GTCAAAGAAT ACGACCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
 651 CGCCGCGAAT CAGGAAAAAG CCAACTGGTT CGAACTCTTA AAAACCGCGC
 701 CTAAAGTGTT TTGGACGGTT ACTCCGGTAC AGTTTTTCTG CTGGTTTCGCC
 751 TTCCGGTATA TGTGGACTTA CTCGGCAGGC GCGATTGCAG AAAACGCTCTG
 801 GCACACTACC GATGCGTCTT CCGTAGGCCA TCAGGAGGCG GGCACCGGT
 851 ACGGCGTTT GCGGCGGTG TAGTCGGTTG CCGCGGTGAT TTGTTCTGTT
 901 ATTCTGGCAA AAGTACCGAA TAAATACCAT AAGGCGGTT ATTTCGGCTG
 951 TTTGGCTTTG GCGGCGCTCG GTTCTTCTC TATCTTCTC ATCTACAATC
 1001 AATACGCACT CATCTGTCT TATATCTTAA TCGGCATCGC TTGGGCGGGC
 1051 ATTATCACTT ATCCGCTGAC GATTGTGGCC AACGCTTTGT CGGGCAAACA
 1101 CATGGATACT TATTTGGGCC TGTTtaacg ctctgtCTGT ATGCcgcaaa
 1151 tcgTcgctTC GctgttgAGT TTCGTGCTTT TCCCGATGCT GGGCGGCCAT

1201 CAGGCAACCA TGTCTTGGT TGCAGGCGCA GTCTTGCTGC TGGGAGCCTT
1251 CTCAGTCTGT CTGATTAAAG AGATCCACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 566; ORF 143.ng>:

g143.pep
1 MLSFGYLGVQ TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP
51 IVGYSDRTW K~~PRLGRR~~LP YLLYGT~~LI~~AV IVMILMPNSG SFGFGYASLA
101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDM VNEEQKSYAY GIOSFLANTD
151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL IITSAFTISK
201 VKEYDPETYA RYHGIDVAAN QEKANWFELL KTAPKVFWTV TPVQFFCWFA
251 FRYMWTYSAG AIAENVWHTT DASSVGHQEA GNRYGVLA~~AV~~ *SVA~~AVIC~~SF
301 ILAKVPNKYH KAGYFGCLAL GALGFFS~~IFF~~ IYNQYALILS YILIGIAWAG
351 IITYPLTIVA NALSGK~~HMDT~~ YLGLFN~~GSVC~~ MPQIVASLLS FVLFPMLGGH
401 QATMFLVAGA VLLLGAFSVC LIKEIHGGV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 567>:

m143.seq
1 ATGCTCAGTT TCGGCTTTCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAG
51 CTCGCAAATG AGCCGCATTT TTCAAACGCT AGGCGCAGAC CCGCACAAAT
101 TGGGCTGGTT TTTCATCCTG CCGCCGCTGG CGGGGATGCT GGTGCAGCCG
151 ATTGTGCGCC ATTACTCCGA CCGCACTTGG AAGCCGCGTT TGGGCGGCCG
201 CCGTCTGCCG TATCTGCTTT ATGGCACGCT GATTGCGGTT ATTGTGATGA
251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG
301 GCTTTGTCGT TCGGCGCGCT GATGATTGCG CTGTTAGACG TGTCGTCAA
351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGACATG GTCAACGAGG
401 AGCAGAAAGG CTACGCCTAC GGGATTCAA~~A~~ GTTCTTAGC AAATACGGGC
451 GCGGTCGTGG CCGCGATTCT GCCGTTGTG TTTGCGTATA TCGGTTTGGC
501 GAACACCGCC GAGAAAGGCG TTGTGCCGCA GACCGTGGTC GTGGCGTTTT
551 ATGTGGGTGC GGCCTTGCTG GTGATTACCA GCGCGTTCAC GATTTTCAA
601 GTGAAGGAAT ACGATCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
651 CGCCGCGAAT CAGGAAAAAG CCAACTGGAT CGAACTCTTG AAAACCGCGC
701 CTAAGGCGTT TTGGACGGTT ACTTTGGTGC AATTCTTCTG CTGGTTCCGC
751 TTCCAATATA TGTGGACTTA CTCGGCAGGC GCGATTGCGG AAAACGTCTG
801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACGGT
851 ACGGCGTTTT GCGCGCGGTG CAGTCGGTTG CGGCGGTGAT TGTTCGTTT
901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGGCGGGTT ATTTCCGGCTG
951 TTTGGCTTTG GCGCGCTCG GCTTTTCTC CGTTTTCTC ATCGGCAACC
1001 AATACGCGCT GGTGTTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CGGGCAAGCA
1101 TATGGGCACT TACTTGGGCT TGTTTAACGG CTCTATCTGT ATGCCTCAA
1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG
1201 CAGGCCACTA TGTCTTGGT AGGGGGCGTC GTCCTGCTGC TGGGCGCGTT
1251 TTCCGTGTTT CTGATTAAAG AAACACACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 568; ORF 143>:

m143.pep
1 MLSFGFLGVQ TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP
51 IVGHSDRTW K~~PRLGRR~~LP YLLYGT~~LI~~AV IVMILMPNSG SFGFGYASLA
101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDM VNEEQKGYAY GIOSFLANTG
151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK
201 VKEYDPETYA RYHGIDVAAN QEKANWIELL KTAPKAFWTV TLVQFFCWFA
251 FQYMW~~WTYS~~AG AIAENVWHTT DASSVGYQEA GNWYGVLA~~AV~~ QSVA~~AVIC~~SF
301 VLAKVPNKYH KAGYFGCLAL GALGFFSVFF IGNQYALVLS YTLIGIAWAG
351 IITYPLTIVT NALSGK~~HMT~~ YLGLFN~~GSIC~~ MPQIVASLLS FVLFPMLGGL
401 QATMFLVGGV VLLLGAFSVF LIKETHGGV*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m143 / g143 93.9% identity in 429 aa overlap

10

20

30

40

50

60

406

m143.pep	MLSFGFLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW
g143	MLSFGYLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGYSDRTW
	10 20 30 40 50 60
m143.pep	70 80 90 100 110 120
	KPRLGGRRLPYLLYGTLIAVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
g143	KPRLGGRRLPYLLYGTLIAVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
	70 80 90 100 110 120
m143.pep	130 140 150 160 170 180
	QPFKMMVGDVNEEQKGYAYGIQSFLANTGAVVAAILPFVFAYIGLANTAEGKVVPQTVV
g143	QPFKMMVGDVNEEQKSYAYGIQSFLANTDAVVAAILPFVFAYIGLANTAEGKVVPQTVV
	130 140 150 160 170 180
m143.pep	190 200 210 220 230 240
	VAFYVGAALLVITSFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV
g143	VAFYVGAALLIITSFTISKVKEYDPETYARYHGIDVAANQEKANWFELLKTAPKVFWTV
	190 200 210 220 230 240
m143.pep	250 260 270 280 290 300
	TLVQFFCWFAFQYMWITYSAGAIENVWHTTDASSVGYQEAGNWXVLAQSVAAVICSF
g143	TPVQFFCWFAFRYMWITYSAGAIENVWHTTDASSVGHQEAGNRYGVLAQSVAAVICSF
	250 260 270 280 290 300
m143.pep	310 320 330 340 350 360
	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT
g143	ILAKVPNKYHKAGYFGCLALGALGFFSIFFIYNQYALILSYILIGIAWAGIITYPLTIVA
	310 320 330 340 350 360
m143.pep	370 380 390 400 410 420
	NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLFPMGLGGLQATMFLVGGVLLLGAFSVF
g143	NALSGKHMGTYLGLFNGSVCMQIVASLLSFVLFPMGLGGLQATMFLVAGAVLLLGAFSVC
	370 380 390 400 410 420
m143.pep	430
	LIKETHGGVX
g143	LIKEIHGGVX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 569>:

a143.seq	1	ATGCTCAGTT	TCGGCTTTCT	CGGCGTTCAG	ACGGCCTTTA	CCCTGCAAA
	51	CTCGCAGATG	AGCCGCATCT	TCCAGACGCT	CGGTGCCGAT	CCGCACAGCC
	101	TCGGCTGGTT	CTTTATCCTG	CCGCCGCTGG	CGGGGATGCT	GGTGCAGCCG
	151	ATTGTGCGCC	ATTACTCCGA	CCGCACTTGG	AAGCCGCGTT	TGGGCGGCCG
	201	CCGTCTGCCG	TATCTGCTTT	ATGGCACGCT	GATTGCGGTT	ATTGTGATGA
	251	TTTTGATGCC	GAACTCGGGC	AGCTTCGGTT	TCGGCTATGC	GTCGCTGGCG
	301	GCTTTGTCGT	TCGGCGCGCT	GATGATTGCG	CTGTTAGACG	TGTCGTCAAA
	351	TATGGCGATG	CAGCCGTTTA	AGATGATGGT	CGGCGACATG	GTCAACGAGG
	401	AGCAGAAAGG	CTACGCCTAC	GGGATTCAAA	GTTTCTTAGC	GAATACGGGC
	451	GCGGTCTGGT	CGGCGATTCT	GCCGTTTGTG	TTTGCGTATA	TCGGTTTGGC
	501	GAACACCGCC	GAGAAAGGCG	TTGTGCCGCA	GACCGTGGTC	GTGGCGTTTT
	551	ATGTGGGTGC	GGCGTTGCTG	GTGATTACCA	GCGCGTTCAC	GATTTTCAAA
	601	GTGAAGGAAT	ACAATCCGGA	AACCTACGCC	CGTTACCACG	GCATCGATGT
	651	CGCCGCGAAT	CAGGAAAAAG	CCAACCTGAT	CGAACTCTTG	AAAACCCGCG
	701	CTAAGGCGTT	TTGGACGGTT	ACTTTGGTGC	AATTCTTCTG	CTGGTTCGCC

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751 TTCCAATATA TGTGGACTTA CTCGGCAGGC GCGATTGCGG AAAACGTCTG
801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACGGT
851 ACGGCGTTTT GCGGCGGTG CAGTCGGTTG CCGCGGTGAT TTGTTCGTTT
901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGCGGGGT ATTTCGGCTG
951 TTTGGCTTTG GCGCGCTCG GCTTTTCTC CGTTTCTTC ATCGGCAACC
1001 AATACGCGCT GGTGTTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CGGGCAAGCA
1101 TATGGGCACT TACTTGGGCC TGTTTAACGG CTCTATCTGT ATGCCGCAA
1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG
1201 CAGGCCACTA TGTTCTTGGT AGGGGCGTC GTCTGCTGC TGGGCGCGTT
1251 TTCCGTGTTC CTGATTAAAG AAACACACGG CGGGGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 570; ORF 143.a>:

```

a143.pep
1  MLSFGLGVQ TAFTLQSSQM SRIFQTLGAD PHSLGWFFIL PPLAGMLVQP
51  IVGHYSVRTW KPRLGGRRLP YLLYGTLIIV VMILMPNSG SFGFGYASLA
101 ALSFALMIA LLDVSSNMAM QPFKMMVGD VNEEQGYAY GIQSFLANTG
151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK
201 VKEYNPETYA RYHGIDVAAN QEKANWIELL KTAPKAFWTV TLVQFFCWFA
251 FQYMWYSAG AIAENVWHTT DASSVGQEA GNWYGVLAIV QSVAAVICSF
301 VLAKVPNKYH KAGYFGCLAL GALGFFSVFF IGNQYALVLS YTLIGIAWAG
351 IITYPLTIVT NALSGKHMGT YLGLFNGSIC MPQIVASLLS FVLFPMLGGL
401 QATMFLVGGV VLLLGAFSVF LIKETHGGV*

```

m143/a143 99.5% identity in 429 aa overlap

	10	20	30	40	50	60
m143.pep	MLSFGLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSVRTW					
a143	MLSFGLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSVRTW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m143.pep	KPRLGGRRLPYLLYGTLIIVVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM					
a143	KPRLGGRRLPYLLYGTLIIVVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m143.pep	QPFKMMVGDVNEEQGYAYGIQSFLANTGAVVAAILPFVFAYIGLANTAIEKGVVPQTVV					
a143	QPFKMMVGDVNEEQGYAYGIQSFLANTGAVVAAILPFVFAYIGLANTAIEKGVVPQTVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m143.pep	VAFYVGAALLVITSAFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV					
a143	VAFYVGAALLVITSAFTIFKVKEYNPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m143.pep	TLVQFFCWFAFQYMWYSAGAIENVWHTTDASSVGQEAQGNWYGVLAIVQSVAAVICSF					
a143	TLVQFFCWFAFQYMWYSAGAIENVWHTTDASSVGQEAQGNWYGVLAIVQSVAAVICSF					
	250	260	270	280	290	300
	310	320	330	340	350	360
m143.pep	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT					
a143	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT					
	310	320	330	340	350	360
	370	380	390	400	410	420
m143.pep	NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLFPMLGGLQATMFLVGGVVLLLGAFSVF					

408

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a143      |||||
          NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLFPMLGGLQATMFLVGGVLLLGAFSVF
          370      380      390      400      410      420

          430
m143.pep  LIKETHGGVX
          |||||
a143      LIKETHGGVX
          430

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 571>:

```

g144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGCCTGATCG ACGGGCGGGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGTGC GTCTTCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC CCGTGGTGTC GTTCGACGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGTAGGACTT ACCGCGTGGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTCGCAC GGGCTGGCCG TTACCcgtTT
351 CAACGCGGTG GCGGCAGACG GccgacggTt atCCCAACGA TTTGgatatt
401 TCctaccgCT TGGACGAGGA CCGCCGGCTT ACCGTtaccT ATCGCGCCAC
451 CGCgctCGGC GACACGGTGT TCGACCCGAC GCTGCACATT TACTGGCGGC
501 TGGACGCGGG CCTGCACGAT GCGGTTCTGC ATATTCCGCA GGGCGGACAT
551 ATTCCGGCCG ATGCCGAAAA ACTGCCCGTC TTAACGGTTT CAGACGGCCT
601 CGAAGTATTT GA

```

This corresponds to the amino acid sequence <SEQ ID 572; ORF 144.ng>:

```

g144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTC VFVLDLGGIV QEFSVLADGV
51  RENPVVSFDD AASYADNPFQ INKQIGRVAG RIRGAAFDIN GRTRYVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRRLSQR FGyFLPLGRG RPAYRYLSRH
151 RARRHGVRPD AAHLLAAGRG PARCGSAYSA GRTYSGRCRK TARLNGFRRP
201 RSI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 573>:

```

m144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGTCTGATCG ACGGGCGTGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGCGT GTCTGCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC TCGTGGTGTC GTTCGATGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAAC AGATAGGGCG CGTGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGCAGGACTT ACCGCGTGGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTCGCAC GGGCTGGCCG TTACCCGTTT
351 CAACGCGGTG GCGGCAGACG GCCGTTCCGT GGTGCTGCGC AGCCGCCTGg
401 CAACAGTCGG CCGACGGTTA TCCCAACGAT TTGGATTGG ATATTTCTTA
451 CCGCTTGGAC GAGGACGACC GGCTTACCGT TAcCTATCGC GCCACCGCGC
501 TCGGCGACAC GGTGTTTCGAC CCGACGCTGC ACATTTACTG GCGGCTGGAC
551 GCGGGCCTGC ACGATGCGGT TCTGCATATT CCGCAGGGCG GACATATGCC
601 GGCCGATGCC GAAAACTGC CCGTCTCAAC GGTTCAGAC GACCTCGAAG
651 TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 574; ORF 144>:

```

m144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTR VCVLDLGGIV QEFSVLADGV
51  RENLVVSFDD AASYADNPFQ INKQIGRVAG RIRGAAFDIN GRTRYVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRSVVLR SRLATVGRRL SQREGFGYFL
151 PLGRGRPAYR YLSRHRARRH GVRPDAAHLL AAGRGPARGC SAYSAGRTYA
201 GRCRK TARLN GFRRPRSI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m144 / g144 91.3% identity in 218 aa overlap

```

      10      20      30      40      50      60
m144.pep  MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD
          |||
g144      MSDTPATRDFGLIDGRAVTGYVLSNRRGTCVFVLDLGGIVQEFSVLADGVRENPFVVSFDD
          10      20      30      40      50      60

      70      80      90      100     110     120
m144.pep  AASYADNPFQINKQIGRVAGRIRGAAFDINGRTYRVEANEGRNALHGGSHGLAVTRFNAV
          |||
g144      AASYADNPFQINKQIGRVAGRIRGAAFDINGRTYRVEANEGRNALHGGSHGLAVTRFNAV
          70      80      90      100     110     120

      130     140     150     160     170     180
m144.pep  AADGRSVVLRSLATVGRRLSQRFGFGYFLPLGRGRPAYRYLSRHRARRHGVRPDAAHLL
          |||
g144      AAD-----GRRLSQRFG--YFLPLGRGRPAYRYLSRHRARRHGVRPDAAHLL
          130     140     150     160

      190     200     210     219
m144.pep  AAGRGPARCGSAYSAGRTYAGRCRKRTARLNGFRRPRSI
          |||
g144      AAGRGPARCGSAYSAGRTYSGRCRKRTARLNGFRRPRSI
          170     180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 575>:

```

a144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGCCTGATCG ACGGGCGGTGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGCGT GTCTGCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTTGGC AGACGGCGTG
151 CGCGAAAACC TCGTGGTGTC GTTCGACGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGCAGGACTT ACCGCGTGGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTTCGCAC GGGCTGGCCG TTACCCGTTT
351 CAACGCGGTG GCGGCAGACG GCCGTTTCGGT GGTGCTGCGC AGCCGCTG.
401 CAACAGTCGG CCGACGGTTA TCCAACGAT TTGGATTGG ATATTTCTTA
451 CCGCTTGGAC GAGGACGACC GGCTTACCGT TACCTATCGC GCCACCGCGC
501 TCGGCGACAC GGTGTTTCGAC CCGACGCTGC ACATTTACTG GCGGCTGGAC
551 GCGGGCCTGC ACGATGCGGT TCTGCATATT CCGCAGGGCG GACATATCC
601 GGCCGATGCC GAAAACTGC CCGTCTCAAC GGTTCAGAC GACCTCGAAG
651 TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 576; ORF 144.a>:

```

a144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTR VCVLDLGGIV QEFSVLADGV
51  RENLVVSFDD AASYADNPFQ INKQIGRVAG RIRGAAFDIN GRTYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRSVVLR SRLXTVGRRL SQRFGFGYFL
151 PLGRGRPAYR YLSRHRARRH GVRPDAAHLL AAGRGPARCG SAYSAGRTYS
201 GRCRKRTARLN GFRRPRSI*

```

m144/a144 99.1% identity in 218 aa overlap

```

      10      20      30      40      50      60
m144.pep  MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD
          |||
a144      MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD
          10      20      30      40      50      60

      70      80      90      100     110     120
m144.pep  AASYADNPFQINKQIGRVAGRIRGAAFDINGRTYRVEANEGRNALHGGSHGLAVTRFNAV

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410

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|||||
a144  AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV
      70      80      90      100     110     120

      130     140     150     160     170     180
m144.ppep AADGRSVVLRSLATVGRRLSQRFGGYFLPLGRGRPAYRYLSRHRARRHGVRPDAAHLL
|||||
a144  AADGRSVVLRSLXTVGRRLSQRFGGYFLPLGRGRPAYRYLSRHRARRHGVRPDAAHLL
      130     140     150     160     170     180

      190     200     210     219
m144.ppep AAGRGPARGCSAYSAGRTYAGRCRKRTARLNGFRRPRSIX
|||||
a144  AAGRGPARGCSAYSAGRTYSGRCRKRTARLNGFRRPRSIX
      190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 577>:

```

g146.seq
1  ATGAAGCAAA TCCCCCTCCG CCTTCTCCAG GTCGTCATTG ACCACGACAA
51  AGTCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCCTT CGACAGCCTC
101 CTTTGGATAA ctTCCCGACT GTCCGTCCCG CGCctTTGA GGCGCGCGGC
151 AAGCACGTCG AAAGAAGGCG GCAGGATAAA GATACCGACA GCTTCCGGCA
201 GCGCGTTGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAGCCTG CCGCCGCCAA CGCATTACAG CCCTCCGTGC TTGTGCCGTA
301 ATAGTTGCCG AATACGTCTG CGTATTCCAA AAAAGCCTCC TGCGCGATAA
351 GCGATTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGGCGGGCG CGTCGTATGC GACACGGAAG CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTG CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAA CCGATTGTAT CACAACGGAC ACCCTATTTT
601 ATATTTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 578; ORF 146.ng>:

```

g146.ppep
1  MKQIPLRLQ VVIDHDKVEQ YGLDFMPCL RQPPLDNFPT VRPAPFEARG
51  KHVERRRQDK DTDSFRQVA NLRRALNVDF QNHVIACRRQ RIHALRACAV
101 IVAEYVCVFQ KSLLRDKRFK LFFGNKVIMY AVCFAFTRRA RMRHGNNAQT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPYF
201 IFADAHILPL LF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 579>:

```

m146.seq
1  ATGGCGCAAA TCCTCCTCCG CTCGCGCCAA GTCGTCATTG ACCACGACAA
51  AGTCAAACAA TACGGACTGC TCGATTTCAT GCCTTGCCTT CGACAGCCTC
101 CTTTGGATAA CTTCCTCGACT GTCCGTCCCG CGTCCGTGTA GGCGCGCGGC
151 AAGTACGTCG AAAGAAGGCG GCAGGATAAA GATGCCGACG GCTTCCGGCA
201 GCGCGTCGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAGCCTG CCGCCGCCAA CGCATTACAG CCCTCCGCGC CTGTGCCGTA
301 ATAGTTGCCA AATACGTCCG CGTATTCCAA AAAAGCTTCC TGCGCGATAA
351 GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGGCGGGCG CGTCGTGTGC GACACGGAAG CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTG CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAATGGAC ACCCAGTTTC
601 CTATTTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 580; ORF 146>:

```

m146.ppep
1  MAQILLRSRQ VVIDHDKVKQ YGLDFMPCL RQPPLDNFPT VRPASVEARG
51  KYVERRRQDK DADGFGQVA NLRRALNVDF QNHVIACRRQ RIHTLRACAV
101 IVAKYVGVFQ KSFLLDKRLK LFFGNKVIMY AVCFAFTRRA RRVHGNNAQT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQWTPSF
201 LFADAHILPL LF*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m146 / g146 90.1% identity in 212 aa overlap

m146.pep	10	20	30	40	50	60
	MAQILLRSRQVVIDHDKVKQYGLLDFMPCLRQPPLDNFPTVRPASVEARGKYVERRRRQDK					
g146						
	10	20	30	40	50	60
	MKQIPLRLLQVVIDHDKVEQYGLFDFMPCLRQPPLDNFPTVRPAPFEARGKHVERRRRQDK					
m146.pep	70	80	90	100	110	120
	DADGFGQRVANLRRALNVDFQNHVIACRRQRIHTLRACAVIVAKYVGVFQKSFLRDKRLK					
g146	: :					
	70	80	90	100	110	120
	DTDSFRQRVANLRRALNVDFQNHVIACRRQRIHALRACAVIVAEYVCVFQKSLLRDKRFK					
m146.pep	130	140	150	160	170	180
	LFFGNKVIMYAVCFATRRARRVRHGNQAQTMVCQQPRHQRFARAGSGRNDKDVAFSIS					
g146						
	130	140	150	160	170	180
	LFFGNKVIMYAVCFATRRARRMRHGNQAQTMVCQQPRHQRFARAGSGRNDKDVAFSIS					
m146.pep	190	200	210			
	GHIFYLYIFQPIVSQWTPSFLFADAHILPLLEFX					
g146						
	190	200	210			
	GHIFYLYIFQPIVSQRTPYFIFADAHILPLLEFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 581>:

a146.seq

1	ATGGCGCAAA	TCCTCCTCCG	CCCGCGCCAA	GTCATCATTTG	ACCACGACAA
51	AATCGAACAA	TACGGACTGT	TCGATTTCAT	GCCTTGCCTT	CGACAGCCTC
101	CTTTGGATAA	CTTCCCGACT	GTCCGTCCCG	CGTCCGTGTA	GACGCGCAGC
151	AAGCACATCG	AAAGACGGCG	GCAGGATAAA	GATGCCGACG	GCTTCGGGCA
201	GCGCATCTCG	AACCTGAGCC	GCGCCCTGAA	CGTCGATTTC	CAAAATCACG
251	TCATAACCTG	CCGCCGCCAA	CGCATTCACA	CCCTCCGCGC	TTGTGCCGTA
301	ATAGTTGCCG	AACACGTCCG	CGTATTCCAA	AAAAGCCTCC	TGCGCGATAA
351	GCGACTCAAA	CTCTTCTTTG	GAAACAAAGT	GATAATGTAC	GCCGTTTGCT
401	TCGCCTTCAC	GCGGCGGACG	CGTCGTGTGC	GACACGGAAA	CGCGCAAACC
451	GTTATGTTT	GCCAACAGCC	GCGACACCAG	CGTGGTTTTG	CCCGTGCCGG
501	AAGCGGCCGA	AATGATAAAG	ATGTTGCCTT	TTGATAAGC	GGACATATTT
551	TTTACCTGTA	TATTTTCCAG	CCGATTGTAT	CACAACGGAC	ACCGGTTTC
601	CTATTTGCCG	ATGCCCATAT	TTGCGCGCTA	TTGTTTGA	

This corresponds to the amino acid sequence <SEQ ID 582; ORF 146.a>:

a146.pep

1	MAQILLRPRQ	VIIDHKIEQ	YGLDFMPCL	RQPPLDNFPT	VRPASVETR
51	KHIERRRQDK	DADGFGQRIS	NLSRALNVDF	QNHVITCRRQ	RIHTLRACAV
101	IVAETHVRVFQ	KSLLRDKRLK	LFFGNKVIMY	AVCFATRRRT	RRVRHGNQAQ
151	VMVCQQPRHQ	RGFARAGSGR	NDKDVAFSIS	GHIFYLYIFQ	PIVSQRTPGF
201	LFADAHILPL	LF*			

m146/a146 90.6% identity in 212 aa overlap

m146.pep	10	20	30	40	50	60
	MAQILLRSRQVVIDHDKVKQYGLLDFMPCLRQPPLDNFPTVRPASVEARGKYVERRRRQDK					
a146						
	10	20	30	40	50	60
	MAQILLRPRQVIIDHKIEQYGLFDFMPCLRQPPLDNFPTVRPASVETRSHIERRRQDK					
	70	80	90	100	110	120

```

m146.pep      DADGFGQVRANLRRALNVDFQNHVIACRRQRRIHTLRACAVIVAKYGVVFQKSLFRDKRLK
|||||:::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a146          DADGFGQRISNLSRALNVDFQNHVITCRRQRRIHTLRACAVIVAEHVRVVFQKSLLRDKRLK
              70          80          90          100         110         120

              130         140         150         160         170         180
m146.pep      LFFGNKVIMYAVCFAFTRRRARRVRHGNQATVMVCQQPRHQRGFARAGSGRNDKDVAFSIS
|||||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a146          LFFGNKVIMYAVCFAFTRRRTRVRHGNQATVMVCQQPRHQRGFARAGSGRNDKDVAFSIS
              130         140         150         160         170         180

              190         200         210
m146.pep      GHIFYLYIFQPIVSQWTPSELFADAHILPLLFX
||||| | | | | | | | | | | | | | | | | | | | | | | |
a146          GHIFYLYIFQPIVSQRTPGFLFADAHILPLLFX
              190         200         210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 583>:

```
g147.seq (partial)
1  ..ATGCGACGAG AAGCCAAAAT GGCACAAATC ACAC TCAAAC CCATTGTTTT
51  ATCAATTCTT TTAATCAACA CACCCCTCCT CGCCCAAGCG CATGAAACTG
101 AGCAATCGGT GGGCTTGGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTCCG
151 CGCGCGACTT CGGGGCTGCT GCACACTCGC ACCGCCTCCG ACAAAATCAT
201 CTCCGGCGAT ACTTTGCGCC AAAAAGCCGT CAACTTGGGC GACGCTTTGG
251 ACGGCGTACC GGGCATCCAC GCTTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC GGGCAGACGG ATTAAGTAT TGAACCATCA
351 CGGCGAAACG GGCGATATGG CGGACTTTTC TCCCGATCAC GCCATTATGG
401 TAGATACAGC CTTGTCGCAA CAGGTGAAA TCCTGCGCGG GCCGGTTACG
451 CTCTTGTAAC GCTCGGgcaa tgtggccgGG GCTGGtcaat gttgccgatg
501 qAAAAAtccc ccaaaaAatg cc..
```

This corresponds to the amino acid sequence <SEQ ID 584; ORF 147.ng>:

```
g147.pep (partial)
1  ..MRREAKMAQI TLKPIVL SIL LINTPLLAQA HETEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRQGTGRR IKVLNHHGET GDMADFSPDH AIMVDTALSQ QVEILRGFVT
151 LLYSSGNVAG AGQCCRWNKP PKNA..
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 585>:

ml47.seq	(partial)				
1	..CCGCATAAAA	CTGAGCAATC	GGTGGATTTG	GAAACGGTCA	GCGTCGTCGG
51	CAAAAGCCGT	CCGCGCGCCA	CGTCGGGGCT	GTTGCACACT	TCGACCGCCT
101	CCGACAAAT	CATCTCCGGC	GATACCTTGC	GCCAAAAAGC	CGTCAACTTG
151	GGCGACGCT	TAGACGGCGT	ACCGGCGCAT	CACGCTTCGC	AATACGGCGG
201	CGGCGCGTCT	GCTCCCCTCA	TTCGCGGTCA	AACAGGCAGG	CGGATTAAAG
251	TGTTGAACCA	TCACGGCGAA	ACAGGCGATA	TGGCGGATTT	TTCGCCCGAT
301	CACGCCATTA	TGGTAGATAC	CGCCTTGTCG	CAACAGGTCG	AAATCCTGCG
351	CGGGCCGGTT	ACGCTCTTGT	ACAGCTCGGG	CAATGTGGCG	GGGCTGGTCG
401	ATGTTGCCGA	TGGCAAAAAT	CCCGAAAAAA	TGCCTGAAAA	CGCGGTATCG
451	GATCGAATCG	GATTGCGTTT	GAGCAGCGGC	ACTCTGAAAA	AACTCACGTC
501	CGGCGGCATC	AATATCGGTT	TGGGCAAAAA	CTTTGTATTG	CACACGGAAG
551	GGCTGTACCG	CAAATCGGGG	GATTACGCCG	TACCGCGTTA	CCGCAATCTG
601	AAACGCCTGC	CCGACAGCCA	CGCCGATTCT	CAAACGGGGC	GCATCGGGCT
651	GTCTTGGGTT	GGCGAAAAAG	GTTTTATCGG	CGTAGCGTAC	AGCGACCGTC
701	GCGACCAATA	TGGTCTGCCT	GCCCACACGC	ACGAATAACA	TGATTGCCAC
751	GCCGACATCA	TCTGGCAAAA	GACTTGATT	AACAAACGCT	ATTTACAGCT
801	TTATCCGCAC	CTGTTGACCG	AAGAAGACAT	CGATTACGAC	AATCCGGGCT
851	TGAGCTGCGG	CTTCCACGAC	GACGATAATG	CACACGCACA	CACCCACAGC
901	GGCAGACCGT	GGATAGACCT	GCGCAACAAA	CGCTACGAAC	TCCGTGCCGA
951	ATGGAAGCAA	CCGTTCCCCG	GTTTTGAAGC	CCTGCGCGTA	CACCTGAACC
1001	GCAACGACTA	CCGCCACGAC	GAAAAAGCAG	GCATGCGAGT	CGAAAACTTT
1051	TTTAACAACC	AAACGCAAAA	CGCCCGCATC	GAGTTGCGCC	ACCAACCCAT

413

```

1101 AGGTCGTCTG AAAGGCAGCT GGGGCGTGCA ATATTACAA CAAAAATCCA
1151 GTGCTTTATC TGCCATATCC GAAGCGGTTA AACAAACCGAT GCTGCTTGAC
1201 AACAAAGTGC AACATTACAG CTTTTTCGGT GTAGAACAGG CAAACTGGGA
1251 CAACTTCACG CTTGAAGGAG GCGTACGCGT GGAAAAACAA AAAGCCTCCA
1301 TTCAGTACGA CAAAGCATTG ATTGATCGGG AAAACTACTA CAACCACCCC
1351 CTGCCCAGAC TCGGCGCGCA CCGCCAAACC GCCCGCTCAT TCGCACTTTC
1401 GGGCAACTGG TATTTCACGC CACAACACAA ACTCAGCCTG ACCGCCTCCC
1451 ATCAGGAACG CCTGCCGTCA ACGCAAGAGC TGTACGCACA CGGCAAAACAC
1501 GTCGCCACCA ACACCTTTGA AGTCGGCAAC AAACACCTCA ACAAAGAGCG
1551 TTCCAACAAT ATCGAACTCG CGCTGGGCTA CGAAGGCGAC CGCTGGCAAT
1601 ACAATCTGGC ACTCTACCGC AACCGCTTCG GTAACCTACAT TTACGCCCAA
1651 ACCTTAAACG ACGGACGCGG CCCCAAATCC ATCGAAGACG ACAGCGAAAT
1701 GAAGCTCGTG CGCTACAACC AATCCGGCGC CGACTTCTAC GGCGCGGAAG
1751 GCGAAATCTA CTTCAAACCG ACACCGCGCT ACCGCATCGG CGTTTCCGGC
1801 GACTATGTAC GAGGCGGTCT GAAAAACCTG CCTTCCCTAC CCGGCAGAGA
1851 AGATGCCTAC GGCAACCGTC CTTTCATCGC ACAGGACGAC CAAAATGCCC
1901 CCCGTGTTCC GGCTGCGCGC CTCGGCTTCC ACCTGAAAGC CTCGCTGACC
1951 GACCGTATCG ATGCCAATTT GGACTACTAC CGCGTGTTCC CCAAAACAA
2001 ACTCGCCCGC TACGAAACGC GCACGCCCGG ACACCATATG CTCAACCTCG
2051 GCGCAAACTA CCGCCGCAAT ACGCGCTATG GCGAGTGGA TTGCTACGTC
2101 AAAGCCGACA ACCTGCTCAA CCAATCCGTT TACGCCACG GCAGCTTCT
2151 CTCTGATACG CCGCAAATGG GCCGCAGCTT TACCGGCGGC GTGAACGTGA
2201 AGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 586; ORF 147>:

```

m147.pep (partial)
1  ..PHKTEQSVDL ETVSVVGKSR PRATSGLLHT STASDKIISG DTLRQKAVNL
51  GDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGE TGDMAFSPD
101 HAIMVDTALS QQVEILRGPV TLLYSSGNVA GLVDVADGKI PEKMPENGVS
151 GELGLRLSSG NLEKLTSGGI NIGLGKNFVL HTEGLYRKSG DYAVPRYRNL
201 KRLPDSHADS QTGSIGLSWV GEKGFIVGAY SDRRDQYGLP AHSHEYDDCH
251 ADIIWQKSLI NKRYLQLYPH LLTEEDIDYD NPGLSCGFHD DDNAHAHTHS
301 GRPWIDLRNK RYELRAEWKQ PFPGFELRV HLNRRNDYRD EKAGDAVENF
351 FNNQTQNARI ELRHQPIGRL KGSWGVQYLQ QKSSALS AIS EAVKQPMLLD
401 NKVQHYSFFG VEQANWDNFT LEGGVRVEKQ KASIQYDKAL IDRENYNHP
451 LPDLGAHRQT ARSFALSGNW YFTPQHKLSL TASHQERLPS TQELYAHGKH
501 VATNTFEVGN KHLNKRSSNN IELALGYEGD RWQYNLALYR NRFGNYIYAQ
551 TLNDGRGPKS IEDDSEMCLV RYNQSGADFY GAEGEYFKP TPRYRIGVSG
601 DYVRGRKLNL PSLPGREDAY GNRPFIAQDD QNAPRVPAAR LGFHLKASLT
651 DRIDANLDYY RVFAQNKLAR YETRTPGHHM LNLGANYRRN TRYGEWNWYV
701 KADNLLNQSV YAHSSFLSDT PQMGRSFTGG VNVKE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m147 / g147 92.3% identity in 142 aa overlap

```

                                10      20      30
m147.pep                      PHKTEQSVDLETVSUVGKSRPRATSGLLHTS
                                |:||||| |||||
g147      MRREAKMAQITLKPIVLSILLINTPLLAQAHETEQSVGLETVSUVGKSRPRATSGLLHTS
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m147.pep      TASDKIISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGET
|||||
g147      TASDKIISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGET
                                70      80      90      100     110     120

                                100     110     120     130     140     150
m147.pep      GDMADFSPDHAIMVDTALSQQVEILRGPVTLTYSSGNVAGLVDVADGKIPEKMPENGVS
|||||
g147      GDMADFSPDHAIMVDTALSQQVEILRGPVTLTYSSGNVAGAGQCCRWNPPKNA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 587>:

```

a147.seq
1  ATGCGACGAG AAGCCAAAAT GGCACAAACT ACACTCAAAC CCATTGTTTT
51  ATCAATTCTT TTAATCAACA CACCCTCCT CTCCAAGCG CATGGAAGCTG
101 AGCAATCAGT GGGCTTGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTCGG
151 CGCGCCACTT CGGGGCTGCT GCACACTTCT ACCGCCTCCG ACAAATCAT
201 CAGCGGCGAC ACCTTGCAC AAAAAGCCGT CAACTTGGGT GATGCTTTAG
251 ACGGCGTACC GGGCATTCT GCCTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC AGGCAGACGG ATTAAAGTGT TGAACCATCA
351 CGGCGAAACG GGCACATGG CGGACTTCTC TCCAGACCAT GCAATCATGG
401 TGGACAGCGC CTGTGCGCAA CAGGTCGAAA TCCTGCGCGG TCCGGTTACG
451 CTCTTGTAACA GCTCGGGCAA TGTGGCGGGG CTGGTCGATG TTGCCGATGG
501 CAAAATCCCC GAAAAAATGC CTGAAAACGG CGTATCGGGC GAACTCGGAT
551 TGCCTTTGAG CAGCGGCAAT CTGAAAAAAC TCACGTCCGG CGGCATCAAT
601 ATCGGTTTGG GCAAAAACCTT TGTATTGCAC ACGGAAGGGC TGTACCGCAA
651 ATCGGGGGAT TACGCCGTAC CGGTTACCG CAATCTGAAA CGCCTGCCCG
701 ACAGCCACGC CGATTGCGAA ACGGGCAGCA TCGGGCTGTC TTGGGTTGGC
751 GAAAAAGGCT TTATCGGCGC AGCATACAGC GACCGTCGCG ACCAATATGG
801 TCTGCCGTGCC CACAGCCACG AATACGATGA TTGCCACGCC GACATCATCT
851 GGCAAAAGAG TTTGATTAAAC AAACGCTATT TGCAGCTTTA TCCGCACCTG
901 TTGACCGAAG AAGACATCGA TTACGACAAT CCGGGCTTGA GCTGCGGCTT
951 TCACGACGAC GATGATGCAC ACGCCCATGC CCACAACGGC AAACCTTGGA
1001 TAGACCTGCG CAACAAACGC TACGAACTCC GCGCCGAATG GAAGCAACCG
1051 TTCCCCGGTT TTGAAGCCCT GCGCGTACAC CTGAACCGCA ACGACTACCG
1101 CCACGACGAA AAAGCAGGCG ATGCAGTAGA AAACCTTTTT AACAACCAAA
1151 CGCAAAACGC CCGTATCGAG TTGCGCCACC AACCCATAGG CCGTCTGAAA
1201 GGCAGCTGGG GCGTGCAATA TTTGGGACAA AAATCCAGTG CTTTATCTGC
1251 CACATCCGAA GCGGTCAAAC AACCAGTGCT GCTTGACAAT AAAGTGCAAC
1301 ATTACAGCTT TTTCGGTGTA GAACAGGCAA ACTGGGACAA CTTACGCTT
1351 GAAGGCGGCG TACGCGTGGA AAAACAAAAA GCCTCCATCC GCTACGACAA
1401 AGCATTGATT GATCGGGAAA ACTACTACAA CCATCCCCTG CCCGACCTCG
1451 GCGGCGACCG CCAAACCGCC CGCTCATTCG CACTTTCGGG CAACTGGTAT
1501 TTCACGCCAC AACACAAACT CAGCCTGACC GCCTCCCATC AGGAACGCCCT
1551 GCCGTCAACG CAAGAGCTGT ACGCACACGG CAAACACGTC GCCACCAACA
1601 CCTTTGAAGT CGGCAACAAA CACCTCAACA AAGAGCGTTC CAACAATATC
1651 GAACTCGCGC TGGGCTACGA AGGCGACCGC TGGCAATACA ATCTGGCACT
1701 CTACCGCAAC CGCTTCGGCA ACTACATTTA CGCCCAAACC TTAAACGACG
1751 GACGCGGCCC CAAATCCATC GAAGACGACA GCGAAATGAA GCTCGTGCGC
1801 TACAACCAAT CCGGTGCGGA CTTCTACGGC GCGGAAGGCG AAATCTACTT
1851 CAAACCGACA CCGCGCTACC GCATCGGCGT TTCCGGCGAC TATGTACGAG
1901 GCCGTCTGAA AAACCTGCCT TCCCTACCCG GCAGGGAAGA CGCCTACGGC
1951 AACCGCCAC TCATTGCCCA AGCCGACCAA AACGCCCTC GCGTTCGGC
2001 TGCGCGCCTC GCGTCCACC TGAAAGCCTC GCTGACCGAC CGCATCGATG
2051 CCAATTTGGA CTACTACCGC GTGTTGCGCC AAAACAAACT CGCCCGCTAC
2101 GAAACGCGCA CGCCCGGACA CCATATGCTC AACCTCGGCG CAAACTACCG
2151 CCGCAATACG CGCTATGGCG AGTGGAATTG GTACGTCAA GCGGACAACC
2201 TGCTCAACCA ATCCGTTTAC GCCCACAGCA GCTTCCTCTC TGATACGCCG
2251 CAAATGGGCC GCAGCTTTAC CGGCGGCGTG AACGTGAAGT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 588; ORF 147.a>:

```

a147.pep
1  MRREAKMAQT TLKPIVLSIL LINTPLLSQA HGTEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHHGET GDMADFSPPH AIMVDSALSQ QVEILRGVPT
151 LLYSSGNVAG LVDVADGKIP EKMPENGVSQ ELGLRLSSGN LEKLTSGGIN
201 IGLGKNFVLH TEGLYRKSGD YAVPRYRNLK RLPDSHADSQ TGSIGLSWVG
251 EKGFIGAAYS DRRDQYGLPA HSHEYDDCHA DIIWQKSLIN KRYLQLYPHL
301 LTEEDIDYDN PGLSCGFHDD DDAHAHAHNG KPWIDLRNKR YELRAEWKQP
351 FPGFEALRVH LNRNDYRHDE KAGDAVENFF NNQTQNARIE LRHQPIGRLE
401 GSWGVQYLGQ KSSALSATSE AVKQPMMLDN KVQHSFFGV EQANWDNFTL
451 EGGVRVEKQK ASIRYDKALI DRENYNHPL PDLGAHRQTA RSFALSGNWI
501 FTPQHKLST ASHQLRPST QELYAHGKHV ATNTFEVGNK HLNKERSNNI
551 ELALGYEGDR WQYNLALYRN RFGNYIYAQT LNDGRGPKSI EDDSEMKLVR

```


	10	20	30	40	50	60
m147.pep	PHKTEQSV DLETVSVVGKSRPRATSGLLHSTS					
a147	MRREAKMAQTTLKPIVLSILLINTPLLSQAHGTEQSVGLETVSVVGKSRPRATSGLLHSTS					
	10	20	30	40	50	60
	40	50	60	70	80	90
m147.pep	TASDKIISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGET					
a147	TASDKIISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGET					
	70	80	90	100	110	120
	100	110	120	130	140	150
m147.pep	GDMADFS PDHAIMVDTALSSQQVEILRGPV TLLYSSGNVAGLVDVADGKIPEKMPENGVS G					
a147	GDMADFS PDHAIMVDSALSSQQVEILRGPV TLLYSSGNVAGLVDVADGKIPEKMPENGVS G					
	130	140	150	160	170	180
	160	170	180	190	200	210
m147.pep	ELGLRLSSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRN LKRLPDSHADSQ					
a147	ELGLRLSSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRN LKRLPDSHADSQ					
	190	200	210	220	230	240
	220	230	240	250	260	270
m147.pep	TGSIGLSWVGEGKGF IGVAYS DRRDQYGLPAHSHEYDDCHADI IWQKSLINKRYLQLYPHL					
a147	TGSIGLSWVGEGKGF IGAAYS DRRDQYGLPAHSHEYDDCHADI IWQKSLINKRYLQLYPHL					
	250	260	270	280	290	300
	280	290	300	310	320	330
m147.pep	LTEEDIDYDN PGLSCGFHDDDNAHAH THSGRPWIDL RNKRYELRAEWKQFPFGFEALRVH					
a147	LTEEDIDYDN PGLSCGFHDDDDAH AHANGKPWIDL RNKRYELRAEWKQFPFGFEALRVH					
	310	320	330	340	350	360
	340	350	360	370	380	390
m147.pep	LNRNDYRHDEKAGDAVENFFNNQTQ NARIELRHQPIGR LKGSWGVQYLGQKSSALS AIS E					
a147	LNRNDYRHDEKAGDAVENFFNNQTQ NARIELRHQPIGR LKGSWGVQYLGQKSSALSATSE					
	370	380	390	400	410	420
	400	410	420	430	440	450
m147.pep	AVKQPM LLDNKNVQHYSFFGVEQANW DNF TLEGGVRVEKQKAS IRYDKALIDRENYN HPL					
a147	AVKQPM LLDNKNVQHYSFFGVEQANW DNF TLEGGVRVEKQKAS IRYDKALIDRENYN HPL					
	430	440	450	460	470	480
	460	470	480	490	500	510
m147.pep	PDLGAHRQTAR SFALSGN WYFT PQHKLSLTASHQERLPSTQ ELYAHGKHVATNTFEVGNK					
a147	PDLGAHRQTAR SFALSGN WYFT PQHKLSLTASHQERLPSTQ ELYAHGKHVATNTFEVGNK					
	490	500	510	520	530	540
	520	530	540	550	560	570
m147.pep	HLNKERSNNIELALGYEGDRWQYNLALYRN RFGNYIYAQT LNDGRGPKSIEDDSEMKLVR					
a147	HLNKERSNNIELALGYEGDRWQYNLALYRN RFGNYIYAQT LNDGRGPKSIEDDSEMKLVR					

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	550	560	570	580	590	600
	580	590	600	610	620	630
m147.pep	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFIAQDDQ					
a147	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPPLIAQADQ					
	610	620	630	640	650	660
	640	650	660	670	680	690
m147.pep	NAPRVPAARLGFHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNT					
a147	NAPRVPAARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNT					
	670	680	690	700	710	720
	700	710	720	730		
m147.pep	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
a147	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
	730	740	750	760		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 589>:

```

g148.seq
1  ATGGCGTTAA  AAACATCAAA  CTTGGAACAC  GCAATGctgg  ttcaTCCCGA
51  AgctATgagt  gtcggcgCGC  TTGccgAcaa  AATCCGCAAA  AtcgaAAact
101 gGCCGCAAAA  AGgcaTCTTA  TTCCACGACA  TCACGCCCGT  CCTGCAAAGT
151 GCGGAATACT  TCCGCCTTTT  GGTTCGATTG  CTGGTTTACC  GCTATATGGA
201 TCAGAAAATC  GACATCGTTG  CCGGCTTGGA  CGCGCGCGGC  TTCATTATCG
251 GCGCGGCACT  CGCCTACCAG  CTCAaCGtgc  gctTCGTCCC  CATCCGCAAA
301 AAAGGCAAGC  TGCCTTTTGA  AACCGTATCG  CAAAGCTAcg  cgCTCGAATA
351 CGGGGAAGCT  GCGGTGGAAA  TCCACACCGa  tgccgTCAAA  CCCGGTTCGC
401 GCGTCCTGCT  GGTTCGATGAT  TTGGTTGCCA  CGGGCGGCAC  AATGCTTGCC
451 GGGCTGGAAC  TGATCCGCAA  ACTCGGCGGG  GAAATTGTCT  AAgccgcgcg
501 CATTTTGGA  TTTACCGACC  TTCAAGGCGG  CAAGAATATC  CGCGCAAGTG
551 GCGCGCCCTT  ATTTACCCTG  CTTCAAAACG  AAGGCTGCAT  GAAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 590; ORF 148.ng>:

```

g148.pep
1  MALKTSNLEH  AMLVHPEAMS  VGALADKIRK  IENWPQKGIL  FHDITPVLOS
51  AEYFRLLVDL  LVYRYMDQKI  DIVAGLDARG  FIIGAALAYQ  LNVGFVPIRK
101 KGKLPFETVS  QSYALEYGEA  AVEIHTDAVK  PGRSVLLVDD  LVATGGTMLA
151 GLELIRKLGG  EIVEAAAILE  FTDLQGGKNI  RASGAPLFTL  LQNEGCMKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 591>:

```

m148.seq
1  ATGGCGTTAA  AAACATCAAA  CTTGGAACAC  GCAATGCTGG  TTCATCCCGA
51  AGCTATGAGT  GTCGGCGCGC  TTGCCGACAA  AATCCGCAAA  ATCGAAAAC
101 GGCCGCAAAA  AGGCATCTTA  TTCCACGACA  TCACGCCCGT  CCTTCAAAGC
151 GCGGAATACT  TCCGCCTTTT  GGTTCGATTG  TTGGTTTACC  GCTATATGGA
201 TCAGAAAATC  GACATCGTTG  CCGGTTTGGA  CGCGCGCGGC  TTCATTATCG
251 GCGCGGCACT  CGCCTACCAG  CTCAACGTCG  GTTTCGTCCC  CATCCGCAAA
301 AAAGGCAAGC  TGCCTTTTGA  AACCGTATCG  CAAAGCTACG  CGCTCGAATA
351 CGGGGAAGCT  GCGGTGGAAA  TCCACACCGA  TGCCGTCAAA  CTCGGTTCGC
401 GCGTGCTGCT  GGTTCGATGAT  TTGATTGCCA  CGGGCGGCAC  GATGCTTGCC
451 GGAATGGAAC  TGATCCGCAA  ACTCGGCGGA  GAAATTGTCT  AAGCCGCCGC
501 CATTTTGGA  TTTACCGACC  TTCAAGGCGG  CAAGAATATC  CGTGCAAGCG
551 GCGCGCCCTT  ATTTACCCTG  CTTCAAAACG  AAGGCTGTAT  GAAGGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 592; ORF 148>:

```

m148.pep
1  MALKTSNLEH  AMLVHPEAMS  VGALADKIRK  IENWPQKGIL  FHDITPVLOS
51  AEYFRLLVDL  LVYRYMDQKI  DIVAGLDARG  FIIGAALAYQ  LNVGFVPIRK

```

101 KGKLPFETVS QSYALEYGEA AVEIHTDAVK LGSRVLLVDD LIATGGTMLA
 151 GLELIRKLGG EIVEAAAILE FTDLQGGKNI RASGAPLFTL LQNEGCMKG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m148 / g148 99.0% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
g148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m148.pep	LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
g148	LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m148.pep	AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI					
g148	AVEIHTDAVKPGSRVLLVDDLVATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI					
	130	140	150	160	170	180
	190	200				
m148.pep	RASGAPLFTLLQNEGCMKGX					
g148	RASGAPLFTLLQNEGCMKGX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 593>:

a148.seq

1	ATGGCGTTAA	AAACATCAAA	CTTGGAACAC	GCAATGCTGG	TTCATCCCGA
51	AGCTATGAGT	GTCGGTGCGC	TTGCCGACAA	AATCCGCAAA	ATCGAAAAC
101	GGCCGCAAAA	AGGCATCTTA	TTCCACGACA	TCACGCCCGT	CCTGCAAAGC
151	GCGGAATACT	TCCGACTTTT	GGTTGATTTA	TTGGTTTACC	GCTATATGGA
201	TCAGAAAATC	GACATCGTTG	CCGGTTTGGA	CGCGCGCGGC	TTCATTATCG
251	GCGCGGCACT	CGCCTACCAG	CTCAACGTCG	GTTTCGTCCC	CATCCGCAAA
301	AAAGGCAAGC	TGCCTTTTGA	AACCGTATCG	CAAAGCTACG	CGCTCGAATA
351	CGGGGAAGCT	GCGGTGGAAG	TCCACACCGA	TGCCGTCAAA	CTCGGTTGCG
401	GCGTGCTGCT	GGTCGATGAT	TTGGTTGCCA	CGGGCGGCAC	GATGCTTGCC
451	GGACTGGAGC	TGATCCGCAA	ACTCGGCGGG	GAAATTGTCT	AAGCCGCCGC
501	CATTTTGGAA	TTTACCGACC	TTCAAGGCGG	CAAGAATATC	CGTGCAAGCG
551	GCGCGCCCTT	ATTTACCCTG	CTTCAAAACG	AAGGCTGTAT	GAAGGGCTGA

This corresponds to the amino acid sequence <SEQ ID 594; ORF 148.a>:

a148.pep

1	MALKTSNLEH	AMLVHPEAMS	VGALADKIRK	IENWPQKGIL	FHDITPVLQS
51	AEYFRLLVDL	LVYRYMDQKI	DIVAGLDARG	FIIGAALAYQ	LNVGFPVIRK
101	KGKLPFETVS	QSYALEYGEA	AVEIHTDAVK	LGSRVLLVDD	LVATGGTMLA
151	GLELIRKLGG	EIVEAAAILE	FTDLQGGKNI	RASGAPLFTL	LQNEGCMKG*

m148/a148 99.5% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
a148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m148.pep    LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a148        LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA
              70      80      90      100     110     120

              130      140      150      160      170      180
m148.pep    AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
              ||||||||||||||||:|||||||||||||||||||||||||||||||||
a148        AVEIHTDAVKLGSRVLLVDDLVAATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
              130      140      150      160      170      180

              190      200
m148.pep    RASGAPLFTLLQNEGCMKGX
              |||||||||||||||
a148        RASGAPLFTLLQNEGCMKGX
              190      200

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 595>:

g149.seq

```

1   ATGTTGATTG ACAACAATGT CCGCCATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAATTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC
101 AAAAAGCCTC CATCCGGTAC GACAAAGCAT TGATTGATCG AGAAACTAC
151 TACAACCAGC CCCTGCCCCG CCTCGGCGCG CACCGCCAAA CCGCCCCTC
201 GTTCGCACTT TCGGGCAACT GGTATTTTAC GCCACACCAC AAACCTAGCC
251 TGACCGCCTC CCATCAGGAa cgCCTGCCGT CAACGCaagA actGtACgca
301 cacggcAAGC ACGtcgccac CAACACCTTT GAagtccgca acaaACACCT
351 CAACAAAGaG CgttccaacA atatcgaACT CGCGCTGGgc tAcaaaggcg
401 accGCTGGCA ATACAATCTG GCAGCCTACC GCAACCGAtT CGGCAACTAC
451 ATTTACGCCC AAACCTTaaa cgacggacgC GGCCCCAAAT CCATCgaaga
501 cgacagcgaa ATGaagcTCG TGCCTACAA CCAATCCGGT GCCGACTTCT
551 ACGgcgcggA aggcgaaatc tACTTcaaaC CGACACCGCG CTACCGCATC
601 GGTGTTTCCG GCGACTatgt acgaggccgT CTGAAAAACC TGCCGTCCCT
651 ACCCGGCAGG gaagatccCT AcggcAAACG TCccttcaTC GCACAAGCCG
701 ACCAAAACGC CCCCCTGATT cgggtGCGC GCCTCGGCTT CCACCTGAAA
751 ACCTCGCTAA CCGACCGTAT CGATGCCAAT TTGGACTION ACCGCGTGTT
801 CGCCCAAAAC AAACCTCGCCC GCTACGAAAC GCGTACGCCC GGACACCATA
851 TGCTCAACCT CGGTGCAAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGGTACG TCAAAGCCGA CAACCTGctc aACcaatCcg tTTACGCCCa
951 cAGCAGCTTC CTCTCTGATA CGCCGCAAAt gGGCCGCAGC TTtgccgGCg
1001 gcgtaAACGT GaAGTTttaA

```

This corresponds to the amino acid sequence <SEQ ID 596; ORF 149.ng>:

g149.pep

```

1   MLIDNNVRHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
51  YNQPLPDLGA HRQTARSFAL SGNWYFTPHH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YKGDRWQYNL AAYRNRFGNY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVSGDYVRGR LKNLPSLPGR EDPYGKRPF I AQADQNAPRI PAARLGFHLK
251 TSLTDRIDAN LDYYRVFAQN KLARYETRTP GHMMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FAGGVNVKF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 597>:

m149.seq

```

1   ATGCTGCTTG ACAACAAAGT GCAACATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAATGAG GACAACTTCA CGCTTGAAGG AGGCGTACGC GTGGAAAAAC
101 AAAAAGCCTC CATTCACTAC GACAAAGCAT TGATTGATCG GGAAACTAC
151 TACAACCACC CCCTGCCCCG CCTCGGCGCG CACCGCCAAA CCGCCCCTC
201 ATTCGCACTT TCGGGCAACT GGTATTTTAC GCCACAACAC AAACCTAGCC
251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA
301 CACGGCAAAC ACGTCGCCAC CAACACCTTT GAAGTCGGCA ACAAACACCT
351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGGCG
401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGTAACCTAC

```

m149.pep

m149/g149

	10	20	30	40	50	60
m149.pep	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIQYDKALIDRENYYNHPLPDLGA :: : : :					
g149	MLIDNNVRHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYYNQPLPDLGA 10 20 30 40 50 60					
	70	80	90	100	110	120
m149.pep	HRQTARSFALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGKNHLNKE : : : : :					
g149	HRQTARSFALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGKNHLNKE 70 80 90 100 110 120					
	130	140	150	160	170	180
m149.pep	RSNNIELALGYEGDRWQYNLALYRNRFNGNIYAQTLNDGRGPKSIEDDSEMKLVRYNQSG : : : : :					
g149	RSNNIELALGYKGDRWQYNLAAYRNRFNGNIYAQTLNDGRGPKSIEDDSEMKLVRYNQSG 130 140 150 160 170 180					
	190	200	210	220	230	240
m149.pep	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGLKNLPSLPGREDAYGNRPFIAQDDQNAPRV : : : : :					
g149	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGLKNLPSLPGREDPYGKRPFIAQADQNAPRI 190 200 210 220 230 240					
	250	260	270	280	290	300
m149.pep	PAARLGPHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEW : : : : :					
g149	PAARLGPHLKTSLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEW 250 260 270 280 290 300					
	310	320	330	340		
m149.pep	NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNKFX : : : : :					

420

g149 NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFAGGVNVKFX
 310 320 330 340

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 599>:

a149.seq
 1 ATGCTGCTTG ACAATAAAGT GCAACATTAC AGCTTTTTCG GTGTAGAACA
 51 GGCAAACTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC
 101 AAAAAGCCTC CATCCGCTAC GACAAAGCAT TGATTGATCG GGAAACTAC
 151 TACAACCATC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
 201 ATTCGCACTT TCGGGCAACT GGTATTTCAC GCCACAACAC AAATCAGCC
 251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA
 301 CACGGCAAAC ACGTCGCCAC CAACACCTTT GAAGTCGGCA ACAAACACCT
 351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGGCG
 401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGCAACTAC
 451 ATTTACGCCC AAACCTTAA CGACGGACGC GGCCCAAAT CCATCGAAGA
 501 CGACAGCGAA ATGAAGCTCG TGCGCTACAA CCAATCCGGT GCGGACTTCT
 551 ACGGCGCGGA AGGCGAAATC TACTTCAAAC CGACACCGCG CTACCGCATC
 601 GCGGTTTCCG GCGACTATGT ACGAGGCCGT CTGAAAAACC TGCCTTCCCT
 651 ACCCGCAGG GAAGACGCCT ACGGCAACCG CCCACTCATT GCCCAAGCCG
 701 ACCAAACGC CCCTCGCGTT CCGGCTGCGC GCCTCGGCGT CCACCTGAAA
 751 GCCTCGCTGA CCGACCGCAT CGATGCCAAT TTGGACTACT ACCGCGTGTT
 801 CGCCAAAAC AAATCGCCC GCTACGAAAC GCGCAGCCC GGACACCATA
 851 TGCTCAACCT CCGCGCAAAC TACCGCCGCA ATACGCGCTA TGGCGACTGG
 901 AATTGGTACG TCAAAGCCGA CAACCTGCTC AACCAATCCG TTTACGCCCA
 951 CAGCAGCTTC CTCTCTGATA CGCCGCAAAT GGGCCGAGC TTTACCGGCG
 1001 GCGTGAACGT GAAGTTTAA

This corresponds to the amino acid sequence <SEQ ID 600; ORF 149.a>:

a149.pep
 1 MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
 51 YNHPLPDLGA HRQTARSFAL SGNWYFTPQH KLSLTASHQE RLPSTQELYA
 101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YEGDRWQYNL ALYRNRFNGY
 151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
 201 GVSVDYVRGR LKNLPSLPGR EDAYGNRPLI AQADQNAPRV PAARLGVHLK
 251 ASLTDRIDAN LDYYRVFAQN KLARYETRTP GHMMLNLGAN YRRNTRYGEW
 301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FTGGVNVKF*

m149/a149 98.8% identity in 339 aa overlap

	10	20	30	40	50	60
m149.pep	MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY YNHPLPDLGA					
a149	MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY YNHPLPDLGA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m149.pep	HRQTARSFAL SGNWYFTPQH KLSLTASHQE RLPSTQELYA HGKHVATNT FEVGNKHLNKE					
a149	HRQTARSFAL SGNWYFTPQH KLSLTASHQE RLPSTQELYA HGKHVATNT FEVGNKHLNKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m149.pep	RSNNIELALG YEGDRWQYNL ALYRNRFNGY IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG					
a149	RSNNIELALG YEGDRWQYNL ALYRNRFNGY IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m149.pep	ADFYGAEGEI YFKPTPRYRIGVSGDYVRGR LKNLPSLPGR EDAYGNRPLI AQADQNAPRV					
a149	ADFYGAEGEI YFKPTPRYRIGVSGDYVRGR LKNLPSLPGR EDAYGNRPLI AQADQNAPRV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m149.pep	PAARLGFHLK ASLTDRIDAN LDYYRVFAQN KLARYETRTP GHMMLNLGAN YRRNTRYGEW					

a149

m149.pcp

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 601>:

g149-1.seq

1	ATGGCACAAA	TCACACTCAA	ACCCATTGTT	TTATCAATTG	TTTTAATCAA
51	CACACCCCTC	CTCGCCCAAC	CGCATGAAC	TGAGCAATCG	GTGGGCTTGG
101	AAACGGTCAG	CGTCGTCCGG	AAAAGCCGTC	CCTCGCGCAG	TTCCGGGGCTG
151	CTGCACACTT	CGCGCCGCTC	GCACAAAATC	ATCGCCGGCG	ATACTTTGCG
201	CCAAAAAGCC	GTCAAACTTG	GCGACGCTTT	GGACGGCGTA	CCGGGCATCC
251	ACGCTTCGCA	ATACGGCGGC	GCGCATCTCG	CTCCGCTTAT	TCGCGGTCAA
301	ACGGGCAGAC	GGATTAAAGT	ATTGAACCAT	CACGGCGAAA	CGGGCGATAT
351	GGCGGACTTT	TCTCCGATC	AGCCCAATTG	GTAGATACCC	CGCTTGTGCG
401	AACAGGTTGA	AATCCTGCGC	GGGCCGGTTA	CGCTCTTGTA	CAGCTCGGGC
451	AATGTGGCGG	GGCTGGTCGA	TGTTGCCGAT	GGAAAAATCC	CGAAAAAAT
501	GCCTGAAAA	GGCGTATCCG	GCGAagccgg	ATTGCGTTTG	AGCAGCGCGA
551	ATTTGAAAA	ACTGACATCG	CAGGCATCA	ATATCGGACT	GGGCAAAAA
601	TTCTGTGCTG	ATACCGAAGG	CTTGATCCGC	AAATCGGGCG	ATTACGGCGT
651	ACCGCGTTAC	CGCAATCTGA	AACGCCTGCC	CGACAGCCAT	CGCGATTGCG
701	AAACGGGCAG	CATCGGGGTG	TCTTGGGTGG	GCGAAAAAGG	CTTTATCGGC
751	CGAGCATACA	CGACCCGTCG	CGACCGCTAC	CGCTGCGCT	CCCATAGCCA
801	CGAATTACGAT	GATTGCCACG	CGACATCAT	GTGCAAAAAG	AGTTTGATCA
851	ACAAACGCTA	TTTGCACTTT	TATCCGCACT	TGTTGACCGA	AGAAGACATC
901	GATTACGACA	ATCCGGGCTT	GAGCTCGCGC	TTCCACGACG	CGCAGCGGTG
951	ACACGCACAC	ACCCACAACG	GCAAACCGTG	GATAGACCTG	CGCAACAAC
1001	GCTACGAACT	CCGCGCCGAA	TGGAAGCAGG	CATTCCCCGG	TTTTGAAGCC
1051	CTGCGCGTAC	ATCTGAACCG	CAATGACTAC	CACCACGACG	AAAAAGCAGG
1101	CGATGCAGTA	GAAAACTTCT	TCAACAACAA	AACACACAA	GCCCGTATCG
1151	AGTTGCGCCA	CCAACCCATA	GGCCGTCTGA	AAGGCAGCTG	GGGCGTGCAA
1201	TATTTGGGAC	AAAAATCCAG	CGCGCTTTCC	GCCATTCCCG	AAACCGTCCA
1251	ACAACCGATG	TTGATTGACA	ACAATGTCCG	CCATTACAGC	TTTTTCGGTG
1301	TAGAACAGCG	AAATTGGGAC	AACCTCACGC	TTGAAGGCGG	CGTACGCGTG
1351	GAAAAACAAA	AAGCTTCCAT	CCGGTACGAC	AAAGCATTTG	TTGATCGAGA
1401	AAACTACTAC	AACGAGCCCC	TGCCGCACTT	CGCGCGCAGC	CGCAAAACCG
1451	CCCGCTCGTT	CGCACTTTTC	GGCAACTGGT	ATTTACAGCC	ACACCACAAA
1501	CTCAGCCTGA	CCGCTTCCCA	TCAGGAACGC	CTGCGGTCAA	CGCAAGAACT
1551	GTACGCGACG	GGCAAGCAGC	TCCGACCAAA	CACCTTTTGA	GTCGCGCAACA
1601	AACACCTCAA	CAGAGAGCGT	TCCAACAATA	TCGAATCTCG	GCTGGGCTAC
1651	GAAGGCGACC	GCTGGCAATA	CAATCTGGCA	GCCTACCGCA	ACCGATTCCG
1701	CAACTACATT	TACGCCCAAA	CCTTAAACGA	CGGACGCGCG	CCCAATATCC
1751	TCGAAGACGA	CAGCGAAATG	AAGCTCGTGC	GCTACAACCA	ATCCGGTGCC
1801	GACTTCTACG	CGCGGGAAGG	GAGAACTAC	TTCAAAACGA	CACCGCGCTA
1851	CCGATACGGT	GTTTCCGGCG	ACTATGTACG	AGGCCGTCTG	AAAAACCTGC
1901	CGTCCTTACC	CGGCGGGGAA	GATCCCTACG	GCAAACGTCC	CTTCATCGCA
1951	CAAGCCGACC	AAAAACCCCG	CCGCATTCCG	GCTCGCGCGC	TCGGGTTCCA
2001	CCTGAAAAAC	TCGCTAACCC	ACCGTATCGA	TGCCAAATTG	GACTACTACC
2051	GCGTGTTCCG	CCAAAAACAA	CTCGCCCGCT	ACGAAACGCG	TACGCCCGGA
2101	CACCATATGC	TCAACCTCGG	TGCAAACTAC	CGCCGCAATA	CGCGCTATGG
2151	CGAGTGGAAAT	TGGTACGTCA	AAGCGACAAA	CCTGCTCAAC	CAATCCGTTT
2201	ACGCCACACG	CAGCTTCTCT	TCTGATACGC	CGAAATGGG	CCGAGCTTT
2251	ACGGCGGGCG	TAAACGTGAA	GTTTTAA		

This corresponds to the amino acid sequence <SEQ ID 602; ORF 149-1.ng>:

g149-1.pep

1	MAQITLKPIV	LSILLINTPL	LAQAHETEQS	VGLETVSUVG	KSRPRATSGL
51	LHTSTASDKI	ISGDTLRQKA	VNLGDALDVT	PGIIHQSOYGG	GASAPVIRRGQ
101	TGRRIKVLNH	HGETGDMADF	SPDGHAMDMV	ALSQQSOVEILR	GPVTVLLYSSG
151	NVAGLVVDVAD	GKIPKMPEN	GVSGEAGLRL	SSGNLEKLTFS	AGNIGLGNK
201	FVLHTEGLYR	KSGDYAVPRY	RNLKRLPDSH	ADSQTSGISGL	SWWGEKGFTG
251	AAYSRRDRYR	GLPAHSHEYD	DCHADIIWQK	SILNKRYLRLQ	YPHLLTEEDI
301	YDYNFGLSCG	FHDGDGAHAH	THNGKPWIDL	RNKRVELRAE	WKOPFPGEFA

```

351 LRVHLNRNDY HHDEKAGDAV ENFFNNKTHN ARIELRHQPI GRLKGSWGVO
401 YLGQKSSALS AIPETVQOPM LIDNNVRHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENY NQPLPDLGAH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
551 EGDWRQYNLA AYRNRFNGYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEYI FKPTPRYRIG VSGDYVRGRL KNLPSLPGRE DPGYKRPFIA
651 QADQNAPRIP AARLGFHLKT SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 603>:

m149-1.seq

```

1 ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATTC TTTTAATCAA
51 CACACCCCTC CTCGCCCAAG CGCATGAAAC TGAGCAATCG GTGGATTGG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGGCCAC GTCGGGGCTG
151 TTGCACACTT CGACCGCTC CGACAAAATC ATCTCCGGCG ATACCTTGCG
201 CCAAAAAGCC GTCAACTTGG GCGACGCTT AGACGGCGTA CCGGGCATCC
251 ACGCTTCGCA ATACGGCGGC GCGCGCTCG CTCCCGTCAT TCGCGGTCAA
301 ACAGGCAGGC GGATTAAAGT GTTGAACCAT CACGGCGAAA CAGGCGATAT
351 GCGCGATTTC TCGCCCGATC ACGCCATTAT GGTAGATACC GCCTTGTCGC
401 AACAGGTCGA AATCCTGCGC GGGCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCGA TGTGCGGAT GGCAAAATCC CCGAAAAAAT
501 GCCTGAAAAC GCGGTATCGG GCGAACTCGG ATTGCGTTTG AGCAGCGGCA
551 ATCTGAAAAA ACTCACGTCC GCGGGCATCA ATATCGGTTT GGGCAAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCCGT
651 ACCGCGTTAC CGCAATCTGA AACGCTGCC CGACAGCCAC GCCGATTTCG
701 AAACGGGCAG CATCGGGCTG TCTTGGGTG GCGAAAAAGG TTTTATCGGC
751 GTAGCGTACA GCGACCGTCG CGACCAATAT GGTCTGCCTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGCTTGATTA
851 ACAAACGCTA TTTACAGCTT TATCCGACCC TGTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTCCACGACG ACGATAATGC
951 ACACGCACAC ACCCACAGCG GCAGACCGTG GATAGACCTG CGCAACAAAC
1001 GTACGAATCT CCGTGCCGAA TGGAAGCAAC CGTTCGCCGG TTTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAAGCAGG
1101 CGATGCAGTC GAAAACTTTT TTAACAACCA AACGCAAAAC GCCCGCATCG
1151 AGTTGCGCCA CCAACCCATA GGTCGTCTGA AAGGCAGCTG GGGCGTGCAA
1201 TATTTACAAAC AAAAATCCAG TGCTTTATCT GCCATATCCG AAGCGGTTAA
1251 ACAACCGATG CTGCTTGACA ACAAAGTGCA ACATTACAGC TTTTTCGGTG
1301 TAGAACAGGC AAATGAGGAC AACTTCACGC TTGAAGGAGG CGTACGCGTG
1351 GAAAAACAAA AAGCCTCCAT TCAGTACGAC AAAGCATTGA TTGATCGGGA
1401 AAATACTTAC AACCACCCCT TGCCCCGACT CGGCGCGCAC CGCCAAACCG
1451 CCCGCTCAT CGCACTTTCG GGCAACTGGT ATTTACGCCC ACAACACAAA
1501 CTCAGCCTGA CCGCCTCCCA TCAGGAACGC CTGCCGTCAG CGCAAGAGCT
1551 GTACGCACAC GGCAACACG TCGCCACCAA CACCTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGGCGACC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 TAATACATT TACGCCCAA CTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GCTACAACCA ATCCGGCGCC
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTTCGGCGC ACTATGTACG AGGCCGCTG AAAAACCTGC
1901 CTTCCTTACC CGGCAGAGAA GATGCCATAC GCAACCGTCC TTTTATCGGA
1951 CAGGACGACC AAAATGCCCC CCGTGTTCGG GCTGCGCGCC TCGGCTTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGTATCGA TGCCAATTG GACTACTACC
2051 GCGTGTTCGC CCAAAACAAA CTCGCCGCT ACGAAACGCG CACGCCCGGA
2101 CACCATATG TCAACCTCGG CGCAAACTAC CGCCGCAATA CGCGCTATGG
2151 CGAGTGGAA TGGTACGTCA AAGCCGACAA CCTGCTCAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTCTC TCTGATACGC CGCAATGGG CCGCAGCTTT
2251 ACCGGCGGCG TGAACGTGAA GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 604; ORF 149-1>:

m149-1.pep

```

1 MAQTTLKPIV LSILLINTPL LAQAHETEQS VDLETVSUVG KSRPRATSGL
51 LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDT ALSQQVEILR GPVTLLYSSG
151 NVAGLVDVAD GKIPEKMPEN GVSSELGLRL SSGNLEKLTS GGINIGLGN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGEKGFIF
251 VAYSDDRDQY GLPAHSHEYD DCHADIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPLGSCG FHDDDNAHAH THSGRPWIDL RNKRYELRAE WKQFPFGFEA
351 LRVHLNRNDY HHDEKAGDAV ENFFNNQTON ARIELRHQPI GRLKGSWGVO
401 YLQKSSALS AISEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIYD KALIDRENY NHPLPDLGAH RQTARSFALS GNWYFTPQHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY

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551 EGDWRQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
 601 DFYGAEGEIIY FKPTPRYRIG VSGDYVRGRL KNLPSPGREG DAYGNRPFIA
 651 QDDQNAPRVP AARLGFHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG
 701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
 751 TGGVNVKF*

m149-1/g149-1 96.2% identity in 758 aa overlap

	10	20	30	40	50	60
m149-1.pep	MAQTTLKPIVLSILLINTPLLAQAHETE	QSV	QV	LET	VS	VVGKSRPRATSGLLHTSTASDKI
g149-1	MAQITLKPIVLSILLINTPLLAQAHETE	QSV	QV	LET	VS	VVGKSRPRATSGLLHTSTASDKI
	10	20	30	40	50	60
	70	80	90	100	110	120
m149-1.pep	ISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF				
g149-1	ISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m149-1.pep	SPDHAIMVDTALSQQVEILRGPVTL	LYSSGNVAGLV	VDVADGKIPEKMPENGVS	GELGLRL		
g149-1	SPDHAIMVDTALSQQVEILRGPVTL	LYSSGNVAGLV	VDVADGKIPEKMPENGVS	GEAGLRL		
	130	140	150	160	170	180
	190	200	210	220	230	240
m149-1.pep	SSGNLEKLTSGGINIGLGKNFVLHTE	GLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL				
g149-1	SSGNLEKLTSGGINIGLGKNFVLHTE	GLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL				
	190	200	210	220	230	240
	250	260	270	280	290	300
m149-1.pep	SWVGEKGFIVGAYSDRRDQYGLPAHS	HEYDDCHADIWQKSLINKRYLQLYPHLLTEEDI				
g149-1	SWVGEKGFIVGAYSDRRDQYGLPAHS	HEYDDCHADIWQKSLINKRYLQLYPHLLTEEDI				
	250	260	270	280	290	300
	310	320	330	340	350	360
m149-1.pep	DYDNPGLSGCFHDDDNAHAH	THSGRPWIDLRNKRYELRAEWKQFPFGFEALRVHLNRNDY				
g149-1	DYDNPGLSGCFHDDDNAHAH	THSGRPWIDLRNKRYELRAEWKQFPFGFEALRVHLNRNDY				
	310	320	330	340	350	360
	370	380	390	400	410	420
m149-1.pep	RHDEKAGDAVENFFNNQTNARIELRH	QPIGRLKSGVQYLGQKSSALS	SAISEAVKQPM			
g149-1	HHDEKAGDAVENFFNNKTHNARIELRH	QPIGRLKSGVQYLGQKSSALS	SAIPETVQQPM			
	370	380	390	400	410	420
	430	440	450	460	470	480
m149-1.pep	LLDNKVQHYSFFGVEQANWDNFTLEGG	VRVEKQKASIQYDKALIDRENYNHPDLGAH				
g149-1	LIDNNVRHYSFFGVEQANWDNFTLEGG	VRVEKQKASIRYDKALIDRENYNQPLDLGAH				
	430	440	450	460	470	480
	490	500	510	520	530	540
m149-1.pep	RQTARSFALSGNWFYTPQHKL	SLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER				
g149-1	RQTARSFALSGNWFYTPHHKL	SLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER				
	490	500	510	520	530	540
	550	560	570	580	590	600
m149-1.pep	SNNIELALGYEGDRWQYNLALYRNR	FGNYIYAQTLNDGRGPKSIEDDSEM	KLVRYNQSGA			
g149-1	SNNIELALGYEGDRWQYNLAAYRNR	FGNYIYAQTLNDGRGPKSIEDDSEM	KLVRYNQSGA			
	550	560	570	580	590	600
	610	620	630	640	650	660
m149-1.pep	DFYGAEGEIIYFKPTPRYRIGVSGDY	VRGRLKNLPSPGREGDAYGNRPFIAQDDQNAPRVP				
g149-1	DFYGAEGEIIYFKPTPRYRIGVSGDY	VRGRLKNLPSPGREDPYGKRPFIQAQADQNAPRIP				
	610	620	630	640	650	660

	670	680	690	700	710	720
m149-1.pep	AARLGFLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN					
g149-1	AARLGFLKTSLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN					
	670	680	690	700	710	720
	730	740	750	759		
m149-1.pep	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
g149-1	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
	730	740	750			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 605>:

a149-1.seq

```

1  ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATTC TTTAATCAA
51  CACACCCCTC CTCTCCCAAG CGCATGGAAC TGAGCAATCA GTGGGCTTGG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGCGCCAC TTCGGGGCTG
151 CTGCACACTT CTACCGCCTC CGACAAAATC ATCAGCGGCG ACACCTTGCG
201 ACAAAAAGCC GTCAACTTGG GTGATGCTT AGACGGCGTA CCGGGCATTG
251 ATGCTCGCGA ATACGGCGGC GCGCATCCG TCCTCGTTAT TCGCGGTCAA
301 ACAGGCAGAC GGATTAAAGT GTTGAACCAT CACGGCGAAA CGGGCGACAT
351 GGGGGAATTC TCTCCAGACC ATGCAATCAT GGTGGACAGC GCCTTGTCGC
401 AACAGGTCGA AATCCTGCGC GGTCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCTGA TGTGCGGAT GGCAAAATCC CCGAAAATAA
501 GCCTGAAAAC GCGGTATCGG GCGAACTCGG ATTGCGTTTG AGCAGCGGCA
551 ATCTGGAATA ACTCACGTCC GCGGCATCA ATATCGGTTT GGGCAAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCCGT
651 ACCGCGTTAC CGCAATCTGA AACGCTGCC CGACAGCCAC GCCGATTCGC
701 AAACGGGCAG CATCGGGCTG TCTTGGGTTG GCGAAAAGG CTTTATCGGC
751 GCAGCATACA GCGACCGTCG CGACCAATAT GGTCTGCTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGTTTGATTA
851 ACAACGCTA TTTGCAGCTT TATCCGCACC TGTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTTCACGACG ACGATGATGC
951 ACACGCCCAT GCCCACAACG GCAAACCTTG GATAGACCTG CGCAACAAAC
1001 GCTACGAACT CCGCGCCGAA TGAAGCAAC CGTTCGCCG TTTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC GCCACGACG AAAAAGCAGG
1101 CGATGCAGTA GAAAACCTTT TTAACAACCA AACGCAAAAC GCCCGTATCG
1151 AGTTGCGCCA CCAACCCATA GGCGTCTGA AAGGCAGCTG GGGCGTGCAA
1201 TATTGGGAC AAAAATCCAG TGCTTTATCT GCCACATCCG AAGCGGTCAA
1251 ACAACGATG CTGCTTGACA ATAAAGTGCA ACATTACAG TTTTTCGGTG
1301 TAGAACAGGC AACTGGGAC AACTTCACGC TTGAAGGCGG CGTACGCGTG
1351 GAAAAACAAA AAGCCTCCAT CCGCTACGAC AAAGCATGTA TTGATCGGGA
1401 AACTACTAC AACCATCCCC TGCCGACCT CGCGCGCAC CGCCAAACCG
1451 CCGCTCAAT CGCACTTTCG GGCAACTGGT ATTTACGCC ACAACACAAA
1501 CTGACGCTGA CCGCTCCCA TCAGGAACGC CTGCCGTCAA CGAAGAGCT
1551 GTACGCACAC GGCAACACG TCGCCACCA CACCTTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAATCGC GCTGGGCTAC
1651 GAAGGCGACC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 CAACTACATT TACGCCCAA CCTTAAACGA CGGACGCGGC CCCAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GCTACAACCA ATCCGGTGCG
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGCG GTTTCGGCG ACTATGTACG AGGCCGTCTG AAAAACCTGC
1901 CTCCCTACC CGGCAGGGAA GACGCCTACG GCAACCGCCC ACTCATTGCC
1951 CAAGCCGACC AAAACGCCCC TCGCGTTCCG GCTGCGCGCC TCGGCGTCCA
2001 CCGTGAAGCC TCGCTGACCG ACCGCATCGA TGCCAATTTG GACTACTACC
2051 GCGTGTTTCG CCAAAACAAA CTCGCCGCT ACGAAACGCG CACGCGCGGA
2101 NVAGLVDVAD GKIPEKMPEN GVSSELGLRL SSGNLEKLTG GINIGLGN
2151 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGEKGFIG
2201 AAYSDRRDQY GLPAHSHEYD DCHADIIWQK SLINKRYLQL YPHLLTEEDI
2251 DYDNPLGSCG FHDDDDAHAA AHNGKPWIDL RNKRYELRAE WKQPPFGFEA

```

This corresponds to the amino acid sequence <SEQ ID 606; ORF 149-1.a>:

a149-1.pep

```

1  MAQTLKPIV LSILLINTPL LSQAHGTEQS VGLETVSQVG KSRPRATSGL
51  LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDS ALSQQVEILR GPVTLLYSSG
151 NVAGLVDVAD GKIPEKMPEN GVSSELGLRL SSGNLEKLTG GINIGLGN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGEKGFIG
251 AAYSDRRDQY GLPAHSHEYD DCHADIIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPLGSCG FHDDDDAHAA AHNGKPWIDL RNKRYELRAE WKQPPFGFEA

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```

351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTON ARIELRHQPI GRLKGSWGVO
401 YLGQKSSALS ATSEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENNY NHPLPDLGAH RQTARSFALS GNWYFTPQHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
551 EGDWRQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEYI FKPTPRYRIG VSGDYVRGRL KNLPSPGRE DAYGNRPLIA
651 QADQNAAPRV AARLGVHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

a149-1/m149-1 98.0% identity in 758 aa overlap

	10	20	30	40	50	60
a149-1.pep	MAQTTLKPIVLSILLINTPLLSQAHGTEQSVGLETVSVVGKSRPRATSGLLHTSTASDKI					
m149-1	MAQTTLKPIVLSILLINTPLLAQAHETEQSVLDLETVSVVGKSRPRATSGLLHTSTASDKI					
	10	20	30	40	50	60
a149-1.pep	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
m149-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
	70	80	90	100	110	120
a149-1.pep	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
m149-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
	70	80	90	100	110	120
a149-1.pep	SPDHAIMVDSALSQQVEILRGPVTLTYSSGNVAGLVVDVADGKIPEKMPENGVSSELGLRL					
m149-1	SPDHAIMVDTALSQQVEILRGPVTLTYSSGNVAGLVVDVADGKIPEKMPENGVSSELGLRL					
	130	140	150	160	170	180
a149-1.pep	SSGNLEKLTSGGINIGLGNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL					
m149-1	SSGNLEKLTSGGINIGLGNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL					
	190	200	210	220	230	240
a149-1.pep	SSGNLEKLTSGGINIGLGNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL					
m149-1	SSGNLEKLTSGGINIGLGNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL					
	190	200	210	220	230	240
a149-1.pep	SWVGEKGFIGAAYSDDRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHLLTEEDI					
m149-1	SWVGEKGFIVAYSDDRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHLLTEEDI					
	250	260	270	280	290	300
a149-1.pep	DYDNPGLSCGFHDDDDAHAAHNGKPWDLRNKRYELRAEWKQFPFGFEALRVHLNRNDY					
m149-1	DYDNPGLSCGFHDDDDNAHAHNSGRPWDLRNKRYELRAEWKQFPFGFEALRVHLNRNDY					
	310	320	330	340	350	360
a149-1.pep	DYDNPGLSCGFHDDDDAHAAHNGKPWDLRNKRYELRAEWKQFPFGFEALRVHLNRNDY					
m149-1	DYDNPGLSCGFHDDDDNAHAHNSGRPWDLRNKRYELRAEWKQFPFGFEALRVHLNRNDY					
	310	320	330	340	350	360
a149-1.pep	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGQVYLGQKSSALSATSEAVKQPM					
m149-1	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGQVYLGQKSSALSAISEAVKQPM					
	370	380	390	400	410	420
a149-1.pep	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENNYNHPLPDLGAH					
m149-1	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIYDKALIDRENNYNHPLPDLGAH					
	430	440	450	460	470	480
a149-1.pep	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENNYNHPLPDLGAH					
m149-1	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIYDKALIDRENNYNHPLPDLGAH					
	430	440	450	460	470	480
a149-1.pep	RQTARSFALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
m149-1	RQTARSFALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
	490	500	510	520	530	540
a149-1.pep	RQTARSFALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
m149-1	RQTARSFALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
	490	500	510	520	530	540
a149-1.pep	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMCLVRYNQSGA					
m149-1	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMCLVRYNQSGA					
	550	560	570	580	590	600
a149-1.pep	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMCLVRYNQSGA					
m149-1	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMCLVRYNQSGA					
	550	560	570	580	590	600
	610	620	630	640	650	660

a149-1.pep	DFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPLIAQADQNAPRVP
m149-1	DFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFIAQDDQNAPRVP
	610 620 630 640 650 660
a149-1.pep	670 680 690 700 710 720
a149-1.pep	AARLGVLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
m149-1	AARLGFLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
	670 680 690 700 710 720
a149-1.pep	730 740 750 759
a149-1.pep	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
m149-1	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
	730 740 750

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 607>:

g150.seq (partial)

```

1  ..TACTGCAAGG CAGACCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAAAT
51  CACCGCCCGC CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTTGA
101 GCGGTTTCGA TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGGTTT
151 GACAAACGATC CGGCACTGGT CGGGGAAATC CTAGACCTGC TCGGCATCAA
201 TCCGCAACG GAAATACAGG CGGGCGGAAA AACCTGCCG GTGCCTCCG
251 CACTGTTATC CCATTTCGAA CTCACGCAA ACACCCCGC CTTTGTCAA
301 GGCTATGCCA CGTTCGCCGA TAATGACGAA CTCGACCGTA TTGCTGCCGA
351 CAACGCCGTT TTGCAAGGCT TTGTGCAAAG CACGCCGATT GCCGGTGTGC
401 TGCACCGCTT CCCGGCAAAA CTGACGGCGG AACAAATCGC CGGCCTGCTG
451 CGCCCGCTTG CGCCGCGCCT GTATTGATT TCCTCGTCGC AGGCGGAAGC
501 GGGGACGAA GTGCACCTGA CCGTCGGCGC AGTGCGTTT GAACACGAA
551 GGCAGCCAG GGCAGCGGC GCATCGGTT TCTTGCCGA CCGCTGGAA
601 GAGGACGGCA CGGTGCGCGT GTTTCGGAA CGCAACGACG GCTTCAGGCT
651 GCCCGAAGAC AGCCGCAAGC CGATTGTGAT GATCGGCTCC GGTACCGGCG
701 TCGACCGTT CCGCGCCTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA
751 GGCAGAACT GGCTGATTTT CGGCAATCCG CATTTTGCCG CCGACTTCCT
801 CTATCAGACC GAATGGCAGC AGTTTGCAA AGACGGCTTC CTGCACAGAT
851 ATGACTTCGC CTGGTCGCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC
901 AAAATCCGCG AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC
951 GCAATATCTAT GTGTGCGCG ATGCGGCAA AATGGCAAAA GAAGTGAAG
1001 CCGCCTTGCT GGATGTGATT ATCGGGGAG GGCATTGCGA CGAAGACGGC
1051 GCAGAAGGAT ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA
1101 TGTTTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 608; ORF 150.ng>:

g150.pep (partial)

```

1  ..YCKADPPFAA LLANQKITAR QSDKDVRHIE IDLSGSDLHY LPGDALGVWF
51  DNDPALVGEI LDLLGINPAT EIQAGGKTLV VASALLSHFE LTQNTPAFVK
101 GYATFADNDE LDRIAADNAV LQGFVQSTPI AGVLHRFPK LTAEQFAGLL
151 RPLAPRLYSI SSSQAEAGDE VHLTVGAVRF EHEGRARAGG ASGFFADRLE
201 EDGTVRVFAE RNDGFRLPED SRKPIVMIGS GTGVAPFRAF VQORAAENAE
251 GRNWLIFGNP HFAADFLYQT EWQQFAKDG LHRYPFAWSR DQEEKIYVQD
301 KIREQAEGLW QWLQEGAHY VCGDAAKMAK EVEAALLDVI IGAGHSDEDE
351 AEGYLDMLRE EKRYQRDVY*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 609>:

m150.seq

```

1  ATGCAGAACA CAAATCCGCC ATTACCGCT CTGCCGCCCG AAATCACGCA
51  GCTCTGTGCG GGGCTGGACG CGGCACAATG GCGTGGCTG TCCGGCTACG
101 CTTGGGCAAA AGCAGGAAAC GGGCATCTG CAGGACTGCC CGCGCTTCAG
151 ACGGCATTGC CGGCGGCAGA ACCTTTTTC GTAACCGTCC TTTCCGCCTC
201 GCAAACCGGC AATGCGAAAT CCGTTGCCGA CAAAGCGGCG GACAGCCTGG
251 AAGCCGCCG CATCCAAGTC AGTCGCGCCG AACTGAAAGA CTATAAGGCG
301 AAAACATCG CCGCGAAGC CCGCTGCTG CTGGTTACCT CCACCAAGG
351 CGAAGGCGAA CCGCGAAGG AAGCGTCGT GCTGCACAAA CTGCTGAACG
401 GCAAAAAAGC CCCGAAATTG GACAACTCC AATTGCGCT ACTGGGTTTG

```

451 GCGACAGTT CCTATCCGAA TTTCTGTCAG GCAGGTAAAG ATTTGACCG
 501 GCGTTTTGAA GAATTGGGCG CAAAACGGCT GCTCGAACGC GTTGATGCGG
 551 ATTTGGACTT TACCGCCTCC GCAAACGCCT GGACAGATAA TATCGCCGCA
 601 CTCTTAAAAG AAGAAGCCGC AAAAAACCGG GCAACGCCCG CGCCGCAGAC
 651 AACGCCCCC GCGGCCTTC AGACGGCACC GGATGGCAGG TACTGCAAGG
 701 CAGCCCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAAT CACCGCCCGC
 751 CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTGGA GCGGTTCCGA
 801 TTTGCACTAC CTCCGGGCG ACGCGCTCGG CGTTTGGTTT GACAACGATC
 851 CGGCACTGGT CAGGGAAATC CTAGACCTGC TCGGCATCGA TCCGGCAACG
 901 GAAATACAGG CGGGCGGAAA GATGATGCCG GTTGC GCGCG CACTTTCATC
 951 TCATTTTCGAA CTCACGCAAA AACTCCGGC TTTCGTCAAA GGCTATGCCG
 1001 CGTTCGCCCA TTATGAAGAA CTCGATAAAA TCATTGCCGA TAACGCCGTT
 1051 TTGCAGGATT TCGTGCAAAA CACGCCTATT GTCGATGTGC TGCACCGCTT
 1101 CCCGGCAAGC CTGACGGCAG AACAATTCAT CCGTTTACTG CGTCCGCTTG
 1151 CACCCCGTTT GTATTGATT TCTTCAGCAC AGGCGGAAGT GGGCGATGAA
 1201 GTGCATTTAA CTGTCGGCGT GGTTCGTTT GAACACGAAG GCCGCGCCAG
 1251 AACGGGCGGC GCATCGGGT TCCTTGCCGA CCGGCTGGAA GAGGACGGCA
 1301 CCGTGCGCGT GTTTGTGGA CGCAACGACG GCTTCAGGCT GCCCGAAGAC
 1351 AGCCGCAAGC CGATTGTGAT GATCGGCTCG GGCACCGCG TCGCACCGTT
 1401 CCGCGCTTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA GGCAAAACT
 1451 GGCTGATTTT CGGCAATCCG CATTTTGCCC GTGATTTTCT CTATCAAACC
 1501 GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGGT ACGATTTCCG
 1551 CTGGTCCCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC AAAATCCGCG
 1601 AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC GCATATCTAT
 1651 GTGTGCGGCG ATGCGGCAAA AATGGCAAAA GACGTGGAAG CCGCCTTGCT
 1701 GGATGTGATT ATCGGGGCG GACATTTGGA CGAAGAGGGC GCAGAAGAAT
 1751 ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA TGTTTATTGA

This corresponds to the amino acid sequence <SEQ ID 610; ORF 150>:

m150.pep

1 MQNTNPPLPP LPPEITQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ
 51 TALPAAEPFS VTVLSASQTG NAKSVADKAA DSLEAAGIQV SRAELKDYKA
 101 KNIAGERRL LVTSTQGEGE PPKEAVVLHK LLNGKKAPKL DKLQFAVLGL
 151 GDSSYPNFCQ AGKDFDRRFE ELGAKRLLER VDADLDFTAS ANAWTDNIAA
 201 LLKEEAAKNR ATPAPQTPP AGLQTAPDGR YCKAAPFPAA LLANQKITAR
 251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI LDLLGIDPAT
 301 EIQAGGKMMP VARALSSHFE LTQNTPAFVK GYAAFAHYEE LDKIIADNAV
 351 LQDFVQNTPI VDVLRFPAS LTAEQFIRLL RPLAPRLYSI SSAQAEVGDE
 401 VHLTVGVVRF EHEGRARTGG ASGFLADRLE EDGTVRVFVE RNDGFRLPED
 451 SRKPIVMIGS GTGVAPFRAF VQRAAENAE GKNWLIFGNP HFARDFLYQT
 501 EWQQFAKDF LHRDYFAWSR DQEEKIYVQD KIREQAEGLW QWLQEGAHY
 551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG AEEYLDMLRE EKRYQRDVY*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 150 shows 91.3% identity over a 369 aa overlap with a predicted ORF (ORF 150.ng) from *N. gonorrhoeae*:

m150/g150

	210	220	230	240	250	260
m150.pep	LLKEEAAKNRATPAPQTPPAGLQTAPDGRYCKAAPFPAA LLANQKITARQSDKDVRHIE					
g150	YCKADFPFAALLANQKITARQSDKDVRHIE					
	10 20 30					
	270	280	290	300	310	320
m150.pep	IDLSGSDLHYLPGDALGVWFDNDPALVREILDLLGIDPATEIQAGGKMMPVARALSSHFE					
g150	IDLSGSDLHYLPGDALGVWFDNDPALVGEILDLLGINPATEIQAGGKTLFPVASALLSHFE					
	40 50 60 70 80 90					
	330	340	350	360	370	380
m150.pep	LTQNTPAFVKGYAAFAHYEELDKIIADNAV LQDFVQNTPIVDVLRFPASLTAEQFIRLL					

	: : :
g150	LTQNTPAFVKGYATFADNDELDRIAADNAVLQGFGVQSTPIAGVLHRFPAKLTAEQFAGLL
	100 110 120 130 140 150
m150.pep	390 400 410 420 430 440 RPLAPRLYSISSAQAEVGDEVHSLTVGVVRFEHEGRARTGGASGFLADRLEEDGTVRVFVE
g150	: : : : RPLAPRLYSISSSQAEAGDEVHSLTVGAVRFEHEGRARAGGASGFFADRLEEDGTVRVFAE
	160 170 180 190 200 210
m150.pep	450 460 470 480 490 500 RNDGFRLPEDSRKPIVMIGSGTGVAPFRAFVQQRAAENAEGKNWLIFGNPHFARDFLYQT
g150	: RNDGFRLPEDSRKPIVMIGSGTGVAPFRAFVQQRAAENAGRNLWIFGNPHFAADFLYQT
	220 230 240 250 260 270
m150.pep	510 520 530 540 550 560 EWQQFAKDGLHRYDFAWSRDQEEKIYVDKIREQAEGWLQWLQEGAHIYVCGDAAKMAK
g150	: EWQQFAKDGLHRYDFAWSRDQEEKIYVDKIREQAEGWLQWLQEGAHIYVCGDAAKMAK
	280 290 300 310 320 330
m150.pep	570 580 590 600 DVEAALLDVII GAGHLDEEGAEYLDM LREEKRYQRDVYX
g150	: : EVEAALLDVII GAGHSDEGDGAEGYLDMLREEKRYQRDVYX
	340 350 360 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 611>:

a150.seq

1	ATGCAGAACA	CAAATCCGCC	ATTACCGCCT	ATGCCGCCCG	AAATCACGCA
51	GTCCTGTCTG	GGGCTGGACG	CGGCACAATG	GGCGTGCTG	TCCGCTACG
101	CTTGGGCAA	AGCAGGAAAC	GGGGCATCTG	CAGGACTGCG	CGCGCTTCAG
151	ACGGCATTGC	CGACGGCAGA	ACCTTTTTTC	GTAAACGTC	TTTCCGCCTC
201	GCAAACTGGC	AATGCGAAAT	CCGTTGCCGA	CAAAAGCGCG	GACAGCCTGG
251	AAGCCGCCGG	CATCCAAGTC	AGTCGCGCCG	AACTGAAAGA	CTATAAGGCG
301	AAAAACATCG	CCGGCGAACG	CCGCCTGCTG	CTGGTTACCT	CCACCCAAGG
351	CGAAGGCGAA	CCGCCGGAAG	AAGCCGTCGT	GCTGCACAAA	CTGCTGAACG
401	GCAAAAAAGC	CCCAGAAATTG	GACAAACTCC	AATTTGCCGT	ACTGGGTTTG
451	GGCGACAGCT	CCTATCCGAA	TTTCTGCCGG	GCGGGCAAA	ATTTTCGACAA
501	ACGTTTTTGA	GAATTTGGCG	CAAAACGCAT	GCTCGAACGC	TTTGATGCGG
551	ATTTGGACTT	TGCGCGCCGC	GCAGACGGAT	GGACAGATAA	TATCCGCGCA
601	CTCTTAAAG	AAGAAGCCGC	AAAAAACCGG	GCAACGCCCG	CGCCGCAGAC
651	AACGCCCCC	GCCGGCCTTC	AGACGGCACC	GGATGGCAGG	TACTGCAAGG
701	CAGACCCCTT	TCCCGCCGCC	CTGCTGGCCA	ATCAGAAAAT	CACCGCCCGC
751	CAATCCGATA	AAGACGTGCG	CCACATCGAA	ATCGATTTGA	GCGGTTTCGGA
801	TTTGCACTAC	CTCCCGGGCG	ACGCGCTCGG	CGTTTGGTTT	GACAACGATC
851	CGGCACCTGT	CAGGGAATC	CTAGACCTGC	TCGGCATCTG	TACGGCAACG
901	GAAATACAGG	CGGGCGGAAA	AACCTGCGCG	TTTGCTCCCG	CATGTTATC
951	CCATTTTGA	CTCACGCAA	ACACCCCGCG	CTTTGTCAA	GGCTATGCC
1001	CGTTGCGCGA	TGATGACGAA	CTCGACCGTA	TTGTGCCGA	CAACGCCGTT
1051	TTGCAAGGCT	TTGTGCAAAG	CACGCCGATT	GCCGATGTGC	TGCACCGCTT
1101	CCCGGCAAAA	CTGACAGCGG	AACAATTGCG	CGGCCTACTG	CGCCCGCTTG
1151	CGCCGCGCCT	GTATTGCGAT	TCCTCGTCGC	AGGCGGAAGT	GGGGGACGAA
1201	GTGCACCTGA	CCGTGCGCGC	GGTGCCTTTC	GAACACGAAG	GGCGCGCCAG
1251	GGCGGGCGCG	GCATCGGGTT	TCCTTGCCGA	CCGGTGGAA	GAGGACGGCA
1301	CGGTGCGCGT	GTTTGTGGAA	CGCAACGACG	GCTTCAGGCT	GCCCGAAGAC
1351	AGCCGCAAGC	CGATTGTGAT	GATCGGCTCG	GGCACC GGCG	TCGCACCGTT
1401	CCGCGCTTTT	GTCCAACAAC	GTGCCGCAGA	AAATGCGGAA	GGCAAAAAC
1451	GGCTGTTTTT	CGGCAATCCG	CATTTTGCCC	GTGATTTTCT	CTATCAAACC
1501	GAATGGCAGC	AGTTTGCCAA	AGACGGCTTC	CTGCACAGAT	ACGATTTGCG
1551	CTGGTCGCGC	GATCAGGAAG	AAAAATCTA	TGTGCAGGAC	AAAATCCGCG
1601	AACAGGCGGA	AGGACTTTGG	CAATGGCTGC	AGGAAGCGCG	CGCATCTAT
1651	GTGTGCGGCG	ATGCGGCAAA	AATGGCAAAA	GACGTGGAAG	GCGATCTGCT

1701 GGATGTGATT ATCGGGGCAG GACATTTGGA CGAAGAGGGC GCAGAAGAAT
 1751 ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA TGTTATTGA

This corresponds to the amino acid sequence <SEQ ID 612; ORF 150.a>:

a150.pep
 1 MQNTNPPLPP MPPEITQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ
 51 TALPTAEFFS VTVLSASQTG NAKSVADKAA DSLEAAGIQV SRAELKDYKA
 101 KNIAGERRLL LVTSTQGEGE PEEAVVLHK LLNGKKAPKL DKLQFAVLGL
 151 GDSSYPNFCR AGKDFDKRFE ELGAKRLLER VDADLDFAAA ADGWTDNIAA
 201 LLKEEAAKNR ATPAQOTTPP AGLQTAPDGR YCKADFPFPA LLANQKITAR
 251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI LDLLGIDQAT
 301 EIQAGGKTLP VASALLSHFE LTQNTPAFVK GYAPFADDDE LDRIAADNAV
 351 LQGFVQSTPI ADVLHRFPK LTAEQFAGLL RPLAPRLYSI SSSQAEVGDE
 401 VHLLTVGAVRF EHEGRARAGG ASGFLADRLE EDGTVRVFVE RNDGFRLPED
 451 SRKPIVMIGS GTGVAPFRAF VQRAAENAE GKNWLFVGNP HFARDFLYQT
 501 EWQQFAKDGF LHRYDFAWSR DQEEKIYVQD KIREQAEGLW QWLQEGAHYI
 551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG AEEYLDMLRE EKRYQRDVY*

m150/a150 94.8% identity in 599 aa overlap

	10	20	30	40	50	60
m150.pep	MQNTNPPLPPLPPEITQLLSGLDAAQWAWLSGYAWAKAGNGASAGLPALQTALPAAEPFS					
a150	MQNTNPPLPPMPPEITQLLSGLDAAQWAWLSGYAWAKAGNGASAGLPALQTALPTAEFFS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m150.pep	VTVLSASQTGNAKSVADKAADSLEAAGIQVSRALKDYKAKNIAGERRLLLVSTQGEGE					
a150	VTVLSASQTGNAKSVADKAADSLEAAGIQVSRALKDYKAKNIAGERRLLLVSTQGEGE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m150.pep	PPKEAVVLHKLKLLNGKKAPKLDKLQFAVLGLGDSSYPNFCQAGKDFDRFEELGAKRLLER					
a150	PPKEAVVLHKLKLLNGKKAPKLDKLQFAVLGLGDSSYPNFCRAGKDFDKRFEELGAKRLLER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m150.pep	VDADLDFTASANAWTDNIAALLKEEAAKNRATPAPQTTPPAGLQTAPDGRYCKAAPPFAA					
a150	VDADLDFAAAADGWTDNIAALLKEEAAKNRATPAPQTTPPAGLQTAPDGRYCKADFPFAA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m150.pep	LLANQKITARQSDKDVRHIEIDLSGSDLHYLPGDALGVWFDNDPALVREILDLLGIDPAT					
a150	LLANQKITARQSDKDVRHIEIDLSGSDLHYLPGDALGVWFDNDPALVREILDLLGIDQAT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m150.pep	EIQAGGKMMPVARALSSHFEELTQNTPAFVKGYAAFAHYEELDKIIADNAVLDQFVQNTPI					
a150	EIQAGGKTLPVASALLSHFEELTQNTPAFVKGYAPFADDDELDRIAADNAVLDQGFVQSTPI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m150.pep	VDVLRFPASLTAEQFIRLLRPLAPRLYSISSAQAEVGDEVHLLTVGVVRFHEGRARTGG					
a150	ADVLRFPKLTAEQFAGLLRPLAPRLYSISSAQAEVGDEVHLLTVGAVRFEHEGRARAGG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m150.pep	ASGFLADRLEEDGTVRVFVERNDGFRLPEDSRKPIVMIGSGTGVPFRAFVQRAAENAE					
a150	ASGFLADRLEEDGTVRVFVERNDGFRLPEDSRKPIVMIGSGTGVPFRAFVQRAAENAE					
	430	440	450	460	470	480
	490	500	510	520	530	540
m150.pep	GKNWLIFGNPHFARDFLYQTEWQQFAKDGFHLHRYDFAWSRDQEEKIYVQDKIREQAEGLW					

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a150      GKNWLFFGNPHFARDFLYQTEWQQFAKDGFLHRYDFAWSRDQEEKIYVQDKIREQAEGLW
           490      500      510      520      530      540
m150.pep  QWLQEGAHYVCGDAAKMAKDVEAALLDVIIAGAGHLEEGAEYLDMLREEKRYQRDVYX
           550      560      570      580      590      600
a150      QWLQEGAHYVCGDAAKMAKDVEAALLDVIIAGAGHLEEGAEYLDMLREEKRYQRDVYX
           550      560      570      580      590      600

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 613>:

g151.seq

```

1  ATGAAACAAA TCCGCAACAT CGCCATCATC GCACACGTCG ACCACGGCAA
51  AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGA AAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTG
201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG
251 TGGAGCGCGT TTTGGGGATG GTGGATTGCG TCGTCTTGTT GGTGGACGCA
301 CAGGAAGGTC CGATGCCGCA AACCCGTTTC GTGACCAAAA AAGCCTTGGC
351 TTTGGGGCTG AAACCGATTG TCGTCATCAA CAAAATCGAC AAACCGTCCG
401 CCCGTCCGAG CTGGGTTATC GACCAGACTT TCGAGTTGTT CGACAACTTG
451 GGTGCGACCG ACGAGCAGTT GGATTTCCTG ATTGTTTACG CTTCAGGTTT
501 GAGCGGCTTT GCCAAGCTGG AAGAAAccga CGAGAGCAGC GATATGCGCC
551 CGCgtttcga CACCATCCTA AAATACAcgc ctgCACCGAG CGGCAGCGCG
601 GACGAGCCGC TGCAACTGCA AATTTCCCAA CTCGACTACG ACAACTACAC
651 CGGCCGCCTC GGTATCGGTC GTATCTTGAA CGGACGCATC AAACCCGGCC
701 AAACCGTTGC CGTGATGAAC CACGAGCAGC AAATCGCCCA AGGCCGCATC
751 AACCAGCTTT TGGGTTTCAA AGGCTTGGA CGCGTGCCGC TTGAAGAAGC
801 CGAAGCCGCG GACATTGTGA TTATTTCCGG TATCGAAGAC ATCGGCATCG
851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGGCCTGCC GATGTTGAGC
901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTAAACA CCAGCCCGCT
951 CGCAGGTACA GAAGGCAAAT TCGTGACCAG CCGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGCTGACC AACGTTGCCC TGCGCGTGGA AGACACCGCC
1051 GatgCCGACG TGTTCCGCGT ATCcgGGCGC GGCGAACGTC ACCTGACGAT
1101 TTTGCTGGAA AATATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAGC
1151 CGCGCGTCGT GTACCGAGAC ATCGACGGTC AAAAATGCGA ACCTTATGAA
1201 AACCTGACTG TGGACGTACC cgacgacAAC CAAGGCGCGG TAATGGAAGA
1251 ACTCGGCCGC CGCCGTGGCG AACTGACCAA TATGGAAAGC GACGGCAACG
1301 GacgCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGTTTC
1351 CAAGGCGAAT TCATGACCCT GACGCGCGGC GTCGGGCTGA TGAgccacGT
1401 GTTcgacgac tacgcgcccg tcaAACCCGA TATGCCCGGC CGCCACAACG
1451 GCGTactggt GtcccaAGAG CAGGGCGAGG CGGTTGCTTA CGCCTTGTGG
1501 AATCTTGAAG ACCGCGGCCG TATGTTGTA TCGCCCAACG ACAAATCTA
1551 CGAAGGTATG ATTATCGGCA TCCACAGCCG CGACAACGAT TTGGTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTCACCAATA TCCGTGCCAG CGGTACCGAC
1651 GAAGCGGTGC GCCTGACCAC GCCGATCAAA CTGAcgcTGG AAGGCGCGGT
1701 CGAGTTTATC GACGATGACG AGCTGGTGGA AATCACGCCG CAAtccatcc
1751 gcctgcgcat gcgttacctG AGCGaattgg aacgcccgcg tcaTTTTAAA
1801 AagctgGATT AA

```

This corresponds to the amino acid sequence <SEQ ID 614; ORF 151.ng>:

g151.pep

```

1  MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
51  RGITILAKNT AIDYEGCHIN IVDTPGHADF GGEVERVLGM VDCVLLVDA
101 QEGPMPQTRF VTKKALALGL KPIVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESS DMRPLFDLIL KYTPAPSGSA
201 DEPLQLQISQ LDYDNYTGRL GIGRIILNGRI KPGQTVAVMN HEQQIAQGRI
251 NQLLGFKGLE RVPLEAEAG DIVIISGIED IGIGVTITDK DNPKGLPMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
401 NLTVDVPDDN QGAVMEELGR RRGELTNMES DGNRTRLEY HIPARGLIGF
451 QGEFMTLTRG VGLMSHVDD YAPVKPDMPG RHNGVLVSQE QGEAVAYALW

```


501 NLEDRGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
 551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRMYL SELERRRHFK
 601 KLD*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 615>:

m151.seq

```

1  ATGAAACAAA TCCGCAACAT CGCCATCATC GCCCACGTCG ACCACGGCAA
51  AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG
251 TAGAGCGCGT TTTGGGGATG GTGGACTGCG TCGTCTTGTT GGTGGACGCG
301 CAGGAAGGCC CGATGCCGCA AACCCGTTTC GTGACCAAAA AAGCCTTGGC
351 TTTGGGGCTG AAACCGATTG TCGTCATCAA CAAAATCGAC AAGCCGTCCG
401 CTGCTCCGAG CTGGGTTATC GACCAAACCT TCGAGCTGTT CGACAACCTG
451 GGCGCGACCG ACGAGCAGTT GGATTTCCCG ATTGTTTACG CTTCAGGGTT
501 GAGCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
551 CGCTGTTTCA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
601 GACGAAACGC TGCAACTGCA AATTTCCCAA CTCGACTACG ACAACTACAC
651 CGCCCGCCTC GGTATCGGTC GTATCTTGAA CGGACGCATC AAACCCGGCC
701 AAACCGTTGC CGTCATGAAC CACGATCAGC AAATCGCCCA AGGCCGCATC
751 AACCAGCTTT TGGGTTTCAA AGGTTTGGA AGCGTGCCGC TTGAAGAAGC
801 CGAAGCCGGC GACATCGTGA TTATTTCCGG TATCGAAGAC ATCGGTATCG
851 GCGTAACCAT CACCGACAAA GACAATCCCA AAGGCCTACC GATGTTGAGC
901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGCT
951 GGCGGGTACG GAAGGCAAAT TCGTAACCAG CCGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TCGCGTGGA AGATACCGCC
1051 GATGCCGACG TGTTCGCGT ATCCGGGCGC GGCGAGCTGC ACCTGACCAT
1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAAC
1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAATGCGA ACCGTATGAA
1201 AACCTGACCG TGATGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
1251 ACTCGGCCCG CGCCGTGGCG AACTGACTAA TATGGAAAGC GACGGCAACG
1301 GACGCAACCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGTTTC
1351 CAAGGCGAAT TTATGACCCT GACGCGCGGG GTCGGGTGA TGAGCCACGT
1401 GTTCGACGAT TACGCGCCCG TCAAACCGA TATGCCCGGC CGCCACAACG
1451 GCGTGCTGGT GTCCCAAGAG CAGGGCGAGG CAGTCGCTTA CGCCTTGTTG
1501 AATCTGGAAG ACCGCGGCCG TATGTTGTA TCGCCCAACG ACAAATCTA
1551 CGAAGGCATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
1651 GAAGCCGTTT GCCTGACCAC GCAATCAAG CTGACGCTGG AAGGTGCGGT
1701 TGAGTTTATC GACGATGACG AACTCGTTGA AATCACGCCG CAATCCATCC
1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCCG CCACTTTAAA
1801 AAGCTGGATT GA
```

This corresponds to the amino acid sequence <SEQ ID 616; ORF 151>:

m151.pep

```

1  MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQVDER VMDSNDLEKE
51  RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVLLVDA
101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDLIL KYTPAPSGSA
201 DETLQLQISQ LDYDNYTGRL GIGRIINGRI KPGQTVAVMN HDQQIAQGRI
251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPKGLPMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
401 NLTVDPDDN QGAVMEELGR RRGELTMES DNGRTRLEY HIPARGLIGF
451 QGEFMTLTRG VGLMSHFDD YAPVKPDMPG RHNGVLVSQE QGEAVAYALW
501 NLEDRGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRKRYL SELERRRHFK
601 KLD*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 151 shows 99.2% identity over a 603 aa overlap with a predicted ORF (ORF 151.ng) from *N. gonorrhoeae*:

m151/g151

m151.pep	10	20	30	40	50	60
	MKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMDSDNLEKERGITILAKNT					
g151	MKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMDSDNLEKERGITILAKNT					
	10	20	30	40	50	60
m151.pep	70	80	90	100	110	120
	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGMPQTRFVTKKALALGL					
g151	AIDYEGCHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGMPQTRFVTKKALALGL					
	70	80	90	100	110	120
m151.pep	130	140	150	160	170	180
	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN					
g151	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESS					
	130	140	150	160	170	180
m151.pep	190	200	210	220	230	240
	DMRPLFDTILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN					
g151	DMRPLFDTILKYTPAPSGSADEPLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN					
	190	200	210	220	230	240
m151.pep	250	260	270	280	290	300
	HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
g151	HEQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
	250	260	270	280	290	300
m151.pep	310	320	330	340	350	360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR					
g151	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR					
	310	320	330	340	350	360
m151.pep	370	380	390	400	410	420
	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDVPDDNQGAVMEELGR					
g151	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDVPDDNQGAVMEELGR					
	370	380	390	400	410	420
m151.pep	430	440	450	460	470	480
	RRGELTNMESDGNGRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMPG					
g151	RRGELTNMESDGNGRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMPG					
	430	440	450	460	470	480
m151.pep	490	500	510	520	530	540
	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK					
g151	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK					
	490	500	510	520	530	540
m151.pep	550	560	570	580	590	600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK					
g151	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRMYLSELERRRHFK					
	550	560	570	580	590	600

m151.pep KLDX
 ||||
 g151 KLDX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 617>:

a151.seq

```

1  ATGAAACAAA TCCGCAACAT CGCCATCATC GCCCACGTCG ACCACGGCAA
51  AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG
251 TAGAGCGAGT TTTGGGGATG GTGGACTGCG TCGTCTTGTT GGTGGACGCG
301 CAGGAAGGCC CGATGCCGCA AACCCTTTTC GTGACCAAAA AAGCCTTGGC
351 TTTGGGGCTG AAACCGATTG TCGTCATCAA TAAAATCGAC AAACCGTCCG
401 CCCGTCCGAG CTGGGTCATC GACCAAACCT TCGAGCTGTT CGACAACTTG
451 GGCGCGACCG ACGAGCAGTT GGATTTCCCG ATGTGTTATG CTCCGGTCT
501 GTCCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
551 CGCTGTTCTA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
601 GACGAAACGC TGCAACTGCA AATTTCCTAA CTCGACTACG ACAACTACAC
651 CGGCCGCCTC GGTATCGGTC GTATCTTGAA CGGACGTATC AAGCCCGGTC
701 AAGTTGTTGC CGTCATGAAC CACGATCAAC AAATCGCCCA AGGCCGCATC
751 AACCAGCTTT TGGGTTTCAA AGGTTTAGAA CGCGTGCCGC TTGAAGAAGC
801 CGAAGCCGGC GACATCGTGA TTATTTCCGG TATTGAAGAC ATCGGCATCG
851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGGCCTGCC GATGTTGAGC
901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGTT
951 GGCAGGTACG GAAGGCAAAT TCGTAACCAG CCGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TCGCGTGGA AGATACCGCC
1051 GATGCCGACG TGTTCCGCGT ATCCGGGCGC GGCGAGCTGC ACCTGACCAT
1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAAC
1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAATGCGA ACCGTATGAA
1201 AACCTGACCG TGGACGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
1251 ACTCGGCCGC CGCCGTGGCG AACTGACTAA TATGGAAAGC GACGGCAACG
1301 GACGCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGCTTC
1351 CAAGGCGAAT TTATGACCCT GACGCGCGGG GTCGGGCTGA TGAGCCACGT
1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCCTGGC CGCCACAACG
1451 GCGTGCTGGT GTCCCAAGAG CAGGGCGAGG CAGTCGCTTA CGCCTTGTGG
1501 AATCTGGAAG ACCGCGGCCG TATGTTCTGA TCGCCCAACG ACAAATCTA
1551 CGAAGGTATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
1651 GAAGCCGTTT GCCTGACCAC GCCGATTAAG CTGACGCTGG AAGGTGCGGT
1701 CGAGTTTATC GACGATGATG AGCTGGTAGA AATCACGCCG CAATCCATCC
1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCCG CCATTTCAAA
1801 AAGCTAGATT GA
```

This corresponds to the amino acid sequence <SEQ ID 618; ORF 151.a>:

a151.pep

```

1  MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
51  RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVVLVDA
101 QEGPMPQTRF VTKKALALGL KPIVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDLIL KYTPAPSGSA
201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQVVAVMN HDQQIAQGRI
251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPKGLPMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
401 NLTVDVPDDN QGAVMEELGR RRGELTNMES DGNGRTRLEY HIPARGLIGF
451 QGEFMTLTRG VGLMSHVFDG YAPVKPDMPG RHNGVLVSQE QGEAVAYALW
501 NLEDGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
551 EAVRLTPIK LTLEGAVEFI DDDELVEITP QSIRLRKRYL SELERRRHFK
601 KLD*
```

m151/a151 99.8% identity in 603 aa overlap

10

20

30

40

50

60

m151.pep	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
a151	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
	10 20 30 40 50 60
m151.pep	70 80 90 100 110 120
	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL
a151	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL
	70 80 90 100 110 120
m151.pep	130 140 150 160 170 180
	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN
a151	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN
	130 140 150 160 170 180
m151.pep	190 200 210 220 230 240
	DMRPLFDITILKYTPAPSGSADETLLQLQISQLDYDNYTGRIGIGRIILNGRIKPGQTVAVMN
a151	DMRPLFDITILKYTPAPSGSADETLLQLQISQLDYDNYTGRIGIGRIILNGRIKPGQTVAVMN
	190 200 210 220 230 240
m151.pep	250 260 270 280 290 300
	HDQQIAQGRINQLLGFKGLERVPLEAEAGDIVIISGIEDIGIGVITITDKDNPKGLPMLS
a151	HDQQIAQGRINQLLGFKGLERVPLEAEAGDIVIISGIEDIGIGVITITDKDNPKGLPMLS
	250 260 270 280 290 300
m151.pep	310 320 330 340 350 360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLOKELLTNVALRVEDTADADVFRVSGR
a151	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLOKELLTNVALRVEDTADADVFRVSGR
	310 320 330 340 350 360
m151.pep	370 380 390 400 410 420
	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDVPDDNQAVMEELGR
a151	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDVPDDNQAVMEELGR
	370 380 390 400 410 420
m151.pep	430 440 450 460 470 480
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMPG
a151	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMPG
	430 440 450 460 470 480
m151.pep	490 500 510 520 530 540
	RHNGVLVSQEQGEAVAYALWNLEDGRGMFVSPNDKIYEGMIIGIHSRDNDLVVNPLKGGK
a151	RHNGVLVSQEQGEAVAYALWNLEDGRGMFVSPNDKIYEGMIIGIHSRDNDLVVNPLKGGK
	490 500 510 520 530 540
m151.pep	550 560 570 580 590 600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELEERRRHFK
a151	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELEERRRHFK
	550 560 570 580 590 600
m151.pep	KLDX
a151	KLDX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 619>:

g152.seq

```

1  ATGAAAAaca aAACCaaagt ctgGGacttc cCaccgcgcc ttTTCcactG
51  GctgcttgCC gCATCCctgc CCTTTATGTG gtatagCGCA AAAGCCGGCG
101 GcgataTGCT GcaatgGCAC ACGCGCGTCG GGCTGCTCGT CCTTTTCCTG

```

```

151 CTCGTATTCC GCCTCTGCTG GGCATTGTTGG GGCAGcgATA CCGCCCGTTT
201 CTCccgTtTC GTCCGAGGTT GGGCAGGTAT ACGCGGCTAT CTGAAAAAcg
251 gCATTCCCGA ACAtatcCAG CCCGGACACA ACCCCTTGGG CGCACTgatg
301 gtcGTTGCGC TTTTGgccgc cgtcTCATTT CAagtcggcA CGGGGCTTTT
351 Tgccgccaat gaaaacacct tcagcaCCAa cggctacctc aaccatttgg
401 tttccgaaca tacgGGCAGC CTTATACGGA AAATCCACCT CAACTTTTTTC
451 AAGCTGCTCG CCGTTTTTTC CGCAGTCCAC ATCGCCGCCG TCGCCGCATA
501 CCGCATATTC AAAAAGAAAA ACCTCGTCCG CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 620; ORF 152.ng>:

g152.pep

```

1 MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KAGGDMQLQWH TRVGLLVFL
51 LVFRLCWGIW GSdTARFSRF VRGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAN ENTFTNGYL NHLVSEHTGS LIRKIHLNFF
151 KLLAVFSAVH IAAVAAYRIF KKKNLVRPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAILLLS*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 621>:

m152.seq

```

1 ATGAAAAACA AAACCAAAGT CTGGGACCTC CCCACCCGCC TTTTCCACTG
51 GCTGCTTGCC GCGTCCCTGC CCTTTATGTG GTATAGCGCG AAAGCCGGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTTCGT CCTTTTCCTG
151 CTCGTATTTT GCCTCTGCTG GGCATTGTTGG GGCAGCGATA CCGCCCGTTT
201 TTCCCGTTTC GTCCAAGGCT GGGCAGGCAT ACGCGGCTAT CTGAAAAACG
251 GTATTCCCGA ACACATCCAG CCCGGACACA ACCCCTTGGG CGCACTGATG
301 GTCGTTGCGC TTTTGGCCGC CGTGTCTTTC CAAGTCGGCA CCGGGCTTTT
351 TGCCGCCGAT GAAAACACCT TCAGCACCAA CGGCTACCTC AACCATTGTTG
401 TTTCCGAACA TACGGGCAGC CTTATGCGGA AAATCCACCT CAACTTTTTTC
451 AAGCTGCTCG CCGTTTTTTC TGCAATCCAC ATCGCCGCCG TCGCCGCATA
501 CCGCGTATTC AAAAAGAAAA ACCTCATCCT CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCAGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CTCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 622; ORF 152>:

m152.pep

```

1 MKNKTKVWDL PTRLFHWLLA ASLPFMWYSA KAGGDMQLQWH TRVGLFVLFL
51 LVFRLCWGIW GSdTARFSRF VQGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAD ENTFTNGYL NHLVSEHTGS LMRKIHLNFF
151 KLLAVFSAIH IAAVAAYRVF KKKNLILPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVASLA AAAILLLS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 152 shows 95.4% identity over a 218 aa overlap with a predicted ORF (ORF 152.ng) from *N. gonorrhoeae*:

m152/g152

	10	20	30	40	50	60
m152.pep	MKNKTKVWDL PTRLFHWLLA ASLPFMWYSA KAGGDMQLQWH TRVGLFVLFL LVFRLCWGIW					
	: :					
g152	MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KAGGDMQLQWH TRVGLLVFL LVFRLCWGIW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GSdTARFSRF VQGWAGIRGY LKNGIPEHIQ PGHNPLGALM VVALLAAVSF QVGTGLFAAD					
	: :					
g152	GSdTARFSRF VRGWAGIRGY LKNGIPEHIQ PGHNPLGALM VVALLAAVSF QVGTGLFAAN					
	70	80	90	100	110	120

436

	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSAIHIAAVAAYRVFKKKNLILPMI					
	: : : :					
g152	ENTFSTNGYLNHLVSEHTGSLIRKIHLNFFKLLAVFSAVHIAAVAAYRIFKKKNLVRPMI					
	130	140	150	160	170	180
	190	200	210	219		
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX					
	:					
g152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 623>:

```

a152.seq
1  ATGAAAAACA AAACCAAAGT CTGGGACTTC CCCACCCGCC TTTTCCACTG
51  GCTGCTTGCC GCATCCCTAC CCTTTATGTG GTATAGCGCG AAAACCGGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTTAT CCTTTTCTCG
151 CTCGTATTCC GCCTCTGCTG GGGCATTGCG GGCAGCGATA CCGCCGTTT
201 CTCCCGTTTC GTCCGCGGAT GGTCCGGTAT CAGAGAGTAT ATGAAAAACG
251 GTATCCCGCA ACACGTCCAA CCCGGACACA ACCCCTTGGG CGCACTGATG
301 GTCGTTGCGC TTTTGGCCGC CGTGTCTGTC CAAGTCGGCA CAGGGCTTTT
351 TGCCGCCGAT GTAAACACCT TCAGACCAA CCGGTACCTC AACCATTGCG
401 TTTCCGAACA TACGGGAGC CTTATGCGGA AAATCCATCT CAACTTTTTC
451 AAATGCTCG CCGTTTTTTC CGCAGTCCAC ATCGCCGNCG TCGCCGCATA
501 CCGCGTGTTC AAAAAGAAAA ACCTCGTCTT CCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 624; ORF 152.a>:

```

a152.pep
1  MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KTGGDMLQWH TRVGLFIFLF
51  LVFRLCWGIW GSDTARFSRF VRGWSGIREY MKNGIPEHVQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAD VNTFSTNGYL NHLVSEHTGS LMRKIHLNFF
151 KLLAVFSAVH IAXVAAYRVF KKKNLVLPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAILLS*

```

m152/a152 94.0% identity in 218 aa overlap

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTLRFHWLLAASLPFMWYSAKAGGDMQLQWHTRVGLFVLFLLVFRLCWGIW					
	: : : :					
a152	MKNKTKVWDFPTLRFHWLLAASLPFMWYSAKTGGDMLQWHTRVGLFIFLLVFRLCWGIW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNIGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	: : : :					
a152	GSDTARFSRFVRGWSGIREYMKNIGIPEHVQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSAIHIAAVAAYRVFKKKNLILPMI					
	: : : :					
a152	VNTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSVHIAAXVAAYRVFKKKNLVLPMI					
	130	140	150	160	170	180
	190	200	210	219		
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX					
	:					
a152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 625>:

```
g153.seq
1  atgggggtttg cttacAgat gacgtatatc gaggtCGGga taccggaggc
51  ggcatccgtc ctttCgctGC CCGAGATgat gcgcctgatG GTGTTtCagg
101 attATGGTTT TttggcCGAA GTGATGTTTG TGctgaCTTT cGGCGcgCG
151 GTTCTGTTtC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GGCAGGCGAT GATGGTGGAT GTGTTTTTTG TTCCACTCT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AAAGGTTTCG TTCGGGCCGG CGTTTTATCT
351 GATGTTTCGG CTGTCGGTTA TGCTGATTCT GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTCCAA ATCGGGCGGC TGACGGGGAA TAATGCGGTT
451 CAGACGGCAT CGGAAGGCAA AACCTGTTGC AGCCGCTGCC TGTATTtccg
501 cgacAGTgcc gaatccCCCT GCGGGGTGTg cgCGCggaA CTgtacggcg
551 gacggccgaa aagtCTGAGt atttCgtCGG CGTTTCTgac ggcggcggtT
601 GTTTTGTATT TCCctgCcaa TATCctgccc attatGAttt cgtccAATCc
651 tgccgcccacg GAGGcCAACA CCATCTTTAG CGGCATCGCT TATATGTGGG
701 ACgaggcgA CAGGCTGATT GCGCGGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGGTGC TGAAGATTGC GGCAATGTCG GTTTTGATTG CCGCGGCACG
801 GTTCGCTTTG CCGCGGGCG CAAAGAAATT GTCGCACCTC tacCGCATCA
851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGT GATTATTATT
901 TTGATGTGTT CGTTCCacaC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTTT GACGATGCTG TCCGCCTATT
1001 ATTTcGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAACGAAA CGGAAAAATA TGA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 626; ORF 153.ng>:

```
g153.pep
1  MGFAYSMTYI EVGIPEAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRV M VRLRQAMMVD VFFVSTLVAY
101 IKLSSVAKVR FGPAFYLMFA LSVM LIRTSV SVPQHVVYFQ IGRLTGNNAV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYGGRPKSL S ISSAFLTA AV
201 VLYFPANILP IMISSNPAAT EANTIFSGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIAARFAL PAGAKKLSHL YRITEAVGRW SMIDIFVIII
301 LMCSFH TYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL L WDKRASDGIA
351 FNETEKYD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 627>:

```
m153.seq
1  ATGCGGTTTG CTTACGGTAT GACGTATATC GAGGTCGGGA TACCGGTGTC
51  GGCATCCGTC CTTTCGCTGC CCGAGATGAT GCGCCTGATG GTGTTTCAGG
101 ATTATGGTTT TTTGGCCGAA GTGATGTTTG TGCTGACTTT CCGCGCGCCG
151 GTTCTGTTTC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GACAGGCGAT GATGGTGGAT GTGTTTTTTG TTCCACTTT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AGAGGTTTCG TTCGGGCCGG CGTTTTATCT
351 GATGTTTCGG CTGTCACTTA TGCTGATTCT GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTTCAA ATCGGGCGGC TGACGGGGGA TAATGCGGTT
451 CAGACGGCAT CGGAAGGTAA AACCTGTTGC AGCCGCTGCC TGTATTTCGG
501 CGACAGTGCC GAATCCCCCT GCGGCGTGTG CCGTGCAGAA CTGTACCGCC
551 GACGGCCGAA AAGTCTGAGT ATTTCTGTCG CGTTTCTGAC GCGGCGGTT
601 ATTTTGTATT TCCCTGCCAA TATCCTGCCG ATTATGATTT CGTCCAATCC
651 TGCCGCCACG GAGGTCAATA CCATCCTTAA CCGCATCGCT TATATGTGGG
701 ACGAGGGCGA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCGCGTAC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGTCCGCCCC
801 CTTCCGCTTT CCAACGGGTG CAAAGAAATT GTCGCACCTC TACCGCATCA
851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGT GATTATTATT
901 TTGATGTGTT CGTTCCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTcGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 628; ORF 153>:

```
m153.pep
1  MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRV M VRLRQAMMVD VFFVSTLVAY
```

	10	20	30	40	50	60
m153 .pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFDYGFLAEVMFVLTFGAPVLFLLCLYV					
	: : : : : : : : : :					
g153	MGFAYSMTYIEVGIPGAASVLSLPEMMRLMVFDYGFLAEVMFVLTFGAPVLFLLCLYV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m153 .pep	YAALIRKQAYPALRLRATRVMLRQAAMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
g153	YAALIRKQAYPALRLRATRVMLRQAAMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m153 .pep	LSVMLIRTSVSVPQHVVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSDAESPCGVCGAE					
g153	LSVMLIRTSVSVPQHVVYFQIGRLTGNNNAVQTASEGKTCCSRCLYFRDSDAESPCGVCGAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m153 .pep	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVENTILNGIAYMWDEGDRLI					
g153	LYGGRPKSLSISSAFLTAAVVLYFPANILPIMISSNPAATEANTIFSGIAYMWDEGDRLI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m153 .pep	AAVIFSASILPVCLKIAAMSVLIASARFALPTGAKKLSHLYRITEAVGRWSMIDIFVII					
g153	AAVIFSASILPVCLKIAAMSVLIAAARFALPAGAKKLSHLYRITEAVGRWSMIDIFVII					
	250	260	270	280	290	300
	310	320	330	340	350	359
m153 .pep	LMCSFH TYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLLDWKRASDGIAFNTEKHDX					
g153	LMCSFH TYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLLDWKRASDGIAFNTEKYDX					
	310	320	330	340	350	

a153.seq

1	ATGGCGTTTG	CTTACGGTAT	GACGTATATC	GAGGTCGGGA	TACCGGGTGC
51	GGCATCCGTC	CTTTCGCTGC	CCGAGATGAT	GCGCCTGATG	GTGTTTCAGG
101	ATTATGTTT	TTTGGCCGAA	GTGATGTTT	TGCTGACCTT	CGGCGCGCCG
151	GTTCTGTTT	TGCTGCTGTG	CCTGTATGTC	TATGCCGCGC	TGATACGGAA
201	ACAGGCGTAT	CCTGCGCTGC	GTTTGGCAAC	GC GTGTGATG	GTGCGCTTGA
251	GACAGGCGAT	GATGCTGGAT	GTGTTTTTTG	TTTCCACTTT	GGTGGCGTAT
301	ATCAAGTCT	CGTCTGTGGC	AGAGGTTCCG	TTCGGATCGG	CGTTTTATCT
351	GATGTTCCGC	CTGTGCGTTA	TGCTGATTCG	ATCATCGGTA	TCCGTTCCCC
401	AGCATTGGGT	GTATTTTCAA	ATCGGGCGGC	TGACGGGGGA	TAATGCGGTT
451	CAGACGGCAT	CGGAAGGTAA	AACCTGTTGC	AGCCGCTGCC	TGATATTCCG
501	CGACAGTGCC	GAATCCCCCT	GCGGCGTGTG	CGGTGCGGAA	CTGTACCGCC
551	GACGGCCGAA	AAGTCTGAGT	ATTTCTGCGG	CGTTTCTGAC	GCGGCGGGTT
601	ATTTTGTATT	TCCCTGCCAA	TATCTTGCCG	ATTATGATTT	CGTCCAATCC
651	TGCCGCCACG	GAGGTCAATA	CCATCCTTAA	CGGCATCGCT	TATATGTGGG
701	ACGAGGCGCA	CAGGCTGATT	GCGGCGGTTA	TTTTACGCGC	GAGTATTTTTG
751	GTGCCGGTAC	TGAAGATTGC	GGCAATGTGC	GTTTTGATTG	CGTCCGCCCG
801	CTTCGCTTTG	CCAACGGGTG	CAAAGAAATT	GTCGCACCTC	TACCGCATCA


```

851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGT GATTATTATT
901 TTGATGTGTT CGTTCCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 630; ORF 153.a>:

```

a153.pep
  1 MAFAYGMTYI EVGIPGAASV LSLPEMRLM VFQDYGFLAE VMFVLTFGAP
  51 VLFLLCLYV YAALIRKQAY PALRLATRV VRLRQAMMVD VFFVSTLVAY
 101 IKLSSVAEVR FGSFAYLMFA LSVMLIRTSV SVPQHWVYFQ IGRITGDNV
 151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSL SISAFLTA
 201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDRLI AAVIFSASIL
 251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII
 301 LMCSFHTYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL WDKRASDGIA
 351 FNETEKHD*

```

m153/a153 99.7% identity in 358 aa overlap

m153.pep	10	20	30	40	50	60
	MAFAYGMTYIEVGIPGAASVLSLPEMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLYV					
a153	MAFAYGMTYIEVGIPGAASVLSLPEMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLYV					
	10	20	30	40	50	60
m153.pep	70	80	90	100	110	120
	YAALIRKQAYPALRLATRVVRLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
a153	YAALIRKQAYPALRLATRVVRLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGSAFYLMFA					
	70	80	90	100	110	120
m153.pep	130	140	150	160	170	180
	LSVMLIRTSVSVFPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
a153	LSVMLIRTSVSVFPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
	130	140	150	160	170	180
m153.pep	190	200	210	220	230	240
	LYRRRPKSLSSISAFLTA AVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
a153	LYRRRPKSLSSISAFLTA AVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
	190	200	210	220	230	240
m153.pep	250	260	270	280	290	300
	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII					
a153	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII					
	250	260	270	280	290	300
m153.pep	310	320	330	340	350	359
	LMCSFHTYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGIAFNETEKHDX					
a153	LMCSFHTYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGIAFNETEKHDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 631>:

```

g154.seq
  1 ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCTCAAG CACGCGTCCG
  51 CAAAAACAAC accttctCT CCGCCGCTCG GCTGGTCCCG CTGATCGCGC
 101 TGATTGCCGG CGGCTGGCTT TGGGTTAAG AAATCCGCA CAGGGGGCCT
 151 GTGGTTACGC TCTTGATGGA CAGCGCGGA GGCATCGAAG TCAACAATAC
 201 GGTCAATTAAG GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
 251 TGCGCGACGA CAAAAAGGC GTGGAAGTTA CTGCCAACT CAATGCGGAC
 301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTGGGTGG TCAAGCCGCG
 351 TATCGACCAA AGCGGcgtAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT

```

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401 ACATCGCTTT TACACCCGGC AAAAGCGGCG AGGCAAAAGA CGTGTTCCTAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGcg GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG AccgCATCCT CAACGTcaac AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAATCG AAAGCGCGCA TTTCGAcccG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTTCAT TCCGCCAGCC GTTTTGGCT GGAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTCAGGCG CGATTTTCATT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAGGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAATCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT cggTTCGCTT GtcaATACA AAGGGCTgaa
951 TGTcggCATG GTTTCGATG TCCCTTATTT TGACCGCAAt gacagCCTGC
1001 ACctgtTTGA aaacggctgg aTtcccGtac gCATCCGCAT cgagccTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAGCAAAGC AAAGAGCATT GGAAACAACA
1101 ATTCCAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCGGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TCGGACCGCA TACCGTTTAT GCAGGCGATA CCGTCATCGC
1251 CACACGGGGC GCGGCTTGG ATGACTTGCA GGTCAAATTG GCGGATTGTC
1301 TGGACaaatT CAACAATCTG CCATTggata aAACCGTTGC CGAATTGAAC
1351 GGCTCGCTCG CCGAACTCAA GTCCGCACTC AAATCCGCCA ATGCCGCCCT
1401 AAGCTCCATT GacaAACTGG TCGgcaaTCC GCAGACGCAA AACATCCCGA
1451 ACGAAGTGAA CCAAACCTCTG AAAGAGTTGC GCATAACCTT GCAAGGCGTA
1501 TCGcctCAAT CGCCTATCTa cgGagacgta caAAATAcgc tgCaAAGTTT
1551 GGACAAAAAC TTAaAagacg TtcaACCGT CATTAACTT TTGAaAGAAa
1601 aacCCaaCgc actGATTTtc aacaACAGCA GCAAAGAccc tATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 632; ORF 154.ng>:

g154.pep

```

1 MTDNSPPPNG HAQARVRKNN TFLSAVWLV LIALIAGGWL WVKEIRNRGP
51 VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTL LSGSYIAFTPG KSGEAKDV FQ
151 VQDIPPVTAI QSGSLRLNLI GKNDRI LNVN SPVLYENFMV QIESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETGSGI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAF FKFQ
301 SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQQFQT ALNKGLTATI SSNNLLTGK MIELNDQPSA
401 SPKLRPHTVY AGDTV IATRG GGLDDLQVKL ADLLDKFN NL PLDKTVAELN
451 GSLAELKSAL KSANAALSSI DKLVGNPQTQ NIPNELNQTL KELRITLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NNSSKDPIPK
551 GSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 633>:

m154.seq

```

1 ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51 CAAAAACAAC ACCTTCCTCT CTGCCGCTCG GCTGGTTCGG CTGATCGCGC
101 TGATTGCCCG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCATCAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TCGCGGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCTAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA TTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTTCAT TCCGCCAGCC GTTTTGGCT GGAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTGCGGCG CGATTTTCATT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GCCTGACCGT CGGTTGCGCC GTCGAGTACA AAGGGCTGAA
951 TGTGCGCGTG GTTTCGACG TTTCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATACCCGTAC GCATCCGCAT TGAACCTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAACAAGC AAAGAACATT GGAAACAACA
1101 ATTTCCAGAC GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGAAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCA

```

```

1201 TCACCTAAGC TGCGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GGCAGTTTGG ACGATTGCA GGTCAAATTG GCGGATTGTC
1301 TGGACAAGTT CGACAAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTTCGCTT CCGAGCTCAA ATCCCACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAAACCTG AAAGAGTTGC GCACAACCCT GCAAGGCGTA
1501 TCGCCGCAAT CGCCTATCTA CGGCGACGTA CAAAATACGC TGCAAAGTTT
1551 GGACAAAAC TTAAGAGACG TTCAACCCGT GATTAATACT TTGAAAGAAA
1601 AACCCAACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 634 ORF 154.a>:

m154.pep

```

1 MTDNSPPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51 VVTLMLDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTALQNLAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVFQ
151 VQDIPPVTAI QSGRLRLNLI GKNDRIILNVN SPVLYENFMV QQVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN
451 GSLAEKSTL KSANAALSSI DKLVGKPTQ NIPNELNQLT KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

```

m154 / g154 97.8% identity in 553 aa overlap

	10	20	30	40	50	60
m154.pep	MTDNSPPPNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLMLDSAE					
g154	MTDNSPPPNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLMLDSAE					
	10	20	30	40	50	60
m154.pep	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTALQNLADV SGLIRSDTQ FWVVKPRIDQ					
g154	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTALQNLADV SGLIRSDTQ FWVVKPRIDQ					
	70	80	90	100	110	120
m154.pep	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTALQNLADV SGLIRSDTQ FWVVKPRIDQ					
g154	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTALQNLADV SGLIRSDTQ FWVVKPRIDQ					
	70	80	90	100	110	120
m154.pep	SGVTGLGTLT LSGSYIAFTPG KSDEAKDVFQ VQDIPPVTAI QSGRLRLN LIGKNDRIILNVN					
g154	SGVTGLGTLT LSGSYIAFTPG KSDEAKDVFQ VQDIPPVTAI QSGRLRLN LIGKNDRIILNVN					
	130	140	150	160	170	180
m154.pep	SGVTGLGTLT LSGSYIAFTPG KSDEAKDVFQ VQDIPPVTAI QSGRLRLN LIGKNDRIILNVN					
g154	SGVTGLGTLT LSGSYIAFTPG KSDEAKDVFQ VQDIPPVTAI QSGRLRLN LIGKNDRIILNVN					
	130	140	150	160	170	180
m154.pep	SPVLYENFMV QGVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI					
g154	SPVLYENFMV QGVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI					
	190	200	210	220	230	240
m154.pep	SPVLYENFMV QGVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI					
g154	SPVLYENFMV QGVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI					
	190	200	210	220	230	240
m154.pep	KLNSAPLPAL LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFKQ					
g154	KLNSAPLPAL LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFKQ					
	250	260	270	280	290	300
m154.pep	KLNSAPLPAL LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFKQ					
g154	KLNSAPLPAL LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFKQ					
	250	260	270	280	290	300
m154.pep	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
g154	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
	310	320	330	340	350	360
m154.pep	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
g154	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
	310	320	330	340	350	360
m154.pep	KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATQG					
g154	KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATRG					
	370	380	390	400	410	420

442

	370	380	390	400	410	420
	430	440	450	460	470	480
m154.pep	GGLDDLQVKLADLLDKFDKPLDKTVAEIENGSLAELKSTLKSANAALSSIDKLVGKPQTQ					
g154	GGLDDLQVKLADLLDKFNNLPLDKTVAEIENGSLAELKSALKSANAALSSIDKLVGNPQTQ					
	430	440	450	460	470	480
	490	500	510	520	530	540
m154.pep	NIPNELNQTLKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQVPVINTLKEKPNALIF					
g154	NIPNELNQTLKELRITLQGVSPQSPIYGDVQNTLQSLDKTLKDVQVPVINTLKEKPNALIF					
	490	500	510	520	530	540
	550					
m154.pep	NSSSKDPIPKGSRX					
g154	NSSSKDPIPKGSRX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 635>:

```

a154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGTCTG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTAAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCAATCAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGC GCGACGA CAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGCTCGCCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTTCGACCCG
601 TCCGACCAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTCTGGCTT GGAAAGCGGC ATCAATATCG
701 AAACCAAGG CAGCGGCATC AACTCAATT CCGCCCCTCT GCCTGCCCTG
751 CTGTCGGGCG CGATTTCATT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGATACCGT TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT CGGTTGCGCT GTCGAGTACA AAGGGCTGAA
951 TGTCGGCGTG GTTTCGATG TTCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGCTGG ATTCCCGTAC GCATCCGTAT TGAGCCTTCC
1051 CGTTTGAAAA TCAATGCCGA CGAACAAAGC AAAGAACATT GGAAACAACA
1101 ATTTAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGAACAA
1151 ACCTGCTGAC CGGCAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TCGGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTGTC
1301 TGGACAAGTT CGACAACTG CTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTGCTTGC CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAAAC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAAACCTG AAAGAGTTGC GCACAACCTT GCAAGGCGTA
1501 TCGCCTCAAT CGCCTATCTA CGGCGACGTA CAAAATACGC TGCAAAAGTTT
1551 GGACAAAACC TTAAGAGACG TTCAACCCGT CATTAACACT TTGAAAGAAA
1601 AACCCAACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 636; ORF 154.a>:

```

a154.pep
1  MTDNSPPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVFEQ

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151 VQDIPPVTAI GQSGRLRLNLI GKNDRIILNVN SPVLYENFMV GQVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTGSGI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIAATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN
451 GSLAEKSTL KSANAALSSI DKLVGKPQTQ NIPNELNQTL KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDFIPK
551 GSR*

```

m154/a154 100.0% identity in 553 aa overlap

	10	20	30	40	50	60
m154.pep	MTDNSPPPNHGAQARVRKNNTFLSAVWLVP LIALIAGGWLWVKEIRNRGPVVTLLMDSAE					
a154	MTDNSPPPNHGAQARVRKNNTFLSAVWLVP LIALIAGGWLWVKEIRNRGPVVTLLMDSAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m154.pep	GIEVNNTVIKVL SIDVGRVTRIKLRDDQKGVEVTAQLNADV SGLIRSDTQFWVVKPRIDQ					
a154	GIEVNNTVIKVL SIDVGRVTRIKLRDDQKGVEVTAQLNADV SGLIRSDTQFWVVKPRIDQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m154.pep	SGVTGLGTLLSGSYIAFTPGKSDEAKDV FQVQDIPPVTAIGQSGRLRLNLIKNDRIILNVN					
a154	SGVTGLGTLLSGSYIAFTPGKSDEAKDV FQVQDIPPVTAIGQSGRLRLNLIKNDRIILNVN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m154.pep	SPVLYENFMVGQVESAHFDP SDQSVHYTIFIQSPNDKLIH SASRFWLESG INIETTGSGI					
a154	SPVLYENFMVGQVESAHFDP SDQSVHYTIFIQSPNDKLIH SASRFWLESG INIETTGSGI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m154.pep	KLNSAPLPALLSGAISFDSPKTKNSKNVKS EDSFTLYDSRSEVANLPDDR SLYYTAFFKQ					
a154	KLNSAPLPALLSGAISFDSPKTKNSKNVKS EDSFTLYDSRSEVANLPDDR SLYYTAFFKQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m154.pep	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS					
a154	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS					
	310	320	330	340	350	360
	370	380	390	400	410	420
m154.pep	KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIAATQG					
a154	KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIAATQG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m154.pep	GGLDDLQVKLADLLDKFDKLP LDKTVAELNGSLAEKSTLKSANAALSSIDKLVGKPQTQ					
a154	GGLDDLQVKLADLLDKFDKLP LDKTVAELNGSLAEKSTLKSANAALSSIDKLVGKPQTQ					
	430	440	450	460	470	480
	490	500	510	520	530	540
m154.pep	NIPNELNQTLKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
a154	NIPNELNQTLKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	490	500	510	520	530	540

```

                    550
m154.pep      NSSSKDPIPKGSRX
              |||||
a154          NSSSKDPIPKGSRX
                    550

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 637>:

```

g155.seq
1   atGAAaatcg  GtaccCAGC  CGAGTCAtta  tcCGGCGAAA  cccgcgtagc
51  ctgcAcgccc  gCCACCGTTG  CCctgctggg  caAactAGGC  TTTGAAACCG
101 TTGtcgaAAG  CGGTGCAggt  TTGGCGGCAA  GTTTggaCGA  TGCCGCTTAC
151 CAAACAGCAG  GCGCAACCGT  TGCCGACAAA  GCGGCGGTTT  GGGCCTGCC
201 TTTAATTTAT  AAGGTCAACG  CGCCGTCCGA  AGGCGAGCTG  CCGCTGCTCA
251 AAGAAGGTCA  AACCATCGTC  AGCTTCCTGT  GGCCGCGCCA  AAACGAGGCT
301 TTGGTCGAGG  CCTTGCGCGC  CAAGAAAGTC  AACGCGCTGG  CGATGGACAT
351 GGTTCCCCGC  ATTTCCCGCG  CTCAGGCCTT  GGACGCTTTG  TCTTCAATGG
401 CAAACATCAG  CGGCTACCGC  GCCGTGATTG  AAGCCGCCAA  CGCCTTCGCG
451 CGTTTCTTCA  CCGGTCAAAT  CACTGCCGCC  GGCAAAGTGC  CGCCTGCGCA
501 GGTTTTGGTG  ATTGGCGCCG  GTGTGGCGGG  TTTGGCGGCA  ATCGGTACGG
551 CAAATTCGCT  CGGCGCAGTG  GTGCGCGCGT  TCGATACCCG  CTTGGAAGTG
601 GCGGAACAAA  TCGAATCGAT  GGGCGGTAA  TTcctGAAAC  TCGACTTCCT
651 GCAAGAATCG  GGCGGCAGCG  GAGACGgctA  CGCAAAGTG  ATGAGGACG
701 AATTTATCGC  CGCCGAAATG  AAGCTCTTTG  CCGAACAGGC  GAAAGAAGTG
751 GACATCATCA  TCACCACCGC  CGCCATTCCG  GGCAAACCCG  CTCCCAAGCT
801 GATTACCAA  GAAATGGTGG  AAAGCATGAA  ATCCGATCC  GTCATCGTCG
851 ATTTGGCGGC  GACGGGCGGC  AACTGCGAAC  TCACCCGACC  GGGCGAATTG
901 TCCGTAACCG  GCAACGGCGT  GAAATCATC  GGCTACACCG  ACATGGCAAA
951 CCGCCTTGCC  GGACAGTCTT  CCCAGCTTTA  CGCCACCAAC  TTGGTGAACC
1001 TGACCAAGCT  GTTAAGCCCG  AACAAAGAcg  gcgaAATCAC  GCTGGACTTC
1051 GAAGacgtGA  TTATCCGCAA  TATGACCGTT  ACCCGcgacg  gcgaaATCAC
1101 CTTCCCGCCT  CCGcgaTTc  aggtTTCcgc  ccggccgCAG  CAAAcgccgt
1151 ctgaAAAagc  cgcGCCTGCC  GCCAagcccg  AgccGaaacc  tgttCCcctg
1201 tggaAAAaac  tcgCGCCCGC  CGCcatcgCC  GCCGTATTGG  tgctgtGgt
1251 cggCgcggtc  gcacccgcag  CATTCCTGAA  CCACTTTATC  GTCTTCGTCC
1301 TCGCCTGCGT  CATCGGCTAC  CATGTCGTTT  GgaacgTCAG  CCACTCGCTG
1351 CACACACCGC  TGAgtcggt  aaccaaCgcc  atctccGGCA  tcatggtcgt
1401 cggCGCGCTG  CTGCAAATCG  GTCAGGGcaa  cggttcgtT  TCgctGCTGT
1451 CGTTTGTGTC  CATCCTGATT  GCCGGCATCA  ATATCTTCGG  CGGCTTTGCG
1501 GTTACACGGC  GTATGCTGAA  TATGTTTAAG  AAAGGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 638; ORF 155.ng>:

```

g155.pep
1   MKIGIPRESL  SGETRVACTP  ATVALLGKLG  FETVVESGAG  LAASLDDAAY
51  QTAGATVADK  AAVWACPLIY  KVNAPSEGEL  PLLKEGQTIV  SFLWPRQNEA
101 LVEALRAKKV  NALAMDMVPR  ISRAQALDAL  SSANISGYR  AVIEAANAFG
151 RFFTQITAA  GKVPPAQVLV  IGAGVAGLAA  IGTANSLGAV  VRAFDTRLEV
201 AEQIESMGK  FLKLDFLQES  GSGDGYAKV  MSDEFIAAEM  KLFAEQAKEV
251 DIIITTAIP  GKPAPKLITK  EMVESMKSGS  VIVDLAATGG  NCELTRPGEL
301 SVTGNGVKII  GYTDMANRLA  GQSSQLYATN  LVNLTKLLSP  NKDGEITLDF
351 EDVIIRNMTV  TRDGEITFP  PPIQVSARPO  QTPSEKAAPA  AKPEPKVPPL
401 WKKLAPAAIA  AVLVLWVGAV  APAFLNHFI  VFVLACVIGY  HVVWNVSHSL
451 HTPLMSVTNA  ISGIMVVGAL  LQIQGNGFV  SLLSFVAILI  AGINIFGGFA
501 VTRRMLNMFK  KG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 639>:

```

m155.seq
1   ATGAAATCG  GTATCCCACG  CGAGTCATTA  TCCGGCGAAA  CCCGCGTCGC
51  CTGTACGCCC  GCCACCGTCG  CCCTGCTGGG  CAAACTGGGC  TTTGAAACCG
101 TTGTCGAAAG  CGGTGCAGGT  TTGGCGGCAA  GTTTGGACGA  TGCCGCTTAC
151 CAAACAGCAG  GCGCAACCGT  TGCCGACAAA  GCGGCGGTTT  GGGTCTGCC
201 TTTGATTTAT  AAGGTCAACG  CGCCGTCCGA  ACAGGAACGT  CCGCTTTTGA
251 ACGAAGGTCA  AACCATCGTC  AGCTTCCTGT  GGCCGCGCCA  AAACGAGGCT

```

```

301 TTGGTCGAAG CCTTGCGCGC CAAGAAAGTG AACGCGCTGG CGATGGATAT
351 GGTGCCCCGC ATTTGCGCGC CGCAGGCTTT GGACGCTTTG TCTTCGATGG
401 CAAACATCAG CGGCTACCGC GCCGTAATG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT TACCGCCGCC GGCAAAGTGC CGCCCCGCGA
501 GGTTTTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 ACAAGAATCG GGCGGCAGCG GAGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC AGCCGAGATG AAGCTCTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCT
801 GATTACCAA GAAATGGTGG AAAGCATGAA ATCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGGACGGGC GGCAACTGCG AACTCACCCG CCCGGGCGAA
901 TTGTCCGTAA CCGGCAACGG CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTCCCAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCACG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTTC CGCCCAGCCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGTGCCT GCCGCCAAGC CCGAGCCAAA ACCCGTTCCC
1201 CTGTGGAAAA AACTCGCGCC CGCCGTCATC GCCGCGTCT TGGTACTGTG
1251 GGTGCGGCGC GTGCGACCCG CAGCATTCCT GAACCACTTT ATCGTGTTCG
1301 TTCTCGCCTG CGTCATCGGC TACTACGTCG TCTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTAACCAAC GCCATCTCCG GCATCATCGT
1401 CGTCGGCGCG CTGCTGCAAA TCGGTGAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCGGCA TCAACATCTT CGGCGGCTTT
1501 GCGGTAACAC GCGGTATGCT GAATATGTTT AAGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 640; ORF 155>:

```

m155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWVCPLIY KVNAPSEQEL PLLNEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMPVR ISRAQALDAL SSMANISGYR AVIEAANAFA
151 RFFTGQITAA GKVPQAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGKK FLKLDLPQES GSGDGYAKV MSDEFIAAEM KLFAEQAKEV
251 DIIITTAAP GKPAKLITK EMVESMKSGS VIVDLAAATG GNCELTRPGE
301 LSVTGNVVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDEITLD
351 FEDVIIRNMT VTHDGEITFP PPPIQVSAQP QTPSEKAVP AAKPEPKVP
401 LWKKLAPAVI AAVLVLVWGA VAPAAFLNHF IVEVLACVIG YYVWVNVSHS
451 LHTPLMSVTN AISGIIIVGA LLQIGQGNGF VSLLSFVAIL IAGINIFGGF
501 AVTRRLNMF KKG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 155 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 155.ng) from *N. gonorrhoeae*:

```

m155 / g155 97.9% identity in 513 aa overlap
              10      20      30      40      50      60
m155.pep     MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              |||||
g155          MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              10      20      30      40      50      60

              70      80      90     100     110     120
m155.pep     AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR
              ||||:|||||
g155          AAVWACPLIYKVNAPSEGELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR
              70      80      90     100     110     120

              130     140     150     160     170     180
m155.pep     ISRAQALDALSSMANISGYRAVIEAANAFAFRFFTGQITAAGKVPPAQVLVIGAGVAGLAA
              |||||
g155          ISRAQALDALSSMANISGYRAVIEAANAFAFRFFTGQITAAGKVPPAQVLVIGAGVAGLAA

```

446

	130	140	150	160	170	180
	190	200	210	220	230	240
m155.pep	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
g155	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLQESGGSGDGYAKVMSDEFIAAEM					
	250	260	270	280	290	300
m155.pep	KLFAEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
g155	KLFAEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAA-TGGNCELTRPGE					
	310	320	330	340	350	360
m155.pep	LSVTGNGVKIIGYTDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
g155	LSVTGNGVKIIGYTDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	370	380	390	400	410	420
m155.pep	VTHDGEITFPPPPPIQVSAQPQQTPEKAVPAAKPEPKPVPLWKKLAPAVIAAVLVLVWGA					
g155	VTRDGEITFPPPPPIQVSARPPQQTPEKAAPAAKPEPKPVPLWKKLAPAAIAAVLVLVWGA					
	430	440	450	460	470	480
m155.pep	VAPAAFLNHFIVFVLACVIGYVWVNVSHSLHTPLMSVTNAISGIIIVVGALLQIGQGNGF					
g155	VAPAAFLNHFIVFVLACVIGYHVWVNVSHSLHTPLMSVTNAISGIMVVGALLQIGQGNGF					
	490	500	510			
m155.pep	VSLLSFVAILIAGINIFGGFAVTRRMLNMFKKGX					
g155	VSLLSFVAILIAGINIFGGFAVTRRMLNMFKKGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 641>:

```

a155.seq
1   ATGAAAATCG GTATCCACAG TGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCCG GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTCGAAAG CGGCGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAGCAGCAG GCGCAACCGT TGCCGACAAA GCAGCGGTTT GGGCATACCC
201 TTTAATTTAT AAGGTTAACG CGCCGTCCGA AGACGAGCTG CCGTGCTCA
251 AAGAAGGACA GACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAAG CCTTGCGCGC CAAGAAAGTG AACGCGCTGG CAATGGACAT
351 GGTGCCCCGC ATTTGCGCGC GCGAGGCTTT GGACGNTTGT TCTTNGATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTNTTCA CCGGCCAAAT TACTGCCGCA GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGTGT TCGATACCCG CCTG.AAGTG
601 GCGGAACAAT TAGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 GCAAGAAATCG GGCGGCAGCG GCGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAGATG AAGCTTTTGT CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCN
801 NNTNANCAAA GAAATGGTCG AAAGCATGAA ACCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GGCGACGGGC GGCAACTGCG AACTACCAA ACAGGGCGAA
901 TTGTTCTGTA CCGGCAACGG CGTGAAAATC ATCGGTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTGCGAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGCTGGAC
1051 TTCTGAAGAC TGATTATCCG CAACATGACC GTTACCCGCG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCGCA TTCAAGTTTC CGCCCAACCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGCGCCT GCCGCCAAGC CCGAACCGAA ACCCGTTCCT

```



```

1201 CTGTGGAAAA AACTCGCGCC CGCCNTNATC GCCGCCGTGT TGGTACTGTG
1251 GGTCGGCGCG GTCGCACCCG CAGCATTCCT GAACCACTTT ATCGTCTTCG
1301 TCCTCGCCTG CGTCATCGGC TACTATGTCG TTTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTGACCAAC GCCATTTCCG GCATCATCGT
1401 CGTCGGCGCG CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCAGCA TCAACATCTT CGGCGGCTTC
1501 TTTGTAACGC GCGGATGCT GAATATGTTT AGGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 642; ORF 155.a>:

```

a155.pep
  1 MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
 51 QAAGATVADK AAVWAYPLIY KVNAPSEDEL PLLKEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMPV ISRAQALDXL SXMANISGYR AVIEAANAFA
151 RXFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRVFDTRLXV
201 AEQLESMGGK FLKLDFPQES GSGGDGYAKV MSDEFIAAEM KLFAEQAKEV
251 DIIITTAaip GKPAKXXXX EMVESMKPGS VIVDLAAATG GNCELTKQGE
301 LEVGTNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTRDGEITFP PPPIQVSAQP QQTPSEKAAP AAKPEPKVPV
401 LWKKLAPAXI AAVLVLVWGA VAPAAFLNHF IVFVLACVIG YYVWVNVSHS
451 LHTPLMSVTN AISGIIIVGA LLQIGQGNF VSLLSFVAIL IASINIFGGF
501 FVTRRLNMF RKG*

```

m155/a155 95.3% identity in 513 aa overlap

m155.pep	10	20	30	40	50	60
	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK					
a155	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQAAGATVADK					
	10	20	30	40	50	60
m155.pep	70	80	90	100	110	120
	AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPV					
a155	AAVWAYPLIYKVNAPSEDELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPV					
	70	80	90	100	110	120
m155.pep	130	140	150	160	170	180
	ISRAQALDALSSMANISGYRAVIEAANAFAFRFFTGQITAAGKVPPAQVLVIGAGVAGLAA					
a155	ISRAQALDXLSXMANISGYRAVIEAANAFAFRXFTGQITAAGKVPPAQVLVIGAGVAGLAA					
	130	140	150	160	170	180
m155.pep	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDFPQESGSGGDGYAKVMSDEFIAAEM					
a155	IGTANSLGAVRVFDTRLXVAEQLESMGGKFLKLDFPQESGSGGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
m155.pep	250	260	270	280	290	300
	KLFAEQAKEVDIIITTAaipGKPAKPKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
a155	KLFAEQAKEVDIIITTAaipGKPAKXXXXKEMVESMKPGSVIVDLAAATGGNCELTKQGE					
	250	260	270	280	290	300
m155.pep	310	320	330	340	350	360
	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
a155	LFVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	310	320	330	340	350	360
m155.pep	370	380	390	400	410	420
	VTHDGEITFPPPIQVSAQPQQTPSEKAVPAAPKPEPKVPLWKKLAPAVIAAVLVLVWGA					
a155	VTRDGEITFPPPIQVSAQPQQTPSEKAAPKPEPKVPLWKKLAPAXIAAVLVLVWGA					
	370	380	390	400	410	420

```

g156.seq
1  ATGACTTTTCG CCTATTGGTG CATTCTGATT GCCTGCCTAT TGCCGCTTTT
51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCGGTGT AAAGACAACC
101 ACAATCCTCG CGGTTTTCTG GCACATACGC AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTGCAACCGT TTGCCGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGC ATTGTTTCAT CTGTTCCGCT TCGCCTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT GCGCTCGCTG ATGTGGGCGG GCGGATTTCG
351 CTGCACCGTC GGACTGTTTG TCGCGGCTGC TTGA

```

```
g156.pep
  1  MTFAYWCILI  ACLLPFCAA  YAKKAGGFRF  KDNHNPRGFL  AHTQGAAARA
51  HAAQQNGFEA  FAPFAAAVL  AHATGNAGQA  TVNTLAGLFI  LFLRAFIWCY
101 IADKAALRSL  MWAGGFACTV  GLEVAAA*
```

```
m156.seq
1  ATGACTTTTCG CCTATTGGTG TATTCTGATT GCCTGCCTAT TGCCGCTTTT
51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCGGTGT AAAGACAACC
101 ACAATCCGCG CGGTTTTTCTA GCGCACACGC AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCAC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCCGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC GGCGCAATCG ACCATCAACA
251 CGCTTGCCTG CCTGTTTCAT CTGTTCCGCT TCGCCTTTAT CTGGTGCTAT
301 ATCGCCGACA AAGCCGCTAT GCGCTCACTG ATGTGGGCAG GCGGATTTGC
351 CTGCACCGTC GGGCTGTTTG TCGCGGCTGC TTGA
```

```
m156.pep
  1  MTFAYWCILI  ACLLPFCA  YAKKAGGFRF  KDNHNPRGFL  AHTQGAAARA
51  HAAQONGFEA  FAPFAAVLT  AHATGNAAQ  S  TINTLACLEI  LFLRAFIWCY
101 IADKAAMRSL  MWAGGFACTV  GLFVAAA*
```

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m156.pep	MTFAYWCILIAACLLPLFCAAYAKKAGGRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA					
g156	MTFAYWCILIAACLLPLFCAAYAKKAGGRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m156.pep	FAPFAAAVLTAHATGNAAQSTINTLACLFILFRLAFIWCYIADKAAMRSLMWAGGFACTV					

```

g156      FAPFAAAVLTAHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWAGGFACTV
              70      80      90      100      110      120

m156.pep  GLFVAAAX
           |||||
g156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 647>:

```

a156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTACCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCGCG CGATTTTCTG GCGCGCACGC AAGGCACAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCAGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG CCTGTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT ACGCTCGCTG ATGTGGGTGG GCGGATTGTG
351 CTGCACCGTC GGGCTGTTTG TCGTGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 648; ORF 156.a>:

```

a156.pep
1  MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAAARA
51 HAAQQNGFEA FAPFAAAVLTAHATGNAGQA TVNTLAGLFI LRLAFIWCY
101 IADKAALRSL MWVGGFVCTV GLFVAA*

```

m156/a156 90.6% identity in 127 aa overlap

```

              10      20      30      40      50      60
m156.pep  MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAARAHAAQQNGFEA
           |||||
a156      MTFAYWCILIAYLLPLFCAAYAKKAGGFRFKDNHNPRDFLARTQGTAAARAHAAQQNGFEA
              10      20      30      40      50      60

              70      80      90      100     110     120
m156.pep  FAPFAAAVLTAHATGNAAQSTINTLACLFI LRLAFIWCYIADKAAMRSLMWAGGFACTV
           |||||
a156      FAPFAAAVLTAHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWVGGFVCTV
              70      80      90      100     110     120

m156.pep  GLFVAAAX
           |||||
a156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 649>:

```

g157.seq
1  atgaggaacg aggAAAAACg cgcctgCGc cgcgaattgC gCgGgcgGcg
51 ttcgCAAAATg GgGcgagacg tGCGGgCGGC GGCGGgCgata Aaaatcaacc
101 gcctgctcaa aCGTtatatc AAGCGCggtc gGaAaatcgG CGTGTATTgG
151 cCGATGGGCA AGGAATTGcg TTTGGGCGGc tTgtcCGCG CGGCGCAAAA
201 ACGCGGCGCA AAactctatc tgccttATAT CGAACCGCAC ACGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAACGCGGAA TGGAACGGGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTGCGCATA GACCGGAAG
401 GCTACCGTTT GGGGCGAGCA GCGGCTATT ACGATGCGAC GCTTTCGGCG
451 ATGAAATACC GTTTGCAGGC GAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTCCAC GCGAGGCGCA CGACCTGCCG CTGGACGGTT
551 TTGTATCGGA AGCGGGGATA TTGTGTTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 650; ORF 157.ng>:

```
g157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAAAI KINRLLKRYI KRGRKIGVYW
 51 PMGKELRLGG FVRAAQKRGK KLYLPYIEPH TRRMWFTYPY ERGMERERKR
101 GRAKLHVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGAFACQLVD RLPREAHDLF LDGFVSEAGI LCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 651>:

```
m157.seq
  1 ATGAGGAACG AGGAAAAACG CGCCCTGCGC CGCGAATTGC GCGGGCGGCG
 51 TTCGCAAATG GGGCGGGACG TGGCGGCGGC GGCAACGGTA AAAATCAACC
101 ACCTGCTCAA ACGTTATATT AAAAAAGGGC GGAAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCG GAACTCTACC TGCCTTATAT CGAACCGCGT TCGCGCGGGA
251 TGTGGTTTAC GCCGTATCCT GCCGTAGGAG TAAACAAGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGTCCGA AAAAGCGTGT
351 GCATGATTG AACCTCCTGC TTGTGCCAGT GGTCCGGTATG GACAGGCTGG
401 GCTACCGCTT GGGACAGGCA GCGGCTATT ACGATGCGAC GCTTTCAGCG
451 ATGAAATACC GTTTGCAGGC AAAAACCGTG GCGGTGGGCT TTGCTGCCA
501 GTTGGTGGAC AGGCTGCCGG TCGAGGCGCA CGACCGGTCT TTGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGTTTTT AG
```

This corresponds to the amino acid sequence <SEQ ID 652; ORF 157>:

```
m157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAATV KINHLLKRYI KKGRKIGVYW
 51 PMGKELRLDG FVRAAQKRGK ELYLPYIEPR SRRMWFTYPY ADGVKQERKR
101 GRAKLHVPQF AGRKKRVHDL NLLVPVVGVM DRLGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGAFACQLVD RLPVEAHDRS LDGFVSEAGI LCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m157 / g157 88.1% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALR	RELGRRSQM	GRDVRAAATV	KINHLLKRYI	KKGRKIGVYW	PMGKELRLDG
g157	MRNEEKRALR	RELGRRSQM	GRDVRAAAAI	KINRLLKRYI	KRGRKIGVYW	PMGKELRLGG
	70	80	90	100	110	120
m157.pep	FVRAAQKRG	AELYPYIEP	SRMRWFTYP	PADGVKQER	KRGRAKLHVP	QFAGRKKRVHDL
g157	FVRAAQKRG	AKLYLPYIE	PHTRRMWFT	YPYPERGME	REKRGRAKLH	VPQFAGRKIRVHGL
	130	140	150	160	170	180
m157.pep	NLLVPVVG	MDRLGYRLG	QAGGYDATL	SAMKYRLQAK	TVGVGFACQL	VDRLPVEAHDRS
g157	SVLLVPLV	GIDREGYRL	GQAGGYDAT	LSAMKYRLQAK	TVGVGFACQL	VDRLPREAHDLP
	190					
m157.pep	LDGFVSEAG	ILCFX				
g157	LDGFVSEAG	ILCFX				
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 653>:

```
a157.seq
  1 ATGAGGAACG AGGAAAAACA CGCCTTGCGC CGAGAGTTGC GCCGCGCCCG
 51 CGCGCAGATG GGGCATCAAG GCGGTTGGC GCGGGGCAA ACGATTAACC
```

451

```

101 GCCTGCTCAA ACGTTATATC AAGCGTGGTC GGAAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCA AAACCTTATC TGCCTTATAT CGAACCGCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAAAGCGGAA TGGAAACGGGA GCGCATACGG
301 GGCAGGGCGA AGTTGAACGT GCCGCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTGCGCATA GACCGCGAGG
401 GCTACCGCTT AGGACAGGCA GCGGCTATT ACGATGCGAC GCTTGCGGCG
451 ATGAAATACC GTTTGCAGGC AAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTTGTGGAC AGGCTGCCGC GCGAACCGCA CGATCTGCTG CTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGCTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 654; ORF 157.a>:

a157.pep

```

1 MRNEEKHALR RELRRARAQM GHQGRLAAGQ TINRLLKRYI KRGRKIGVYW
51 PMGKELRLDG FVRAAQKRG A KLYLPYIEPR SRRMWFTYPY ESGMERERIR
101 GRAKLNVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLAA
151 MKYRLQAKTV GVGAFACQFVD RLPREPHDLL LDGFVSEAGI LCF*

```

m157/a157 82.4% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALRRELGRRS	QMGDRVRAAATVKINHL	LKRYIKKGRKIGVYW	PMGKELRLDG		
a157	MRNEEKHALRRELRRARA	QMGHQR	LAAGQTINRLLKRYIKR	GRKIGVYWPMGKELRLDG		
	10	20	30	40	50	60
m157.pep	FVRAAQKRGAE	LYLPYIEPR	SRRMWFTYPY	PADGVKQERKR	GRAKLHVPQF	AGRKKRVHDL
a157	FVRAAQKRGAKLYLPYIEPR	SRRMWFTYPY	PESG	MERERIRGRAKLNVPQF	AGRKIRVHGL	
	70	80	90	100	110	120
m157.pep	NLLLV	PVVGMDRLGYRLG	QAGGYDATLSAMKYRLQAKTV	GVGFACQLVDR	LPVEAHDRS	
a157	SVLLV	PLVGIDREGYRLG	QAGGYDATLAAMKYRLQAKTV	GVGFACQFVDRLPREPHDLL		
	130	140	150	160	170	180
m157.pep	LDGFVSEAGILCFX					
a157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 655>:

g158.seq

```

1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
51 CGGCAGCTTC AGCCGTGCGG CGgagcAGTT GGAGAtggCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGCGT GAACCTGctc
151 aACCGCACCA CGCGGCAACT CAATCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGCTGGCAGT GCACGAAGTA CCGCAAGGCG TGTGCGCGT GGATTCCGCG
301 ATGCcgatgg TGCTGCATCT GCTGGCGCCG CTGGCAGCAA AATTCAACGA
351 ACGCTATCCG CATATCgaC TTTCGCTCGT TTCTTCCGAa ggctatatca
401 atctGattGA Acgcaaagtc gAtatTGCTT TACGGGCCGG AGAATTGGAC
451 GATTCCGGGC TCGTGCACG CCATCTGTTT GACAGCCACT TCCGCTagT
501 cgCCAGTCTT GAATATTTAG CAAAACACGG CACGCCACAA TCTGCAGAAAG
551 atcTTGCCAA CCATCAATGT TTAGGCTTCA CAGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGAtgC GCAGGGAAAT CCCTATAAAA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTGTGTC CTTTCAAGtt
701 gCGGTATTGC TTGCTTATCA GATTTTTTGG TTGACAACGA CATCACTGAA
751 GGAAAGTTAA TTCCcctatt cgCCGAACAA ACCTCCAATA AAACACACCC

```

```

801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG
851 TATTTTTGGA TTTTITAGTG AAGGAACTGG GAAAAAATAT GAATAGAACG
901 AATACCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 656; ORF 158.ng>:

```

g158.pep
  1 MKTNSEELTV FVQVVESGSF SRAAEQLEMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLNLT EEGAQYFRRA QRILQEMAAA ETEMLAVHEV PQGVLRVDSA
101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD
151 DSGLRARHLF DSHFRVVASP EYLAKHGTPQ SAEDLANHQC LGFTEPGSLN
201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSSCGIACLS DFLVDNDITE
251 GKLIPLFAEQ TSNKTHPFNA VYYSKAVNLR RLRVFLDFLV KELGKNMNR
301 NTK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 657>:

```

m158.seq
  1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGAAAG
 51 CGGCAGCTTC AGCCGTGCGG CCGAGCAGTT GGCGATGGCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC
151 AACCGCACCA CGCGGCAACT CAGTCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGCTGGCAGT GCACGAAATA CCGCAAGGCG TGTGAGCGT GGATTCGCGC
301 ATGCCGATGG TGCTGCATCT GCTGGCGCGG CTGGCAGCAA AATTCAACGA
351 ACGCTATCCG CATATCCGAC TTTCGCTCGT TTCTTCCGAA GGCTATATCA
401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCGCG AGAATTGGAC
451 GATTCGGGCG TGCGTGCACG CCATCTGTTT GACAGCCGCT TCCGCGTAAT
501 GCCAGTCCTT GAATACCTGG CAAAACACGG CACGCCGCAA TCTACAGAAG
551 AGCTTGCCGG CCACCAATGT TTAGGCTTCA CCGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGATGC GCAGGGAAAT CCCTATAAGA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGGTT
701 GCGGTATTGT TTGCTTATCA GATTTTTTGG TTGACAACGA CATCGCTGAA
751 GGAAAGTTAA TTCCCCTGCT CGCCGAACAA ACCTCCGATA AAACACACCC
801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAATCTC CGCTTACGCG
851 TATTTTTGGA TTTTITAGTG GAGGAACTGG GAAACAATCT CTGTGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 658; ORF 158>:

```

m158.pep
  1 MKTNSEELTV FVQVVESGSF SRAAEQLAMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLSLT EEGAQYFRRA QRILQEMAAA ETEMLAVHEI PQGVLSVDSA
101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD
151 DSGLRARHLF DSRFRVIASP EYLAKHGTPQ STEELAGHQC LGFTEPGSLN
201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSGCGIVCLS DFLVDNDIAE
251 GKLIPLLAEQ TSDKTHPFNA VYYSKAVNLR RLRVFLDFLV EELGNLNCG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m158 / g158 94.3% identity in 297 aa overlap

```

          10      20      30      40      50      60
m158.pep  MKTNSEELTVFVQVVESGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT
          |||||
g158       MKTNSEELTVFVQVVESGSFSRAAEQLEMANSAVSRIVKRLEEKLGVNLLNRTTRQLNLT
          10      20      30      40      50      60

          70      80      90     100     110     120
m158.pep  EEGAQYFRRAQRILQEMAAAEETEMLAHVHEIPQGVLSVDSAMPMLVHLLAPLAAKFNERYP
          |||||
g158       EEGAQYFRRAQRILQEMAAAEETEMLAHVHEVPQGVLRVDSAMPMLVHLLAPLAAKFNERYP
          70      80      90     100     110     120

```

453

	130	140	150	160	170	180
m158.pep	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
g158	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSHFRVVASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
	: : :					
g158	SAEDLANHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSSCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSKAVNLRRLRVFLDFLVEELGNNLCGX					
		: : :				
g158	DFLVDNDITEGKLIPLFAEQTSNKTHPFNAVYYSKAVNLRRLRVFLDFLVKELGKNMNR					
	250	260	270	280	290	300
g158	NTKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 659>:

a158.seq

1	ATGAAAACCA	ATTGAGAAGA	ACTGACCGTA	TTTGTTCAG	TGGTGGAAAG
51	CGGCAGCTTC	AGCCGTGCGG	CGGAGCAGTT	GGCGATGGCA	AATTCTGCCG
101	TAAGCCGCAT	CGTCAAACGG	CTGGAGGAAA	AGTTGGGTGT	GAACCTGCTC
151	AACCGCACCA	CGCGGCAACT	CAGTCTGACG	GAAGAAGGCG	CGCAATATTT
201	CCGCCGCGCG	CAGAGAAATCC	TGCAAGAAAT	GGCAGCGGCG	GAAACCGAAA
251	TGCTGGCAGT	GCACGAAATA	CCGCAAGGCG	TGTTGCGCGT	GGATTCCGCG
301	ATGCCGATGG	TGCTGCATCT	GCTGGCGCGG	CTGGCAGCAA	AATTCACGCA
351	ACGCTATCCG	CATATCCGAC	TTTCGCTCGT	TTCTTCCGAA	GGCTATATCA
401	ATCTGATTGA	ACGCAAAGTC	GATATTGCCT	TACGGGCCGG	AGAATTGGAC
451	GATTCCGGGC	TGCGTGACAG	CCATCTGTTT	GACAGCCGCT	TCCGCGTAAT
501	CGCCAGTCCT	GAATACCTGG	CAAAACACGG	CACGCCGCAA	TCTACAGAAG
551	AGCTTGCCCG	CCACCAATGT	TAGGCTTCA	CCGAACCCGG	TTCTCTAAAT
601	ACATGGGCGG	TTTTAGATGC	GCAGGAAAT	CCCTATAAGA	TTTCACCGCA
651	CTTTACCGCC	AGCAGCGGTG	AAATCTTACG	CTCGTTGTGC	CTTTCACGTT
701	GCGGTATTGC	TTGCTTATCA	GATTTTTTGG	TTGACAACGA	CATCGCTGAA
751	GGAAAGTTAA	TTCCCCTGCT	CGCCGAACAA	ACCTCCAATA	AAACGCACCC
801	CTTTAATGCT	GTTTATTACA	GCGATAAAGC	CGTCAACCTC	CGCTTACGCG
851	TATTTTGGGA	TTTTTTAGTG	GAGGAACTGG	GAAACAATCT	CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 660; ORF 158.a>:

a158.pep

1	MKTNSEELTV	FVQVVESGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL
51	NRTTRQLSLT	EEGAQYFRRA	QRILQEMAAA	ETEMLAVHEI	PQGVLRVDSA
101	MPMVLHLLAP	LAAGFNERYP	HIRLSLVSE	GYINLIERKV	DIALRAGELD
151	DSGLRARHLF	DSRFRVIASP	EYLAKHGTPQ	STEELAGHQC	LGFTTEPGSLN
201	TWAVLDAQGN	PYKISPHFTA	SSGEILRSLC	LSGCGIACLS	DFLVDNDIAE
251	GKLIPLLAEQ	TSNKTTHPFNA	VYYSKAVNLR	RLRVFLDFLV	EELGNNLCG*

m158/a158 99.0% identity in 299 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVESGSFSRAAEQLAMANS	AVSRIVKR	LEEKLGVNLL	NRTTRQLSLT		
a158	MKTNSEELTVFVQVVESGSFSRAAEQLAMANS	AVSRIVKR	LEEKLGVNLL	NRTTRQLSLT		
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRRAQRILQEMAAE	ETEMLAVHEI	PQGVLSVDS	AMPMVLHLLAP	LAAGFNERYP	
a158	EEGAQYFRRAQRILQEMAAE	ETEMLAVHEI	PQGVLRVDS	AMPMVLHLLAP	LAAGFNERYP	
	70	80	90	100	110	120

	130	140	150	160	170	180
m158.pep	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
a158	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
a158	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
a158	DFLVDNDIAEGKLIPLLAEQTSNKTTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 661>:

```

g160.seq
1  ATGGAcattc  tgGACAAact  ggtcgatCTC  GCccaATTGA  CGGGCAGTGC
51  GGATGTGCAG  TgcctTTTGG  GCGGACAATG  gcATGaaacc  TTGCAACGCG
101 AAGGGCTGGT  ACACATTGTT  ACGGCGGGCA  GCGGTTATCT  CTGCATCGAC
151 GCGGAACTT  CCCGCGTCC  GGTGCGCACG  GCGGATATTG  TATTTTCC
201 GCGCGCTTG  GGTGATGTGT  TGAGCCACGA  CGGAAAATAC  GGAGAAAGTT
251 TACAACCGGA  CATAACGACA  AACGGCACAT  TTATGGTCAA  ACAGTGCGGC
301 AACGGGCTGG  ATATGAGCCT  GTTTTGCGCC  CGTTTCCGCT  ACGACACCCA
351 CGCCGATTG  ATGAACGGGC  TGCCGGAAC  CGTTTTCTG  AACATTGCC
401 ATCCAAGTTT  GCAGTATGTG  GTTCAATGC  TGCAACTGGA  AAGCGAAAA
451 CCTTTGACGG  GGACGGTTTC  CGTGGTCAAC  GCATTACCGT  CCGTCTGCT
501 GGTGCTTATC  CTGCGCGCCT  ATCTCGAACA  GGATAAGGAT  GTCGAACCT
551 CGGCGTATT  GAAAGGTTGG  CAGGACAAAC  GTTTGGGACA  TTTGATCCAA
601 AAGGTGATAG  ACAACCGGA  AGACGAATGG  AATATTGACA  AAATGGTTGC
651 CGCCGCCAAT  ATGTCGCGCG  CGCAACTGAT  GCGCCGCTTC  AAAAGCCAAG
701 TCGGACTCAG  CCCGACGCC  TTTGTGAACC  ATATCCGCCT  GCAAAAAGGC
751 GCATTGCTGC  TGAAGAAAAC  CCCGATTTCG  GTTTTGAGAG  TCGCGCTGTC
801 GGTGGGCTTT  CAGTCGAAA  CGCATTTTCG  CAAGGCGTTC  AAACGGCAAT
851 ATCACGTTTC  GCCGGGGCAA  TACCGGAAAG  AAGCGGGCA  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 662; ORF 160.ng>:

```

g160.pep
1  MDILDKLVDL  AQLTGSADVQ  CLLGGQWHET  LQREGLVHIV  TAGSGYLCID
51  GETSPRPVGT  GDIVFFPRGL  GHVLSHDGKY  GESLQPDIRQ  NGTFMVKQCG
101 NGLDMSLFCA  RFRYDTHADL  MNGLPETVFL  NIAHPSLQYV  VSMLQLESEK
151 PLTGTVSVDN  ALPSVLLVLI  LRAYLEQDKD  VELSGVLKGW  QDKRLGHLIQ
201 KVIDKPEDEW  NIDKMVAAN  MSRAQLMRRF  KSQVGLSPHA  FVNHIRLQKG
251 ALLLKKTPDS  VLEVALSVGF  QSETHFGKAF  KRQYHVSPGQ  YRKEGGQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 663>:

```

m160.seq
1  ATGGACATTC  TGGACAAACT  GGTGATTTTC  GCCCAATTGA  CGGGCAGTGT
51  GGATGTGCAG  TGCCTTTTGG  GCGGACAATG  GTCGGTACGG  CATGAAACCT
101 TGCAACGCGA  AGGATTGGTA  CACATTGTTA  CATCGGGCAG  CGGTATCTC
151 TGCATCGACG  GCGAACTTC  CCCGCGTCCG  GTCAGTACAG  GGGATATTGT
201 ATTTTCCCG  CGCGGCTTGG  GTCATGTGTT  GAGCCACGAC  GGAAAATGCG
251 GAGAAAGTTT  ACAACCGGAT  ATGCGGCAGC  ACGGTGCGTT  TACCGTCAAG
301 CAGTGCGGCA  ACGGACAGGA  TATGAGCCTG  TTTTGCGCCC  GTTTCCGCTA
351 CGACACCCAC  GCCGATTGTA  TGAACGGGCT  GCCTGAAACC  GTTTTCTGA
401 ACATTGCCCA  TCCGAGTTTA  CAGTATGTGG  TTTCAATGCT  GCAACTGGAA
451 AGCAAAAAAC  CTTTGACGGG  GACGTTTCC  ATGGTCAACG  CATGTCTGTC

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455

```

501 CGTCCTGCTG GTGCTTATCC TGC GCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTGACAAA
651 AATGGTGGCG GCTGCCAATA TGTCGCGCGC GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CCGACTCAGC CCGCAGCGCT TTGTGAACCA TATCCGCCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTGTGCGGT
801 CGCACTGTCG GTAGGCTTTC AGTCGGAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAGA AggCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 664; ORF 160>:

```

m160.pep
1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGLQPD MRQHGAFVTK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMAA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m160 / g160 93.4% identity in 301 aa overlap

m160.pep	10	20	30	40	50	60
	MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP					
g160	MDILDKLVDLAQLTGSADVQCLLGGQW---HETLQREGLV HIVTAGSGYL CIDGETSPRP					
	10	20	30	40	50	
m160.pep	70	80	90	100	110	120
	VSTGDIVFFPRGLGHVLSHDGKCGESLQPD MRQHGAFVTK QCGNGQDMSL FCARFRYDTH					
g160	VGTGDIVFFPRGLGHVLSHDGKYGESLQPD IRQNGTFMVKQCGNGLDMSL FCARFRYDTH					
	60	70	80	90	100	110
m160.pep	130	140	150	160	170	180
	ADLMNGLPETVFLNIAHPSLQYVVSMLQLESKKPLTGTVSMVNALSSVLLVLILRAYLEQ					
g160	ADLMNGLPETVFLNIAHPSLQYVVSMLQLESEKPLTGTVSVVNALPSVLLVLILRAYLEQ					
	120	130	140	150	160	170
m160.pep	190	200	210	220	230	240
	DKDVELSGVLKGWQDKRLGHLIQKVIDKPEDEWNVDKMAAANMSRAQLMRRFKSRVGLS					
g160	DKDVELSGVLKGWQDKRLGHLIQKVIDKPEDEWNIDKMAAANMSRAQLMRRFKSQVGLS					
	180	190	200	210	220	230
m160.pep	250	260	270	280	290	300
	PHAFVNHIRLQKGALLLKNPDSVLSVALSVGFQSETHFGKAFKRQYHVSPGQYRKEGGQ					
g160	PHAFVNHIRLQKGALLLKNPDSVLEVALSVGFQSETHFGKAFKRQYHVSPGQYRKEGGQ					
	240	250	260	270	280	290
m160.pep	KX					
g160	KX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 665>:

```

a160.seq
1 ATGGACATTC TGGACAACT GGTCGATTTC GCCCAATTGA CGGGCAGTGT
51 GGATGTGCAG TGCCTTTTGG GCGGACAATG GTCGGTACGG CATGAAACCT

```

```

101 TGCAACGCGA AGGATTGGTA CACATTGTGA CATCGGGCAG CGGCTATCTC
151 TGCATCGACG GCGAAACTTC CCCGCGTCCG GTCAGTACAG GGGATATTGT
201 ATTTTTCCTG CGCGGCTTGG GTCATGTGTT GAGCCACGAC GGAAATGCG
251 GAGAAAGTTT ACAACCGGAT ATGCGGCAGC ACGGTGCGTT TACGGTCAAG
301 CAGTGCGGCA ACGGACAGGA TATGAGCCTG TTTTGCGCCC GTTTCGCGTA
351 CGACACCCAC GCGATTTGA TGAACGGGCT GCCTGAAACC GTTTTCTGA
401 ACATTGCCCA TCCGAGTTTA CAGTATGTGG TTTCAATGCT GCAACTGGAA
451 AGCAAAAAAC CTTTGACGGG GACGGTTTCC ATGGTCAACG CATTGTCGTC
501 CGTCCTGCTG GTGCTTATCC TCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTGCGCGCG GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTTGTCCGT
801 CGCACTGTCG GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAAGA AGGCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 666; ORF 160.a>:

```

a160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
 51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKNP PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

m160/a160 100.0% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||
a160      MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          10      20      30      40      50      60

          70      80      90      100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          |||
a160      VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          70      80      90      100     110     120

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLES KKPLTGTV SMVNALSSVLL VLILRAYLEQ
          |||
a160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLES KKPLTGTV SMVNALSSVLL VLILRAYLEQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          |||
a160      DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          190     200     210     220     230     240

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLLKNP DSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          |||
a160      PHAFVNHIRL QKGALLLKNP DSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          250     260     270     280     290     300

m160.pep KX
          ||
a160      KX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 667>:

```
g161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTCACGTTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTACGC TCGGTGCTGC CGCCGTATTG CGGCGGACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCCT TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGAC AACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTttg GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GGCGGTGCTG CTCCTTGGTT
401 TTGCCGCGCT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTCAAGAA
451 CCGGCGGCAC TCGCCGGGCT GGCGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGCAACC GGCGTGGCGA TGTCGTCggt ttgggcgacg
601 Ctgaccggct ggCACAcccT GTCCTTTcca tcggcagttt ATCtgtCGGG
651 CATCGGCGTG tccgcgCtgA TTGCCCAaCT GtcgatgAcg cGCGcctaca
701 aaGTCGGCGA CAAATTCACG GTTGCTCGC tttcctaTat gaccgtcGTC
751 TTTTCCGCC CTTCTGCGC ATTTTCTCTg ggccaagagc ttttctggCA
801 GGAAATACTC GGTATGTGCA TCATTATcct CAGCGGCATT TTGAGCAGCA
851 TCCGCCCCAT TGCCTTCAAA CAGCGGCTGC AAGCCCTCTT CCGCCAAAGA
901 TAA
```

This corresponds to the amino acid sequence <SEQ ID 668; ORF 161.ng>:

```
g161.pep
1  MDTAKKDILG SGWMLVAAAC FTVMNVLIKE ASAKFALGSG ELVFWRMFLFS
51  TVTLGAAAVL RRDTRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLTTGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVVLL LNPSFRSGQE
151 PAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSAT GVAMSSVWAT
201 LTGWHTLSPF SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPIAFK QRLQALFRQR
301 *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 669>:

```
m161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTTACCATTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA mCTTCCGCAC
201 GCCCCATTGG AAAAACCCT TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGGC CACTGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GGCGGTGCTG CTCCTTGGTT
401 TTGCCGCGCT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTCAAGAA
451 ACGGCGGCAC TCGCCGGGCT GGCGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCGTCGGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTGCTG
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATGACG CGCGCCTACA
701 AAGTCGGCGA CAAATTCACG GTTGCTCGC TTTCTATAT GACCGCTGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTCTCTG GCGGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA
851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA
```

This corresponds to the amino acid sequence <SEQ ID 670; ORF 161>:

```
m161.pep
1  MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMFLFS
51  TVALGAAAVL RRDXFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVVLL LNPSFRSGQE
```

151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
 201 LTGWHTLSFP SAVYLSCIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
 251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
 301 *

Computer analysis of this amino acid sequence gave the following results:
 Homology with a predicted ORF from *N. gonorrhoeae*

m161 / g161 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
	: : : :					
g161	MDTAKKDILGSGWMLVAAACFTVMNVLIKEASAKFALGSGELVFWRMFLSTVTLGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKHNLRSMVGTGAMLLFYAVTHLPLATGVTLSTYSIFLAVFSFLILKE					
	: : : : :					
g161	RRDTFRTPHWKHNLRSMVGTGAMLLFYAVTHLPLTTGVTLSTYSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGFAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	: : : : :					
g161	RISVYTQAVLLLGFAGVLLLNPSFRSGQEPALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFPSAVYLSGIGVSALIAQLSMTRAYKVGDKFT					
	: : : : :					
g161	WRVVFYLSATGVAMSSVWATLTGWHTLSFPSAVYLSGIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	: : : : :					
g161	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPIAFKQRLQALFRQR					
	250	260	270	280	290	300
m161.pep	X					
g161	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 671>:

a161.seq

1	ATGGATACCG	CAAAAAAAGA	CATTTTAGGA	TCGGGCTGGA	TGCTGGTGGC
51	GGCGGCCTGC	TTTACCATTA	TGAACGTATT	GATTAAAGAG	GCATCGGCAA
101	AATTTGCCCT	CGGCAGCGGC	GAATTGGTCT	TTTGGCGCAT	GCTGTTTTCA
151	ACCGTTGCGC	TCGGGGCTGC	CGCCGTATTG	CGTCGGGACA	CCTTCCGCAC
201	GCCCCATTGG	AAAAACCACT	TAAACCGCAG	TATGGTCGGG	ACGGGGGCGA
251	TGCTGCTGCT	GTTTTACGCG	GTAACGCATC	TGCCTTTGGC	CACCGGCGTT
301	ACCCTGAGTT	ACACCTCGTC	GATTTTTTTG	GCGGTATTTT	CCTTCCTGAT
351	TTTGAAAGAA	CGGATTTCCG	TTTACACGCA	GCGGTGCTG	CTCCTTGCTT
401	TTGCCGGCGT	GGTATTGCTG	CTTAATCCCT	CGTTCCGCAG	CGGTCAAGAA
451	ACGGCGGCAC	TCGCCGGGCT	GGCGGGCGGC	GCGATGTCCG	GCTGGGCGTA
501	TTTGAAAGTG	CGCGAACTGT	CTTGGCGGG	CGAACCCGGC	TGGCGCGTCG
551	TGTTTTACCT	TCCGTGACA	GGTGTGGCGA	TGTCATCGGT	TTGGGCGACG
601	CTGACCGGCT	GGCACACCCT	GTCCTTTCCA	TCGGCAGTTT	ATCTGTCTGT
651	CATCGGCGTG	TCCGCGCTGA	TTGCCCACT	GTCGATGACG	CGCGCCTACA
701	AAGTCGGCGA	CAAATTCACG	GTTGCCTCGC	TTTCCTATAT	GACCGCTGTT
751	TTTTCCGCTC	TGTCTGCCGC	ATTTTTTCTG	GCCGAAGAGC	TTTTCTGGCA
801	GGAAATACTC	GGTATGTGCA	TCATCATCCT	CAGCGGTATT	TTGAGCAGCA

851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

This corresponds to the amino acid sequence <SEQ ID 672; ORF 161.a>:

a161.pep
1 MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRLFS
51 TVALGAAAVL RRDTFRTPHW KNHLNRSMSG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPSFRSGQE
151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
201 LTGWHTLSEF SAVYLSICIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL AEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

m161/a161 99.3% identity in 300 aa overlap

m161.pep	10	20	30	40	50	60
	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRLFSTVALGAAAVL					
a161	10	20	30	40	50	60
	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRLFSTVALGAAAVL					
m161.pep	70	80	90	100	110	120
	RRDXFRTPHWKNHLNRSMSGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
a161	70	80	90	100	110	120
	RRDTFRTPHWKNHLNRSMSGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
m161.pep	130	140	150	160	170	180
	RISVYTQAVLLLGAFAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	130	140	150	160	170	180
	RISVYTQAVLLLGAFAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
m161.pep	190	200	210	220	230	240
	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSICIGVSALIAQLSMTTRAYKVGDKFT					
a161	190	200	210	220	230	240
	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSICIGVSALIAQLSMTTRAYKVGDKFT					
m161.pep	250	260	270	280	290	300
	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	250	260	270	280	290	300
	VASLSYMTVVFSALSAAFFLAEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
m161.pep	X					
a161	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 673>:

g163.seq
1 ATGGTTATTT TGACGACTTT GTTTTTGTG TGTGTTTTGG TGGTATTGGT
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG gctCGACCGG GCAAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTATG TTTAACGTT TTCCATTTTt
151 ctgGGTTTTc tgctGATACT CTCGGTCAGC GGTTTGGGAA ACATcagGCT
201 AGGACGGGAT GAAGATGTGC CGGAATTCGG CTCCTGTCTG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCGTGGGCC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGTCGGCG CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GCGGTTACG
401 CCTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC

```

451 CGCTACAAAC TGCCGCTTGC CCTGCGTTCT TGTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCGG
651 CGTGCAGGTC TTGATTATCG CCGCCGTAAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GCGGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTGTGTT TTGGCGGCGG ACCCCACTGT
801 TTACCTGTTG TCGGCATTGC GCGACAACAT AGGGAACACT CTGGAATC
851 TGGTGCGCCT CAGTTTGAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTATTGG GCGTGGTGGT GTTCTTGGgc
951 gcCGTTTGTG GGTTTGTGTTA TCGCCGCGCAT TTCAAAGGGg cgcaccatCc
1001 gcgagtttgt CTTCCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAC TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CCCTGTTTTT TGTAACCTCT GCCGACTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGatgtcTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCGTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTCAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCGGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CACCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GGCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACTG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 674; ORF 163.ng>:

```

m163.pep
1  MVILTTLFFV CVLVVLVLTV PDQVQMWLDR AKEVIFTEFS WFYVLTFESIF
51  LGFLILSVS GLGNIRLGRD EDVPEFGFLS WLAMLFAAGM GVGLMFFGVA
101 EPLMHYFSDI TVGAPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPALARS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFGVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAADPTVYLL SAFGDNIGNY LGNLVRLSLK TYAYEREHKP
301 WFEWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVRIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 675>:

```

m163.seq
1  ATGGTTATTT TGACGACTTT GTTTTTGTG TGTGTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTATG TTTAACGTT TTCCATTTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT
201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCCTGTGC TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCAATTATT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GCGGTTACAG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCAG

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651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGCCTGAAGG TGTTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTTTGT TTGGCGGCGG GACCCACTGT
801 TTACCTGTTG TCGGCATTCT GCGACAACAT AGGGAACCTAC CTCGGAAATC
851 TGGTGCGCCT CAGTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGACCGT GCTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTGTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTCGGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTGT
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGAAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCCAGAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAATTCT GCGGATCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTGAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGT
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACAGACT GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AAATGTTTCA TCGGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GGCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 676; ORF 163>:

```

m163.pep
  1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WIFYVLTFSIF
 51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101  EPLMHYFSDI TAGTPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151  RYKLPALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201  LGAGLQEMGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSLNL
251  GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301  WFESWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGVL
351  WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401  LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451  RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501  FWTGGKWKER LVQIMSQTQE QDILKFLKQT ASPAMHELQR ELSEEYGLSV
551  RVDKMFHRDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601  HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQGEL
651  MAHEQVELAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m163 / g163 98.6% identity in 660 aa overlap

      10      20      30      40      50      60
m163.pep  MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWIFYVLTFSIFLGFLILSVS
          |||
g163      MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWIFYVLTFSIFLGFLILSVS
          |||

      10      20      30      40      50      60

      70      80      90     100     110     120
m163.pep  SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSIDITAGTPEHRQQ
          :|||
g163      GLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSIDITVGAPEHRQQ
          :|||

      70      80      90     100     110     120

      130     140     150     160     170     180

```

m163.pep	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
g163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
	130 140 150 160 170 180
m163.pep	190 200 210 220 230 240
	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
g163	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
	190 200 210 220 230 240
m163.pep	250 260 270 280 290 300
	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
g163	GVKVLSELNLGLAFLLLFFVLAADPTVYLLSAFGDNIGNYLGNLVRLSLKTYAYEREHKP
	250 260 270 280 290 300
m163.pep	310 320 330 340 350 360
	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGLVFTVFGNTAI
g163	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGLVFTVFGNTAI
	310 320 330 340 350 360
m163.pep	370 380 390 400 410 420
	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
g163	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
	370 380 390 400 410 420
m163.pep	430 440 450 460 470 480
	ITSRDKGLSAPRWQAVMWGLMSAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
g163	ITSRDKGLSAPRWQAVMWGLMSAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
	430 440 450 460 470 480
m163.pep	490 500 510 520 530 540
	WKGLSADKKYFETRNVNPTSVFWTGGKWKERLVQIMSQTQEQDILKFLKQTASPAMHELQR
g163	WKGLSADKKYFETRNVNPTSVFWTGGKWKERLVRIMSQTQEQDILKFLKHTASPAMHELQR
	490 500 510 520 530 540
m163.pep	550 560 570 580 590 600
	ELSEEYGLSVRVDKMEHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
g163	ELSEEYGLSVRVDKMEHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
	550 560 570 580 590 600
m163.pep	610 620 630 640 650 660
	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
g163	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
	610 620 630 640 650 660
m163.pep	X
g163	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 677>:

```

a163.seq
1  ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTGG TGGTATTGGT
51  TTAAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTTATG TTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT

```



```

201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GCGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GCGGTTACAG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTTCG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATAGGCTGG ATTGCCGAAA ACAGCTTCAG
651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGTGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGTCTTTCGT TTTTGCTGCT GTTTTTTGTT TTGGCGGCGG GTCCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACATC CTCGGAATC
851 TGGTGCGCCT CAGTTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTGCGGGTT TGCTCATCC CCGGCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAGTG CTCGAAAAGA TGACCTCCTC TCCGGAACCG CTGCTTTTAA
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGAT
1451 TGAGTGCAGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTACAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 678; ORF 163.a>:

```

a163.pep
1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFISF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEIGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSLNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGV LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKHT ASPAMHELQR ELSEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQGEL
651 MAHEQVELAE *

```

m163/a163 99.4% identity in 660 aa overlap

```

              10      20      30      40      50      60
m163.pep    MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFISIFLGFLILSVS
              |||
a163         MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFISIFLGFLILSVS
              10      20      30      40      50      60

              70      80      90     100     110     120
m163.pep    SLGNIRLGRDEDVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ

```

a163		SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ
	70 80 90 100 110 120	
m163.pep	130 140 150 160 170 180	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPLALRSCFYPLLKEKISGRFGDAIDI
a163	130 140 150 160 170 180	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPLALRSCFYPLLKEKISGRFGDAIDI
m163.pep	190 200 210 220 230 240	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
a163	190 200 210 220 230 240	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
m163.pep	250 260 270 280 290 300	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
a163	250 260 270 280 290 300	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
m163.pep	310 320 330 340 350 360	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
a163	310 320 330 340 350 360	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
m163.pep	370 380 390 400 410 420	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
a163	370 380 390 400 410 420	WLNDGVAGGVLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
m163.pep	430 440 450 460 470 480	ITSRDKGLSAPRWQAVMWGLMSAVAVLLMRSGGLGNLQSMTLIVSLP FALLMLIMCFSL
a163	430 440 450 460 470 480	ITSRDKGLSAPRWQAVMWGLMSAVAVLLMRSGGLGNLQSMTLIVSLP FALLMLIMCFSL
m163.pep	490 500 510 520 530 540	WKGLSADKKYFETRVNPTS VFVTGGKWKERLVQIMSQTQEODILKFLKQTAS PAMHELQR
a163	490 500 510 520 530 540	WKGLSADKKYFETRVNPTS VFVTGGKWKERLVQIMSQTQEODILKFLKHTAS PAMHELQR
m163.pep	550 560 570 580 590 600	ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
a163	550 560 570 580 590 600	ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
m163.pep	610 620 630 640 650 660	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
a163	610 620 630 640 650 660	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
m163.pep	X	
	I	
a163	X	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 679>:

```

g164.seq (partial)
1  ..ATGAACACAT TTTTGAAAAA CAGCGAATAC GCGTATATCC TGAACGACTG
51  CAAGGCGCGC TTCCTGTTCG CCTCGGCCGG CCTGTCAAAA GAATTGGCGG
101 GCCTGAAGGC GCAAACGCCG GTCGAAAAAA TCATTGGGAC GGACAAAAGC
151 CGGCCGGCCG GCGAAACGGC GGAAGGCGAT GCCTTTTGTG AAAACGTGCG
201 CCGCTTCCCC GAAAAACCCG ACTTGGGCCG CCAACCCCGG ATAAATGATT
251 TGGCACACAT CATCTACACC TCCGGCACGA CGGGGCATCC CAAAGGCGCG
301 CTAATCAGTT ACGCCAACCT GTTCGCCAAC CTGAACGGCA TCGAACGCAT
351 CTTtaaAATT TCCAAACGCG ACCGCTTTAT CGTTTTCctg ccgatgTTCC
401 ACAGCTTCAC GCTGACGGCT ATGGTGCTGC TGCCGATTTA TATGGCGTGT
451 TCGATTATTT TGGTCAAAtc cgttttCCCC ttttccaacG TTTTGAAACA
501 GGCCCTGCTC AAACGCGCAA CCGTGTTTTT GGGCGTACCC GCGATTACAA
551 CCGCGATGAG CAAGGCAAAA ATCCCTTGGT ATTCAGATG GTTCAACCGC
601 ATCCGCCTGT TTATCAGCGG CGGCGCGCCT TTGGCGGAAC AAACCATCCT
651 CGATTTTAAA GCCAAGTTC CCCGCGCCAA ATTGCTGGAA GGCTACGGAC
701 TGAGCGAAGC CTCGCCCCGTC GTCGCGCTCA ATACGCCCGA ACGGCAAAAA
751 GCCCGCAGCG TCGGCATCCC CCTGCCCGGT TTGGAAGCCA AAGCCGTCGA
801 TGAAGAATTG GTCGAAGTGC CGCGCGCGCA AGTGGCGGAA CTGATCGTCA
851 GGGGCGGTTC GGTGATGCGG GGCTACCTCA ATATGCCTGC CGCCACCGAT
901 GAAACCATCG TCAACGGCTG GTTGAAAACG GGCGATTTCG TTACCATAGA
951 CGAGGACGGC TTTATCTTTA TCGTCGACCG CAAAAAGAT TTGATTATTT
1001 CCAAAGTCA AAACGTCTAT CCGCGCGAGA TCGAAGAAGA AATCCACAAA
1051 CTCGATGCCG TCGAAGCCGC CGCCGTCATC GCGGTGAAAG ACCGTTATGC
1101 CGACGAGGAA ATCGTCGCCT TCGTCCAATT GAAGGAAGGT ATGGATTGG
1151 GCGAGGACGA aatccgccc caccTGCCTA CCGTGTGGC AAATTTCAAA
1201 ATCCCCAAAC AGATCCACTT TAAAGACGGG CTGCCGCGCA ACGCTACGGG
1251 CAAAGTATTG AAACGGGTGC TGAAGGAGCA GTTTGAAGGA AACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 680; ORF 164.ng>:

```

g164.pep (partial)
1  ..MNTFLKNSEY AYILNDCKAR FLFASAGLSK ELAGLKAQTP VEKIIWTDKS
51  RPAGETAEGD AFFENVRRFP EKPDLGRQPR INDLAHIIYT SGTGHPKGA
101 LISYANLFAN LNGIERIFKI SKRDRFIVFL PMFHSFTLTA MVLLPIYMAC
151 SIILVKSVPF FSNVLKQALL KRATVFLGVP AIYTAMSKAK IPWYFRWFNR
201 IRLFISGGAP LAEQTILDFK AKFPRAKLE GYGLSEASPV VAVNTPERQK
251 ARSVGIPLPG LEAKAVDEEL VEVPRGEVGE LIVRGGSVMR GYLNMPAATD
301 ETIVNGWLKT GDFVTIDEDG FIFIVDRKDD LIISKQNVY PREIEEIIHK
351 LDAVEAAAVI GVKDRYADEE IVAFVQLKEG MDLGEDEIRR HLRTVLANFK
401 IPKQIHFKDG LPRNATGKVL KRVLKEQFEG NK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 681>:

```

m164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTCGCCG CCGCCTGCCG
51  CAAAAACGGA AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAG GCCGAAGCCG TCGCGCGGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 AGAATTTATT ACCGCCATT TCGCCATCTC CGCCATCGGC GCGGTCGCCG
251 TACCGATGAA CACATTTTGT AAAACACGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGCGCTGT CAAAAGAATT
351 GCGGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAAATCATT TGGACGGACA
401 AAAGCCGTCC GACCGGCGAA ACGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCGGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGGATAAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GCGCGCTAAT CAGTTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATTTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTACACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTTCGAT TATTTTGGTC AAATCCGTTT TTCCGTTTTT CAACGTTTTG
751 AAACAGACAC TGCTCAAACG CGCGACCGTG TTTTGGGGCG TACCCGCGAT
801 TTACACCGCG ATGAGCAAGG CGAAAATCCC TTGGTATTTT AGATGGTTCA
851 ACCGCATTCG CCTGTTTATC AGCGCGGGCG CGCCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGAAGGCTA

```

```

951  CGGACTGAGC GAAGCCTCTC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGG AGCCAAAGCC
1051 GTCGATGAAG AATTGGTCGA AGTGCCGCGC GCGGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TGCGGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAAATG TCTATCCGCG CGAGATTGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCGCCGCGCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 682; ORF 164>:

```

m164.pep
  1  MNRTYANFYE MLAAACRKNQ NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
 51  IGVKFGDTVLA LAVSNSTEFI TAYFAISAIG AVAVPMNTFL KNSEYAYILN
101  DCKARFLFAS AGLSKELAGL KAQTPVEKII WTDKSRPTGE TAEGDAFFED
151  VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPKGALISYA NLFANLNGIE
201  RIFKISKRDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNV L
251  KQTLKRA TVFLGVPAIYTA MSKAKIPWYF RWFNRIRLFI SGGAPLAEQ T
301  ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEAKA
351  VDEELVEVPR GEVGELIVRG GSVMRGYLMN PAATDETIVN GWLKTGDFVT
401  IDEGDFIFIV DRKKDLIISK GQNVYPREIE EEIYKLDAVE AAVIGVKDR
451  YADEEIVAFV QLKEGMDLGE NEIRRLRTV LANFKIPKQI HFKDGLPRNA
501  TGKVLKRVLK EQFDGNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* m164 / g164 98.6% identity in 432 aa overlap

```

          60      70      80      90      100      110
m164.pep  GDTVALAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSK
          |||||||||||||||||||||||||||||||||||||||
g164      MNTFLKNSEYAYILNDCKARFLFASAGLSK
          10      20      30

          120     130     140     150     160     170
m164.pep  ELAGLKAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPD LGRQPRINDLAHIIYT
          |||||||||||||||||||:|||||||||:|||||||||
g164      ELAGLKAQTPVEKIIWTDKSRPAGETAEGDAFFENVRRFPEKPD LGRQPRINDLAHIIYT
          40      50      60      70      80      90

          180     190     200     210     220     230
m164.pep  SGTTHGHPKGALISYANLFANLNGIERIFKISKRDRFIVFLPMFHSFTLTAMVLLPIYMAC
          |||||||||||||||||||
g164      SGTTHGHPKGALISYANLFANLNGIERIFKISKRDRFIVFLPMFHSFTLTAMVLLPIYMAC
          100     110     120     130     140     150

          240     250     260     270     280     290
m164.pep  SIILVKSVFPFSNV LKQTLKRA TVFLGVPAIYTAMSKAKIPWYFRWFNRIRLFI SGGAP
          |||||||||||||||:|||||||||
g164      SIILVKSVFPFSNV LKQAL KRA TVFLGVPAIYTAMSKAKIPWYFRWFNRIRLFI SGGAP
          160     170     180     190     200     210

          300     310     320     330     340     350
m164.pep  LAEQTILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEAKAVDEEL
          |||||||||||||||
g164      LAEQTILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEAKAVDEEL
          220     230     240     250     260     270

          360     370     380     390     400     410

```

467

```

m164.pep    VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
g164        VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
             280      290      300      310      320      330

             420      430      440      450      460      470
m164.pep    LIISKGQNVYPREIEEEIYKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRR
             ||||||||||||||||:|||||||||||||||||||||||||||||||||||
g164        LIISKGQNVYPREIEEEIHKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGEDEIRR
             340      350      360      370      380      390

             480      490      500      510
m164.pep    HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX
             ||||||||||||||||||||||||||||||||||||||||:|||||
g164        HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFEGNKX
             400      410      420      430

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 683>:

```

a164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTGACCG CCGCCTGCCG
51  CAAAAACGGC AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAA GCCGAAGCCG TTGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 GGAATTTATT ACCGCCTATT TCGCCGTATC CGCCATCGGC GCGGTTGCCG
251 TACCGATGAA CACATTTTGT AAAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GGCGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAATCATT TGGACGGGCC
401 AAAGCCGTCC GGACGGCGAA ATGGCGGAAG GCGATGCCTT TTTGAAGAC
451 GTGCGCCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGATAAAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCCAAG
551 GTGCGCTAAT CAGCTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATCTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTTCGAT TATTTTGGTC AAATCCGTTT TCCCCTTTTC CAACGTTTTG
751 AAACAGGCAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TGCCCGCGAT
801 TTACACCGCG ATGAGCAAGA CGAAATCCC TTGGTATTTT AGATGGTTCA
851 ACCGCATCCG CCTGTTTATC AGCGGCGGAG CACCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGAAGGCTA
951 CGGACTGAGC GAAGCCTCGC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGG AGTCAAAGCC
1051 GTCGATGAAG AATTGGTCGA AGTGCCGCGC GGCGAAGTGG GCGAAGTATG
1101 CGTCAGGGGC GGTTCGGTGA TCGGGGCTA CCTCAATATG CCGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAAATG TCTATCCGCG CGAAATCGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCCGCCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 684; ORF 164.a>:

```

a164.pep
1  MNRTYANFYE MLTAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAVSAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTGQSRPDGE MAEGDAFFED
151 VRRFPEKPD L GRQPRINDLA HIIYTS GTTG HPKGALISYA NLFANLNGIE
201 RIFKISKRDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNVL
251 KQALLKRATV FLGVPPIYTA MSKTKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEVKA
351 VDEELVEVPR GEVGEIVRGG SVMRGYLNM PAATDETIVN GWLKTGDFVT
401 IDEDEGFIFIV DRKKDLIISK QONVYPREIE EEIYKLDVE AAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRLRTV LANFKIPKQI HFKDGLPRNA

```

501 TGKVLKRVLK EQFDGNK*

m164/a164 98.3% identity in 517 aa overlap

	10	20	30	40	50	60
m164.pep	MNRTYANFYEMLAACRKN	NGTAVFDGKEKTAYRAL	KQEA	EAVAAYLQ	NI	GVKFGDTVA
a164	MNRTYANFYEMLTAA	CRKN	NGTAVFDGKEKTAYRAL	KQEA	EAVAAYLQ	NI
	10	20	30	40	50	60
	70	80	90	100	110	120
m164.pep	LAVSNSTEFITAYFAIS	AIGAVAVPMNTFLKNSE	YAYILNDCKARFLFAS	AGLSKELAGL		
a164	LAVSNSTEFITAYFAV	SAIGAVAVPMNTFLKNSE	YAYILNDCKARFLFAS	AGLSKELAGL		
	70	80	90	100	110	120
	130	140	150	160	170	180
m164.pep	KAQTPVEKIIWTDKSRPT	GETAEGDAFFEDVRRF	PEKPD	LGRQPRINDLAHII	YTS	SGTTG
a164	KAQTPVEKIIWTDGSRPD	GEMAE	GDAFFEDVRRFPEKPD	LGRQPRINDLAHII	YTS	SGTTG
	130	140	150	160	170	180
	190	200	210	220	230	240
m164.pep	HPKGALISYANLFANL	NGIERIFKISK	RDRFIVFLPMFHSFT	LTAMVLLPIYMACSII	LV	
a164	HPKGALISYANLFANL	NGIERIFKISK	RDRFIVFLPMFHSFT	LTAMVLLPIYMACSII	LV	
	190	200	210	220	230	240
	250	260	270	280	290	300
m164.pep	KSVFPFSNVLKQTL	LKRATVFLGVP	AIYTAMSKAKIPWYFR	WFRNIRLFISGGAP	LA	EQT
a164	KSVFPFSNVLKQALL	KRATVFLGVP	AIYTAMSKTKIPWYFR	WFRNIRLFISGGAP	LA	EQT
	250	260	270	280	290	300
	310	320	330	340	350	360
m164.pep	ILDFKAKFPRAKL	LEGYGLSEASPV	VAVNTPERQKARS	VGIP	PLPGLEAKAVDEEL	VEVPR
a164	ILDFKAKFPRAKL	LEGYGLSEASPV	VAVNTPERQKARS	VGIP	PLPGLEVKAVDEEL	VEVPR
	310	320	330	340	350	360
	370	380	390	400	410	420
m164.pep	GEVGELIVRGG	SVMRGYLNMPAAT	DETIVNGWLKTG	DFVTIDEDGFIFIV	DRKKDLISK	
a164	GEVGELIVRGG	SVMRGYLNMPAAT	DETIVNGWLKTG	DFVTIDEDGFIFIV	DRKKDLISK	
	370	380	390	400	410	420
	430	440	450	460	470	480
m164.pep	GQNVYPREIEEEIYK	LDAVEAAVIGVK	DRYADEEIVAFVQL	KEGMDLGENEIRRH	LRTV	
a164	GQNVYPREIEEEIYK	LDAVEAAVIGVK	DRYADEEIVAFVQL	KEGMDLGENEIRRH	LRTV	
	430	440	450	460	470	480
	490	500	510			
m164.pep	LANFKIPKQIHFKDGL	PRNATGKVLKRV	LKEQFDGNKX			
a164	LANFKIPKQIHFKDGL	PRNATGKVLKRV	LKEQFDGNKX			
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 685>:

g165.seq

1 ATGGCTGAAG CGACAGACGT TGTCTTGCTG GCGGCGGCA TTATGAGCGC

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51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAagat gTGGCGTTGG AATCGTCAAA cGCGTGGAAC
151 AACGcCGgca CGGGGCATTC CGcGCTGTGc GAATTGAACT AtgcgccGCT
201 GGGtgccggac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctgGTCGC GGAAGGCAAG
301 TTGGAagaCA ATTCTTCAT CAATGCcgtg ccgcatatGT Ctttggtgat
351 gAacgaagac cactgCCgtt acCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtcgcGTGAT TATGCGCGGC CGGgacgaaA ACCAACCCGT
501 CGCCGCCAAC TATTCCGCCG Aaggcacgga tgtcgATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCTCTT CCTCGGCGCG GCGCGCGCG CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GGCGCGCCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCTTACGC
951 AGGTTTCCGT TCCAACCTCC TCAAGCAAGG CTGCTTTATG GATTGCGCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CcTGCTGGgC gAaTTGCgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 686; ORF 165.ng>:

```

g165.pep
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSAIC ELNYAPLGAD GVINPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD VFKTQKLFEN MEFSTDRNKI
151 SDWAPLIMRG RDENQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GLPVSGLFFR NSNPETAEOH NAKVYGOASV GAPPMSPVPHL
301 DTRNVDGKRH LMFPGPYAGFR SNFLKQGSFM DLPLSIHMDN LYPLMLRAGWA
351 NMPLTKYLLG ELR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 687>:

```

m165.seq (partial)
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGCA CGGGGCATTC CGCGCTGTGc GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCAAAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGgTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GGCGCGCCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTGCGCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAA...

```

This corresponds to the amino acid sequence <SEQ ID 688; ORF 165>:

```

m165.pep (partial)
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSAIC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDENQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF

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470

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201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAEQH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMLCAGWA
351 NMPLTK...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m165 / g165 97.2% identity in 356 aa overlap

	10	20	30	40	50	60
m165.pep	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
g165	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m165.pep	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	: : :					
g165	ELNYAPLGADGVINPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m165.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMRGRDENQPVAANYSAEGTDVDF					
	:					
g165	HCRYLQKRYDVFKTQKLFENMEFSTDRNKISDWAPLMRGRDENQPVAANYSAEGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m165.pep	GRLTRQMVKYLGKGKVKTEFNHVEDIKRES DGAWVLKTADTRNPDGQLTLRTRFLFLGA					
g165	GRLTRQMVKYLGKGKVKTEFNHVEDIKRES DGAWVLKTADTRNPDWQLTLRTRFLFLGA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m165.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNKAVYQASVGAPPMSVPHL					
	:					
g165	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNKAVYQASVGAPPMSVPHL					
	250	260	270	280	290	300
	310	320	330	340	350	
m165.pep	DTRNVDGKRHLMFGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTK					
	:					
g165	DTRNVDGKRHLMFGPYAGFRSNFLKQGSFMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG					
	310	320	330	340	350	360
g165	ELRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 689>:

```

a165.seq
  1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GGCGGCGGCA TTATGAGCGC
 51 GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTTG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGCA CGGGGCATT CCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCGGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAAACT TTTTGGAAAT ATGGAATTTT CCACCGATCG GAACAAATTT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCAGATTCT

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471

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601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCTCTT CCTCGGCGCG GCGCGCGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCACCTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGTGGGCG GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACT CCCCAGAGCA AACCCGACG
1151 ACTGGGAACT CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGTT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTGTGGA TATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 690; ORF 165.a>:

```

a165.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQR FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDENQPVAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAEQH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGLM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKGD
401 SEKGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

m165/a165 99.7% identity in 356 aa overlap

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          10      20      30      40      50      60
m165.pep  MAEATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC
a165      MAEATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC
          10      20      30      40      50      60

          70      80      90      100     110     120
m165.pep  ELNYAPLGANGIIDPARALNIAEQFHVSQRFWATLVAEGKLEDNSFINAVPHMSLVMNED
a165      ELNYAPLGANGIIDPARALNIAEQFHVSQRFWATLVAEGKLEDNSFINAVPHMSLVMNED
          70      80      90      100     110     120

          130     140     150     160     170     180
m165.pep  HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAANYSAEGTDVDF
a165      HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAANYSAEGTDVDF
          130     140     150     160     170     180

          190     200     210     220     230     240
m165.pep  GRLTRQMVKYLQKGKVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
a165      GRLTRQMVKYLQKGKVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
          190     200     210     220     230     240

          250     260     270     280     290     300
m165.pep  GGGALLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYQASVGAPPMSVPHL
a165      GGGALLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYQASVGAPPMSVPHL
          250     260     270     280     290     300

```

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	310	320	330	340	350
m165.pep	DTRNVDGKRHLMFGPYAGFRSNFLKQGSMLDLPLSIHMDNLYPMLCAGWANMPLTK				
a165	DTRNVDGKRHLMFGPYAGFRSNFLKQGSMLDLPLSIHMDNLYPMLRAGWANMPLTKYLLG				
	310	320	330	340	350
	370	380	390	400	410
a165	ELRKTKEERFASLLEYYPEANPDWELITAGQVRVQIIKKDSEKGGVLQFGTEIVAHADGS				
	370	380	390	400	410
					420

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 691>:

g165-1.seq

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGgca CGGGGCATTC CGcGCTGTGc GAATTGAACT AtgcgcccGCT
201 GGGtgccgac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctggTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAACGAAGAC CACTGCCGTT ACCTGCAAAA ACCTATGAT GTGTTTAAAA
401 CGCAGAACT TTTTGAATA ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtcgcCTGAT TATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TATTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCGCCACCC
701 GCTTCTCTTT CCTCGGCGCG GCGGCGGCGC CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCGGGCTT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCTTACGC
951 AGGTTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCCG TGACCAAATA CCTGTGGGCG GAATGCGTA AAACCAAAGA
1101 AGAAGCTTt gCCTCCCTGC TGgaatacta cccGaggcag acccGACGAc
1151 ttgtactcat cagcaggnc acGCGTcata tcattanata tgactCgaaa
1201 ctgcgcgtgc tgcagttgta cgagattgtg ccaCGCGacg ctcgctcgcg
1251 cattctggag cgctcgcgcg catcacgctn tgcgctgata tccgctgatg
1301 acactgctcc gaGCGcgccc gtcttggaat gtgtctga

```

This corresponds to the amino acid sequence <SEQ ID 692; ORF 165-1.ng>:

g165-1.pep

```

1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLMVNED HCRYLQKRYD VFKTQKLFEN MEFSTDRNKI
151 SDWAPLIMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAUWLKTA DTRNPDWQLT LRTRELFLLGA GGGALTLLOK
251 SGIPEGKGYG GLPVSGLFFR NSNPETAEOH NAKVYGQASV GAPFMSVPHL
301 DTRNVDGKRH LMGFPYAGFR SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYPRQ TRRLVLITQX TRHIIXYDSK
401 LRVLQLYEIV PRDARSRILE RRGASRXALI SADDTAPSAP VLESV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 693>:

m165-1.seq

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTCTT ATCTTCAAAA ACCTATGAC GCGTTTAAAA
401 CCAAAAACT TTTTGAATA ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGGTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCTGACCC
701 GCTTCTCTTT CCTCGGCGCG GCGGCGGCGC CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCGG TGTCGGGCTT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG

```

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851 TGTACGGGCA GGCTTCCGTC GCGCGCCGCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTCT GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTGTCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGGCA AACCCGACG
1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TCCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGCT CCAGTTTGGT ACGGAGATTG TCGCCACGC
1251 CGACGGCTCA CTCGCCGAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CTGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAGCGCGCC
1351 CCGTCTTGGG AAGACCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCTGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTATTGGA TATTAA

```

This corresponds to the amino acid sequence <SEQ ID 694; ORF 165-1>:

m165-1.pep

```

1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRELFGLA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAQH NAKVYQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFPGYAGFR SNFLKQGSML DLPLSIHMDN LYPMLCAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKGD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERA
451 PSWEDRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

m165-1/g165-1 89.7% identity in 428 aa overlap

	10	20	30	40	50	60
m165-1.pep	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWN	NAGTGHSALC		
g165-1	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWN	NAGTGHSALC		
	10	20	30	40	50	60
	70	80	90	100	110	120
m165-1.pep	ELNYAPLGANGIIDPARALN	IAEQFHVSRQFWATLVAEGK	LEDNSFINAVPHMSLVMNED			
g165-1	ELNYAPLGADGVINPARALN	IAEQFHVSRQFWATLVAEGK	LEDNSFINAVPHMSLVMNED			
	70	80	90	100	110	120
	130	140	150	160	170	180
m165-1.pep	HCSYLQKRYDAFKTQKLFEN	MEFSTDRNKISDWAPLMMRG	RDNQPVAAANYSAEGTDVDF			
g165-1	HCRYLQKRYDVFKTQKLFEN	MEFSTDRNKISDWAPLMRGR	RDNQPVAAANYSAEGTDVDF			
	130	140	150	160	170	180
	190	200	210	220	230	240
m165-1.pep	GRLTRQMVKYLQKGKVKTEF	NRHVEDIKRESDGAWVLKTA	DTRNPDGQLTLRTRFLFLGA			
g165-1	GRLTRQMVKYLQKGKVKTEF	NRHVEDIKRESDGAWVLKTA	DTRNPDGQLTLRTRFLFLGA			
	190	200	210	220	230	240
	250	260	270	280	290	300
m165-1.pep	GGGALTLLQKSGIPEGKGYG	GFPVSGLFFRNSNPETAQH	NAKVYQASVGAPPMSPVPHL			
g165-1	GGGALTLLQKSGIPEGKGYG	GFPVSGLFFRNSNPETAQH	NAKVYQASVGAPPMSPVPHL			
	250	260	270	280	290	300
	310	320	330	340	350	360
m165-1.pep	DTRNVDGKRHLMFPGYAGFR	SNFLKQGSMDLPLSIHMDN	LYPMLCAGWANMPLTKYLLG			
g165-1	DTRNVDGKRHLMFPGYAGFR	SNFLKQGSFMDLPLSIHMDN	LYPMLRAGWANMPLTKYLLG			
	310	320	330	340	350	360
	370	380	390	400	410	420
m165-1.pep	ELRKTKEERFASLLEYYPEA	NPDDWELITAGQRVQIIKGD	SEKGGVLQFGTEIVAHADGS			
g165-1	ELRKTKEERFASLLEYPR-Q	TRRLVLITQXTR-HIIXYDS	-KLRVLQLYEIVPRDARSR			
	370	380	390	400	410	
	430	440	450	460	470	480

m165-1.pep LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNENPERADEIIA
 : |||
 g165-1 ILERRGASRXALISADDTAPSAPVLESVX
 420 430 440

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 695>:

a165-1.seq
 1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GGC GCGGCA TTATGAGCGC
 51 GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
 101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
 151 AACGCCGCGA CGGGGCATTG CGCGCTGTGC GAATTGAACT ATGCGCCGTT
 201 GGGTGCAAAAT GGGATTATCG ATCCGCGCGC CGCCCTCAAT ATTGCCGAAC
 251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTCCG GGAAGGCAAG
 301 CTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
 351 GAATGAAGAC CATTGTCTTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
 401 CCCAAAAACT TTTTAAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
 451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCTG
 501 CGCCGCGCAAC TACTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
 551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
 601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
 651 CAAAACCGCG GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
 701 GCTTCCCTCTT CCTCCGCGCG GCGCGCGCGC CGCTGACCCT GCTGCAAAAA
 751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
 801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
 851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
 901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCTTACGC
 951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCACCTATG GATTTGCCGC
 1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
 1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
 1101 AGAACGCTTC GCCTCCCTGC TGGAAATACTA CCGGAGGCA AACCCGACG
 1151 ACTGGGAACT CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAAGAC
 1201 TCCGAAAAAG GCGGCGTGTG GCAGTTTGGT ACGGAGATTG TCGCACACGC
 1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
 1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
 1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
 1401 GTTGAACGAA AACCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
 1451 AAGTGTGGA TATTTAA

This corresponds to the amino acid sequence <SEQ ID 696; ORF 165-1.a>:

a165-1.pep
 1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
 51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQR FWATLVAEGK
 101 LEDNSFINAV PHMSLVNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
 151 SDWAPLMRGR DENQPVAAAN YSAEGTDVDF GRLTRQMVKY LQGGVKTEF
 201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LTRFLFLGA GGGALTLLQK
 251 SGIPEGKGYG GFPVSGLFRR NSNPETAQEH NAKVYQASV GAPPMSVPHL
 301 DTRNVDGKRH LMFPGYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLRAGWA
 351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA QORVQIIKKD
 401 SEKGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
 451 PSWEGRLEKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

a165-1/m165-1 99.4% identity in 488 aa overlap

	10	20	30	40	50	60
a165-1.pep	MAEATDVVLVGGGIMSATLG VLLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
m165-1	MAEATDVVLVGGGIMSATLG VLLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
	10	20	30	40	50	60
a165-1.pep	ELNYAPLGANGIIDPARALNIAEQFHVSQRFWATLVAEGKLEDNSFINAVPHMSLVNED					
m165-1	ELNYAPLGANGIIDPARALNIAEQFHVSQRFWATLVAEGKLEDNSFINAVPHMSLVNED					
	70	80	90	100	110	120
a165-1.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMRGRDENQPVAAANYSAEGTDVDF					
m165-1	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMRGRDENQPVAAANYSAEGTDVDF					
	130	140	150	160	170	180
a165-1.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMRGRDENQPVAAANYSAEGTDVDF					
m165-1	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMRGRDENQPVAAANYSAEGTDVDF					
	190	200	210	220	230	240

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a165-1.pep  GRLTRQMVKYLGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
|||||
m165-1      GRLTRQMVKYLGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
              190      200      210      220      230      240

              250      260      270      280      290      300
a165-1.pep  GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYQASVGAPPMSVPHL
|||||
m165-1      GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYQASVGAPPMSVPHL
              250      260      270      280      290      300

              310      320      330      340      350      360
a165-1.pep  DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
|||||
m165-1      DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG
              310      320      330      340      350      360

              370      380      390      400      410      420
a165-1.pep  ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
|||||
m165-1      ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
              370      380      390      400      410      420

              430      440      450      460      470      480
a165-1.pep  LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEGRLKELVPGYGIKLNENPERADEIIA
|||||
m165-1      LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNENPERADEIIA
              430      440      450      460      470      480

              489
a165-1.pep  YTAKVLDIX
|||||
m165-1      YTAKVLDIX

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a165-1/p33940

sp|P33940|YOJH_ECOLI HYPOTHETICAL 60.2 KD PROTEIN IN ECO-ALKB INTERGENIC REGION
>gi|1736851|gnl|PID|d1016718 (D90850) ORF ID: o372#5; similar to [SwissProt Accession Number P33940] [Escherichia coli] >gi|1788539 (AE000310) f548; This 548 aa ORF is 100 pct identical to 490 residues of YOJH_ECOLI SW: P33940 (492 aa) but contains 56 additional N-ter aa; 100 pct identical to GB: ECOHU49_33
ACCESSION: U00008 (490 aa) but contains 58 additional N-term resi... Length = 548
Score = 458 bits (1167), Expect = e-128
Identities = 233/490 (47%), Positives = 303/490 (61%), Gaps = 5/490 (1%)

```

Query: 3  EATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALCEL 62
+ TDV+L+GGGIMSATLG L+ELEP W +T++ERLE VA ESSN WNNAGTGHSAL EL
Sbjct: 30 QETDVLLIGGGIMSATLGTYLRELEPEWSMTMVERLEGVAQESSNGWNNAGTGHSALMEL 89

Query: 63 NYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLED-NSFINAVPHMSLVMNEDH 121
NY P A+G I +A+ I E F +SRQFWA V G L SFIN VPHMS V ED+
Sbjct: 90 NYTPQNADGSISIEKAVAINAEAFQISRQFWAHQVERGLRTPRSFINTVPHMSFVWGEDN 149

Query: 122 CSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMGRDENQPVAANYSAGTDDVDFG 181
++L+ RY A + LF M +S D +I +WAPL+M GRD Q VAA + GTDV++G
Sbjct: 150 VNFLRARYAALQQSSLFRGMRYSEDHAQIKWAPLVMGRDPQQKVAATRTEIGTDVNYG 209

Query: 182 RLTRQMVKYLGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTXXXXXXXXXX 240
+TRQ++ LQ K + + V +KR D W + AD +N Q
Sbjct: 210 EITRQLIASLQKKSNSFLQSLSEVRALKRNDNTWTVTVDLKNGTAG-NIRAKFVFIGA 268

Query: 241 XXXXXXXXQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYQASVGAPPMSVPHL 300
Q+SGIPE K Y GFPV G F + NP+ H AKVYG+ASVGAPPMSVPH+
Sbjct: 269 GGAALKLLQESGIPEAKDYAGFPVGGQFLVSENPDVVNHHLAKVYGKASVGAPPMSVPHI 328

Query: 301 DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG 360
DTR +DGKR ++FGP+A F + FLK GSL DL S N+ PM+ G N L KYL+
Sbjct: 329 DTRVLDGKRVLFGPFATFSTKFLKNGSLWDLMSSTTTSNVMPMMHVGLDNFDLVKYLVS 388

Query: 361 ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVXXXXXX 420
++ ++E+RF +L EYYP+A +DW L AGQRVQIIK+D+EKGGVL+ GTE+V
Sbjct: 389 QVMLSEEDRFEALKEYYPQAKKEDWRLWQAGQRVQIIKRAEKGGVLRGTEVVSDDQGT 448

Query: 421 XXXXXXXXXXXXXVPLMIRLMHQCFPER--TPSWEGRLKELVPGYGIKLNENPERADEI 478

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P+M+ L+ + F +R +P W+ LK +VP YG KLN + +
 Sbjct: 449 IAALLGASPGASTAAPIMLNLLKVFGRVSSPQWQATLKAIVPSYGRKLNGDVAATERE 508
 Query: 479 IAYTAKVLDI 488
 + YT++VL +
 Sbjct: 509 LQYTSEVLGL 518

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 697>:

g204.seq
 1 atggcgggcg cggaaataaa acgccccctc gctgtcgatt tccagcacat
 51 agcgctccgtt ctgcacggcg gcatagccgc ttttgccctgc ctgatagggg
 101 tgcagggcg aatgcgaaat caggaatca gtcagtttgc cgccgtcttc
 151 ggcgatattg cccaccagtt tggcaaacaa ggtatggcac acgccgtttt
 201 ccgcccagcc cgaaggcgcg tcctttccgt cggtttccat acatttgccg
 251 acgacggctt ccaagtcgtt gggatgcttt ccggtcagcc ggacggcggt
 301 ttgttccggc aagcctttaa tcggataact gatttgtttt ttgccgtcgt
 351 tggttttgcc ttcgctactt tgtcccaaag ccaaaccggc aatcgccgta
 401 ttgtcgatgt atttgacttt gaaaaccggg ttcggcgcg tttgtgccgc
 451 attttgccgc tgttcgccc gattttcggg tttgccgcag gcggcaagca
 501 gcaggcagcc gcccaacacg gcaaaaggta ttttcagcat tccgcactcc
 551 tgatgggttc aaaatgccgt ctgaaatgcc gtctgaaacg tggcaggcgg
 601 aggttcggac ggcattgggt ttatttcaac gggcggatgc cgaccgcac
 651 gcgtacttta tccaacaatt cgcgcgcttc tttgcgcgct ttttgcgcgc
 701 ctgcctgcaa aatctcttcg atttgcaag gattagaggt caatgcgttg
 751 tag

This corresponds to the amino acid sequence <SEQ ID 698; ORF 204.ng>:

g204.pep
 1 MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVISQFAAVF
 51 GDIAHQFGKQ GMAHAVFRPA RRRVLSVGFH TFADDGFQVV GMLSGQPDGV
 101 LFRQAFNRIT DLFFAVVGFA FATLSQSQTG NRRIVDVDFD ENRFRRLCR
 151 ILRLFRIRIFG FAAGGKQQA AOHGKRYFQH SALLMVSKCR LKCRLLKGRRR
 201 RFGRHWVYFN GRMPTASRTL SNNSRASLRA FCAPACKISS ICEGLEVNAL
 251 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 699>:

m204.seq
 1 ATGGCGGCGG CGGAAATAAA ACGCCCCTTC GCTGTGCGATT TCCAGCACAT
 51 AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCCTGC CTGATAGGGT
 101 TGCAGGGCGG CATGCGAAAC TAGGTAATCC GTCAGTTTGC CGCCGTCTTC
 151 GGCATATTG CCCACCAAGT TGGCAAACAA GGTATGGCAC ACGCCGTTTT
 201 CTGCCCAACC TGCCGGACTG TCCTTATCAT CGGTTTCCAT ACATTTGCCG
 251 CTGACGGCTT CCAAGTCGCC GGGATGCTTG CCGATCAGTC GGATAACATT
 301 TTGTTCCGGC AAGCCTTTAA TCGGATAACT GATTGTGTTT TTGCCGTCGT
 351 TGGTTTTGCC TTCGCTGCTT TGTCCCAAAT CCAAACCGGC AATCGCCGTA
 401 TTGTCGATAT ATATGACTTT GAAAACCGGT TTCGGCGCGC TTTGTACCGC
 451 GTTTTGCAGC TGTACCGCCG TATTTWCGGA TTTGCCGCAC GGCaaRGcAG
 501 CAGGCAGCCG CCCAATACGG CAAAaAwGT wTTCAGCATT CCACaYTCCT
 551 GATGGTTTCA AAATGCCGTC TGAAACGCGG CAGGCGGAGG TTCGGACGGC
 601 ATCGGGTTCA TTTCAACGGG CGGATGcCGA CCGCATCgGT ACTTTGTCCA
 651 ATAATTCGCG TGCTTCTTTA CGCGCTTTCG CCGCGCCTGC CTGCAAAATC
 701 TCTTCGATTG GCGAAGGGTC GGCGGTCAGC TCgTTGTAG

This corresponds to the amino acid sequence <SEQ ID 700; ORF 204>:

m204.pep
 1 MAAAEIKRPF AVDFQHIASV LHGGIAAFAC LIGLQGGMRN *VIRQFAAVF
 51 GDIAHQFGKQ GMAHAVFCPT CRTVLIIGFH TFAADGFQVA GMLADQSDNI
 101 LFRQAFNRIT DLFFAVVGFA FAALSQIQTG NRRIVDIYDF ENRFRRLYR
 151 VLRLYRRIXG FAATAQQQA AQYGKXXXQH STXLMVSKCR LKGRRRRFRG
 201 HRVHFNGRMP TASGTLNNS RASLRAFAAP ACKISSICEG SAVSSL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 204 shows 82.0% identity over a 250 aa overlap with a predicted ORF (ORF 204.ng) from *N. gonorrhoeae*:

m204/g204

		10	20	30	40	50	60
m204.pep		MAAAEIKRPFVDFQHIASVLHGGIAAFACLIGLQGGMNRXVIRQFAAVFGDIAHQFGKQ					
		:					
g204		MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIGLQGGMNRQVISQFAAVFGDIAHQFGKQ					
		10	20	30	40	50	60
		70	80	90	100	110	120
m204.pep		GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
		:					
g204		GMAHAVFRPARRRVLSVGFHTFADDFQVVGMLSGQPDGVLFRQAFNRITDLFFAVVGFA					
		70	80	90	100	110	120
		130	140	150	160	170	180
m204.pep		FAALSQIQTGNRRIVDIYDFENRFRRALYRVRLRYRRIXGFAATAXQQAAAQYKXXXQH					
		:					
g204		FATLSQSQTGNRRIVDVDFENRFRRALCRILRLFRRIFGFAAGGKQAAAQHGKRYFQH					
		130	140	150	160	170	180
		190	200	210	220	230	
m204.pep		STXLMVSKCRLK---RGRRRFRGRHVHFNGRMPTASGTLSNNSRASLRAFAAPACKISS					
		:					
g204		SALLMVSKCRLKCRLLRGRRRFRGRHWVYFNGRMPTASRTLSNNSRASLRAFCAPACKISS					
		190	200	210	220	230	240
		240					
m204.pep		ICEGSAVSSLX					
		:					
g204		ICEGLEVNAL					
		250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 701>:

[illegible]

This corresponds to the amino acid sequence <SEQ ID 702; ORF 204.a>:

a204.pap

1	MAAAEIKRPL	AVDFQHIASV	LHGGIAAFAC	LIGLQGGMRN	QVIRQFAAVF
51	GDIAHQFGKQ	GMAHAVCRPA	RRRALSVEFH	TFADDGFQVV	GMLAGQPDDV
101	LFRQAF....
151KRFRGR
201	HWVYFNGRIP	TASRTLPNNS	RASLRAFCAP	ACKISSICEG	SAVSSL*

m204/a204 54.5% identity in 246 aa overlap

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVDFQHIASVLHGIIAFAACLIQLQGMRNXVIRQFAAVFGDIAHQFGKQ					
a204	MAAAEIKRPLAVDFQHIASVLHGIIAFAACLIQLQGMRNQVIRQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFROAFNRITDLFFAVVGFA					
a204	GMAHAVCRPARRRALSVGFHTFADDGFQVVGMLAGQPDVLFROAF-----					
	70	80	90	100		
	130	140	150	160	170	180
m204.pep	FAALSQIQTNRRIVDIYDFENFRRLALYRVLRLYRRIXGFAATAQQAAAQYKXXXQH					
a204	-----					
	190	200	210	220	230	240
m204.pep	STXLMVSKCRLKRRRFRHRVHFNGRMPASGTLNNRASLRFAAPACKISSICEG					
a204	-----KRFGRHWVYFNGRIPTASRTLNNRASLRFAFCAPACKISSICEG					
	110	120	130	140	150	
m204.pep	SAVSSLX					
a204	SAVSSLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 703>:

```

g205.seq
1  atgctgaaaa taccttttgc cgtgttgggc ggctgcctgc tgcttgccgc
51  ctgcgcaaaa tccgaaaata cggcggaaca gccgcaaat gcggcacaaa
101 gcgcgccgaa accggttttc aaagtcaaat acatcgacaa tacggcgatt
151 gccggtttgg ctttgggaca aagtagcgaa ggcaaaacca acgacggcaa
201 aaaacaaatc agttatccga ttaaaggctt gccggaacaa aacgccgtcc
251 ggctgaccgg aaagcatccc aacgacttgg aagccgtcgt cggcaaatgt
301 atggaaaccg acggaagga cgcgccttcg ggctgggcgg aaaacggcgt
351 gtgccatacc ttgtttgcca aactggtggg caatatcgcc gaagacggcg
401 gcaaactgac tgattacctg atttcgcatt ccgccctgca accctatcag
451 gcaggcaaaa gcggctatgc cgcctgcag aacggacgct atgtgctgga
501 aatcgacagc gagggggcgt tttatttccg ccgccccat tattga

```

This corresponds to the amino acid sequence <SEQ ID 704; ORF 205.ng>:

```

g205.pep
1  MLKIPFAVLG GCLLLAACGK SENTAEQPN AAQSAPKPVF KVKYIDNTAI
51  AGLALQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVCHT LFAKLVGNIA EDGGKLTDL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 705>:

```

m205.seq
1  ATGCTGAAwA CwTyTTTTGC CGTATTGGGC GGCTGCCTGC TGCyTtGCCG
51  tCGCGCAAAT CCGwAAATAC GCGGTACAG CCGCAAAACG CGGTACAAAG
101 CGCGCCGAAA CCGGTTTCA AAGTCATATA TATCGACAAT ACGGCGATTG
151 CCGGTTTGA TTTGGGACAA AGCAGCGAAG GCAAAACCAA CGACGGCAAA
201 AAACAAATCA GTTATCCGAT TAAAGGCTTG CCGGAACAAA ATGTTATCCG
251 ACTGATCGGC AAGCATCCCG GCGACTTGA AGCCGTCAGC GGCAAATGTA
301 TGGAACCGA TGATAAGGAC AGTCCGGCAG GTTGGGCAGA AAACGGCGTG
351 TGCCATACCT TGTtTGCCAA ACTGGTGGG AATATCGCCG AAGACGGCGG
401 CAAACTGACG GATTACCTAG TtTCGATGC CGCCCTGCAA CCTATCAGG
451 CAGGCAAAAG CGGCTATGCC GCCGTGCAGA ACGGACGCTA TGTGCTGGAA
501 ATCGACAGCG AAGGGGCGTT TTATTTCGCG CGCCGCCATT ATTGA

```


This corresponds to the amino acid sequence <SEQ ID 706; ORF 205>:

```
m205.pep
  1  MLXTXFAVLG GCLLXCRCGK SXNTAVQPQN AVQSAPKPVF KVIYIDNTAI
 51  AGLDLGQSSE GKTNDGKKQI SYPIKGLPEQ NVIRLIGKHP GDLEAVSGKC
101  METDDKDSPA GWAENGVCHT LFAKLVG NIA EDGGKLT DYL VSHAALQPYQ
151  AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 205 shows 88.4% identity over a 181 aa overlap with a predicted ORF (ORF 205.ng) from *N. gonorrhoeae*:

```
m205/g205

      10      20      30      40      50      60
m205.pep  MLXTXFAVLGGCLLXCRCGKSXNTAVQPQNAVQSAPKPVFKVIYIDNTAIAGLDLGQSSE
          ||  |||||  |||  ||  |||||:|||||  |||||  |||||
g205      MLKIPFAVLGGCLLLAACGKSENTAEQPQNAASAPKPVFKVKYIDNTAIAGLALGQSSE
          10      20      30      40      50      60

      70      80      90      100     110     120
m205.pep  GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDSPA GWAENGVCHT
          |||||  |||||  |||||:|  ||||:||||  ||:|  |||||
g205      GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT
          70      80      90      100     110     120

      130     140     150     160     170     180
m205.pep  LFAKLVG NIAEDGGKLT DYL VSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
          |||||  |||||  |||||:|:|  |||||  |||||  |||||
g205      LFAKLVG NIAEDGGKLT DYL ISHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
          130     140     150     160     170     180

m205.pep  YX
          |
g205      Y
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 707>:

```
a205.seq (partial)
  1  TCCGAACCTC TTAAAGGCTT GCCGGAACAA AACGTCGTCC GGCTGACCGG
 51  CAAGCATCCC AACGACTTGG AAGCCGTCGT CGGCAAATGT ATGGAAACCG
101  ACGGAAAGGG CGCGCCTTCG GGCTGGGCGG CAAACGGCGT GTGCCATACC
151  TTGTTTGCCA AACTGGTGGG CAATATCGCC GAAGACGGCG GCAAACCTGAC
201  GGATTACCTG ATTTTCGATT CCGCCCTGCA ACCCTATCAG GCAGGCAAAA
251  GCGGCTATGC CGCCGTGCAG AACGGACGCT ATGTGCTGGA AATCGACAGC
301  GAGGGGGCGT TTTATTTCCG CCGCCGCCAT TATTGA
```

This corresponds to the amino acid sequence <SEQ ID 708; ORF 205.a>:

```
a205.pep (partial)
  1  SEPLKGLPEQ NVVRLTGKHP NDLEAVVGKC METDGKGAPS GWAANGVCHT
 51  LFAKLVG NIA EDGGKLT DYL ISHSALQPYQ AGKSGYAAVQ NGRYVLEIDS
101  EGAFYFRRRH Y*
```

m205/a205 88.3% identity in 111 aa overlap

```
      50      60      70      80      90      100
m205.pep  KVIYIDNTAIAGLDLGQSSE GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKC
          |  |:|||||  |:|  ||||:||||  |||
a205      SEPLKGLPEQNVVRLTGKHPNDLEAVVGKC
          10      20      30

      110     120     130     140     150     160
m205.pep  METDDKDSPA GWAENGVCHTLFAKLVG NIAEDGGKLT DYL VSHAALQPYQAGKSGYAAVQ
```

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```

      |||| | :|:|| ||||||||| ||||||||| :| :| |||||||||
a205 METDGKGAPSGWAANGVCHTLFAKLVGNIAEDGGKLT DYLI SHSALQPYQAGKSGYAAVQ
          40           50           60           70           80           90

              170          180
m205.pep NGRYVLEIDSEGA FYFRRRHYX
            ||||| ||||| ||||| ||||| ||||| ||||| |||||
a205 NGRYVLEIDSEGA FYFRRRHYX
             100          110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 709>:

g205-1.seq (partial)

1	ATGCTGAAAA	TACCTTTTGC	CGTGTGGGCG	GGCTGCCTGC	TGCTTGCCCG
51	CTGCGGCAAA	TCCGAAAAATA	CGGCGGAACA	GCCGCAAAAT	GCGGCACAAA
101	GCGCGCCGAA	ACCGGCTTTTC	AAAGTCAAAAT	ACATCGACAA	TACGGCGATT
151	CGCGGTTTGG	CTTTGGGACA	AAGTAGCGAA	GGCAAAACCA	ACGACGGCAA
201	AAAACAAATC	ATTATTCCGA	TTAAGGCTT	GCCGGAACAA	AACGCGCTCC
251	GGCTGACCGG	AAAGCATCCC	AACGACTTGG	AAGCCGTCGT	CGGCAATGT
301	ATGGAACCG	ACGGAAGGA	CGCGCCTTCG	GGCTGGGCGG	AAAACGGCGT
351	GTGCCATACC	TTGTTTGCCA	AACTGGTGGG	CAATATCGCC	GAAGACGGCG
401	GCAAACTGAC	TGATTACCTG	ATTTGCGATT	CCGCCCTGCA	ACCCTATCAG
451	GCAAGCAAAA	GCGGGTATGC	GTCCTGTCAG	AACGGACGCT	ATGTGCTGGA
501	AATCGACAGC	GAGGGGCGCT	TTTA		

This corresponds to the amino acid sequence <SEQ ID 710; ORF 205-1.ng>:

g205-1.pep (partial).

1 MLKIPFAVLG GCLLLAACGK SENTAEPQPN AAQSAPKPVF KVKYIDNTAI
51 AGLALQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVCHT LFAKLVGNIA EDGGKLT DYL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAF

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 711>:

m205-1.seq..

1	ATGCTGAAAA	CATCTTTTGC	CGTATTGGGC	GGCTGCCTGC	TGCTTGCCCG
51	CTGCGGCAAA	TCCGAAAATA	CGGCGGAACA	GCCGCAAAAC	GCGGTACAAA
101	GCGCGCCGAA	ACCGGTTTTT	AAAGTCAAAT	ATATCGACAA	TACGGCGATT
151	CCCGGTTTGG	ATTTGGGACA	AAGCAGCGAA	GGCAAAACCA	ACGACGGCAA
201	AAAACATAAT	AGTTATCCGA	TTAAAGGCTT	GCCGGAACAA	AATGTTATCC
251	GACTGATCGG	CAAGCATCCC	GGCGACTTGG	AAGCCGTCAG	CGGCAAATGT
301	ATGGAACCG	ATGATAAGGA	CAGTCCGGCA	GGTTGGGCAG	AAAACGGCGT
351	GTGCCATACC	TTGTTTGCCA	AAC TTGGTGGG	CAATATCGCC	GAAGACGGCG
401	GCAAACTGAC	GGATTACCTA	GTTTCGCATG	CCGCCCTGCA	ACCCATATCAG
451	CGAGGCAAA	GCGGTATATG	CGCGCTCAG	ACGGAGCGCT	ATGTGCTGGA
501	AATCGACAGC	GAAGGGGCGT	TTTATTTCGG	CCGCGCCAT	TATTGA

This corresponds to the amino acid sequence <SEQ ID 712; ORF 205-1>:

m205-1.pgp

1 MLKTSFAVLG GCLLLAACGK SENTAEQPQN AVQSAPKPVF KVKYIDNTAI
51 AGLDLGQSSE GKTNDGKKQI SYPIKGLPEQ NVIRLIGKHP GDLEAVSGKC
101 METDDKDSPA GWAENGVCHT LFAKLVGNIA EDGGLTDYL VSHAALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y*

m205-1/g205-1 92.0% identity in 174 aa overlap

	10	20	30	40	50	60
g205-1.pep	MLKIPFAVLGGCLLLAACGKSENTAEQPQNAQAQSAKPVPVKYIDNTAIAGLALGQSSE					
m205-1	MLKTSFAVLGGCLLLAACGKSENTAEQPQNAVQSAKPVPVKYIDNTAIAGLDLGQSSE					
	10	20	30	40	50	60
	70	80	90	100	110	120
g205-1.pep	GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT					
m205-1	GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDSAPGWAENGVCHT					


```

51  QGSQELMLHS  LGLIGTPYKW  GGSSTATGFD  CSGMIQLVYK  NALNVKLPR
101  ARDMAAASRK  IPDSRLKAGD  IVFFNTGGAH  RYSHVGLYIG  NGEFIHAPGS
151  GKTIKTEKLS  TPFYAKNYLG  AHTFFTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 717>:

```

m206.seq
1  ATGTTTCCCC  CCGACAAAAC  CCTTTTCCTC  TGTCTCAGCG  CACTGCTCCT
51  CGCCTCATGC  GGCACGACCT  CCGGCAAACA  CCGCCAACCG  AAACCCAAAC
101  AGACAGTCCG  GCAAATCCAA  GCCGTCCGCA  TCAGCCACAT  CGACCGCACA
151  CAAGGCTCGC  AGGAACTCAT  GCTCCACAGC  CTCGGACTCA  TCGGCACGCC
201  CTACAAATGG  GGCGGCAGCA  GCACCGCAAC  CGGCTTCGAT  TGCAGCGGCA
251  TGATTCAATT  CGTTTACAAr  AACGCCCTCA  ACGTCAAGCT  GCCGCGCACC
301  GCCCGCGACA  TGGCGGCGGC  AAGCCGsAAA  ATCCCCGAcA  GCCGcYTCAA
351  GGCCGCGGAC  CTCGTATTCT  TCAACACCGG  CGGCGCACAC  CGCTACTCAC
401  ACGTCGGACT  CTACATCGGC  AACGGCGAAT  TCATCCATGC  CCCCAGCAGC
451  GGCAAAACCA  TCAAACCGA  AAAACTCTCC  ACACCGTTTT  ACGCCAAAAA
501  CTACCTCGGC  GCACATACTT  TTTTACAGA  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 718; ORF 206>:

```

m206.pep..
1  MFPPDKTLFL  CLSALLLASC  GTTSGKHRQP  KPKQTVRQIQ  AVRISHIDRT
51  QGSQELMLHS  LGLIGTPYKW  GGSSTATGFD  CSGMIQFVYK  NALNVKLPR
101  ARDMAAASRK  IPDSRXKAGD  LVFFNTGGAH  RYSHVGLYIG  NGEFIHAPSS
151  GKTIKTEKLS  TPFYAKNYLG  AHTFFTE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

```

m206/g206
      10      20      30      40      50      60
m206.pep  MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS
          || |||||:|||||
g206      MFSPDKTLFLCLGALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS
          10      20      30      40      50      60

      70      80      90      100     110     120
m206.pep  LGLIGTPYKWGGSSTATGFD CSGMIQFVYKNALNVKLPR TARDMAAASRKIPDSRXKAGD
          |||||:|||||
g206      LGLIGTPYKWGGSSTATGFD CSGMIQLVYKNALNVKLPR TARDMAAASRKIPDSRLKAGD
          70      80      90      100     110     120

      130     140     150     160     170
m206.pep  LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX
          :|||||:|||||
g206      IVFFNTGGAHRYSHVGLYIGNGEFIHAPSGKTIKTEKLSTPFYAKNYLGAHTFFTE
          130     140     150     160     170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 719>:

```

a206.seq
1  ATGTTTCCCC  CCGACAAAAC  CCTTTTCCTC  TGTCTCAGCG  CACTGCTCCT
51  CGCCTCATGC  GGCACGACCT  CCGGCAAACA  CCGCCAACCG  AAACCCAAAC
101  AGACAGTCCG  GCAAATCCAA  GCCGTCCGCA  TCAGCCACAT  CGACCGCACA
151  CAAGGCTCGC  AGGAACTCAT  GCTCCACAGC  CTCGGACTCA  TCGGCACGCC
201  CTACAAATGG  GGCGGCAGCA  GCACCGCAAC  CGGCTTCGAT  TGCAGCGGCA
251  TGATTCAATT  CGTTTACAAA  AACGCCCTCA  ACGTCAAGCT  GCCGCGCACC
301  GCCCGCGACA  TGGCGGCGGC  AAGCCGCAA  ATCCCCGACA  GCCGCCTTAA
351  GGCCGCGGAC  CTCGTATTCT  TCAACACCGG  CGGCGCACAC  CGCTACTCAC
401  ACGTCGGACT  CTATATCGGC  AACGGCGAAT  TCATCCATGC  CCCCAGCAGC
451  GGCAAAACCA  TCAAACCGA  AAAACTCTCC  ACACCGTTTT  ACGCCAAAAA
501  CTACCTCGGC  GCACATACTT  TCTTACAGA  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 720; ORF 206.a>:

```
a206.pep
  1 MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
 51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPRTARDMAAASRKIPDSRXKAGD					
a206	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPRTARDMAAASRKIPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLS TPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLS TPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 721>:

```
g209.seq
  1 atgctgcggc atttaggaaa cgacttcgcc ttgggcgcgt tgtttttcga
 51 tgctgcggtt gatgtgccac tgctgggcga tggtcaggag gttgttgacc
101 acccagtaga gaaccaaacc ggcagggaag aagaagaaca tgacggagaa
151 aaccaacggc atgattttca tcattttcgc ctgcatcggg tcggtcggcg
201 gcgggttcag ataggtttg gcaacatcg ttgccgccat aatgatgggc
251 aggatgtagt aggggtcggc gcggctgagg tcggtaatcc agcccagcca
301 aggtgcctgg cgcaattcta cggaggcgaa caatgccag tacaagccga
351 tgaagacggg gatttgcaac agcataggca gacagccgcc cagcgggttg
401 atttcctcgt cttcgaaaag ctgcatcatc gcttgctgtt gcgccatacg
451 gtgcgtcgccg tatttttctt tgatggtctg cagttcgggt gcggcggcac
501 gcattttcgc catcgaacgg taggaggcgt tggatcaatg atacagtacg
551 gctttgacga tgatggtcaa aacgacgatt gccagcccc agttgccgat
601 aatgtttgtc agttggttca ggagccagaa gagcggcgat gcgaaccagt
651 gtactttacc gtagtctttt gccagttgca ggttgctcgc gatgtttcgc
701 ataacggatg tggtttcgg accggcatac aggttgaccg ccattttcgg
751 ttttgcccc cggttggtga tagcgggttaa
```

This corresponds to the amino acid sequence <SEQ ID 722; ORF 209.ng>:

```
g209.pep
  1 MLRHLGNDFE LGALFFDAAV DVPLLGDGQE VVDHPVENQT GREEEHDGE
 51 NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGQDVVG VGAAEVGNPAQP
101 RCLAQFYGGE QCPVQADEDG DLQQHRQTAA QRVDLFLVEK LHHRLLLRHT
151 VVAVFFFDGL QFGCGGTHFR HRTVGGVGQW IQYGFDDDGQ NDDCPAPVAD
201 NVVQLVQPE ERRCEPVYFT VVFCQLQVVG DVCDNGCGLR TGIQVDRHFR
251 FWPPGWDGSG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 723>:

```
m209.seq
  1 ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGgGCGTT GTTTTTCGAT
 51 GCTGCGGTTG ATGTGCCATT GCTGGGCGAT GGTCAGGAGG TTGTTGACTA
101 CCCAGTACAA TACCAGACCG GCAGGGAAGA AGAAGAACAT GACGGAGAAA
151 ACCAACGGCA TGATTTTCAT CATTTTCGCC TGCATCGGTT CCGTCGGCGG
201 CGGGTTCAGA TAAGTTTGGG CGAACATCGT TGCCGCCATA ATGATGGGCA
251 GGATGTAGTA GGGGTCGGCG CGGCTGAGGT CGGTAATCCA ACCCAGCCAA
```

```

301 GGTGCCTGGC GCAATTCTAC GGAGGCGAAC AATGCCCAAT ACAATCCGAT
351 GAAGACGGGG ATTTGCAACA GCATAGGCAG GCAGCCGCCC AGCGGGTTGA
401 TTTTCTCGTC TGTGTAAAGC TGCATCATCG CCTGTTGTTG CGCCATACGG
451 TCGTCGCCGT ATTTCTCTTT GATGGCTTGC AGTTTGGGTG CGGCGGCACG
501 CATTTTCGCC ATAGAGCGGT AAGAGGCGTT GGTCAATGGA TACAGTACGG
551 CTTTGACGAT GATGGTTAAA ACGATAATCG CCCAGCCCCA GTTGCCGATG
601 ATGTTGTGCA GTTGGTTCAG GAGCCAGAAG AGCGGGGAGG CGAACCAGTG
651 TACTTTGCCG TAGTCTTTGG CCAGTTGCAG GTTGTGCGCG ATGTTTGCGA
701 TGACGGATGT GGTCTGCGGG CCGGCGTAGA GGTGATGGA GGCTTCGgTT
751 TCGCGCCGTT TTGGATGGCG GCTAAAGGCA CGCTGACGCT GGTGCTGTAC
801 AGCTTGTCGT TCGGCGGTTT GATGTCGATG TTGCACTCGC CTGCGGCGCA
851 AACGCTTTGT CTGCCTTTAG GTTGGAGAAT CCAGGTGGAC ATGAAGTGGT
901 GTTCAATCAT GCCGAGCCAG CCGGTCGGGG TTTTGC GGAT GTATTGCGCC
951 TCGGATTTCG CGGATTGGC ATCGTCGTCC AAGTCGAAA AGCTGACTTT
1001 TTGGAAGTTG CCTTCAGGGG TATAA

```

This corresponds to the amino acid sequence <SEQ ID 724; ORF 209>:

```

m209.pep
  1 MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYPVQYQTGREEEHHDGE
 51 NQRHDFHHFRLHRVGRRRVQISLGEHRCRHNDGQDVVGVAEVEGNPTQP
101 RCLAQFYGGEQCPIQSDGDLQQHRQAAAQRVDFLVCVKLHHRLLLRHT
151 VVAVFLFDGLQFGCGGTHFRHRAVRGVGQW IQYGFDDDG*NDNRPAFVAD
201 DVVQLVQEPERGGEPVYFAVVFQQLQVVDVCDGCGCLRAGVEVDGGFG
251 FAPFWMAAKGTLTLVLYSLSLRRLMSMLHSPAAQTLCLPLGWRIQVDMKW
301 CSIMPSQPVGLRMYASDL PDLASSSKSEKLTFWKLPSPV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 209 shows 88.5% identity over a 253 aa overlap with a predicted ORF (ORF 209.ng) from *N. gonorrhoeae*:

```

m209/g209
      10      20      30      40      50      60
m209.pep MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYPVQYQTGREEEHHDGENQRHDFHHFR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g209      MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVENQTGREEEHHDGENQRHDFHHFR
          10      20      30      40      50      60

      70      80      90      100     110     120
m209.pep LHRVGRRRVQISLGEHRCRHNDGQDVVGVAEVEGNPTQPRCLAQFYGGEQCPIQSDG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g209      LHRVGRRRVQISLGEHRCRHNDGQDVVGVAEVEGNPAQPRCLAQFYGGEQCPVQADEG
          70      80      90      100     110     120

      130     140     150     160     170     180
m209.pep DLQQHRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g209      DLQQHRQTAAQRVDFLVFEKLLHHRLLLRHTVVAVFFFDGLQFGCGGTHFRHRTVGGVGQW
          130     140     150     160     170     180

      190     200     210     220     230     240
m209.pep IQYGFDDDGXNDNRPAFVADVVQLVQEPERGGEPVYFAVVFQQLQVVDVCDGCGCLR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g209      IQYGFDDDGQNDPCAPVADNVVQLVQEPERRCEPVYFTVVFQQLQVVDVCDNGCCLR
          190     200     210     220     230     240

      250     260     270     280     290     299
m209.pep AGVEVDGGFGF-APFWMAAKGTLTLVLYSLSLRRLMSMLHSPAAQTLCLPLGWRIQVDMK
          :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||
g209      TGIQVDRHFRFWPPGWDG
          250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 725>:

```

a209.seq
  1 ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGCGT TGTTTTTCGA

```

```

51  TGCTGCGGTT GATGTGCCAT TGCTGGGCGA TGGTCAGGAG GTTGTGATC
101  ACCCAGTACA ATACCAGACC GGCAGGGAAG AAGAAGAACA TGACGGAGAA
151  AACCAAAGGC ATGATTTTCA TCATTTTCGC CTGCATCGGG TCGGTCGGCG
201  GCGGGTTCAG ATAGGTTTGG GCGAACATCG TTGCCGCCAT AATGATGGGC
251  AGGATGTAGT AGGGGTCGGC GCGGCTGAGG TCGGTAATCC AACCAGCCA
301  AGGTGCCTGG CGCAATTCTA CGGAGGCGAA CAATGCCCAA TACAATCCGA
351  TGAAGACGGG GATTTGCAAC AGCATAGGCA GGCAGCCGCC CAGCGGGTTG
401  ATTTTCTCGT CTGTGTAAAG CTGCATCATG GCTTGTGCT GCGCCATACG
451  GTCGTCGCGG TATTTCTCTT TGATGGCTTG CAGTTTGGGC GCGGCGGCAC
501  GCATTTTCGC CATCGAACGG TAAGAGGCGT TGGTCAATGG ATACAGTACG
551  GCTTTGACGA TGATGGTTAA AACGATAATC GCCCAGCCCC AGTTGCCGAT
601  GATGTTGTGC AGTTGGTTCA AAAGCCAAA GAGGGGGGAG GCGAACCAGT
651  GTACTTTGCC GTAGTCTTTG GCCAGTTGCA GGTGTGCGC GATGTTTGC
701  ATAACGGATG TGGTCTGTGG GCCGGCGTAG AGGTTGATGG AGGCTTCGGT
751  TTCGCACCGT TTTGGATAGC GGCTAAAGGC ACGCTGACGC TGGTGTCTGA
801  CAGCTTGTCG TTGCGGCGTT TGATGTGCGT ACGGCAGTCG CCAGCGGCGC
851  AAACGCTTTG TCCGCCTTTG GGTTGGAGGA TCCAGGTGGA CATGAAGTGG
901  TGTTCAATCA TGCCGAGCCA GCCGGTCGGG GTTTTGCGGA TGTATTCGGC
951  CTCGGATTTG CCGGATTTGG CATCGTCGTC CAAGTCGGAG AAGCTGACTT
1001 TTTGGAAGTT GCCTTCAGGG GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 726; ORF 209.a>:

```

a209.pep
1  MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEHHDGENQRHDFHHFR
51  NQRHDFHHFR LHRVGRRRVQIGLGEHRCRHNDGQDVVGVAEVEGNPTQPRCLAQFYGGEQCPIQSD
101  RCLAQFYGGE QCPIQSDG DLQQHRQAAAQRVDFLVCVKLHHGLLLRHTVAVFLFDGLQFGRG
151  VVAVFLFDGL QFGRGGTHFRHRTVRGVGQW IQYGFDDDG*NDNRPAPVAD
201  DVVQLVQKPK EGGGEPVYFAVVFQQLQVVG DVCDNGCGLWAGVEVDGGF
251  FAPFWIAAKG TLTLVLYSLRLRLMSIRQSPAAQTLCPPLGWRIQVDMKW
301  CSIMPSQPVGVLRMYSASDLPDLASSSKSEKLTFWKLPSGVX

```

m209/a209 95.6% identity in 341 aa overlap

```

              10      20      30      40      50      60
m209.pep    MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEHHDGENQRHDFHHFR
              |||
a209         MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEHHDGENQRHDFHHFR
              10      20      30      40      50      60

              70      80      90     100     110     120
m209.pep    LHRVGRRRVQISLGEHRCRHNDGQDVVGVAEVEGNPTQPRCLAQFYGGEQCPIQSDG
              |||
a209         LHRVGRRRVQIGLGEHRCRHNDGQDVVGVAEVEGNPTQPRCLAQFYGGEQCPIQSDG
              70      80      90     100     110     120

              130     140     150     160     170     180
m209.pep    DLQQHRQAAAQRVDFLVCVKLHHGLLLRHTVAVFLFDGLQFGRGGTHFRHRAVRGVGQW
              |||
a209         DLQQHRQAAAQRVDFLVCVKLHHGLLLRHTVAVFLFDGLQFGRGGTHFRHRTVRGVGQW
              130     140     150     160     170     180

              190     200     210     220     230     240
m209.pep    IQYGFDDDGXNDNRPAPVADDVVQLVQEPVEERGGEVYFAVVFQQLQVVGDVCDNGCGLR
              |||
a209         IQYGFDDDGXNDNRPAPVADDVVQLVQKPKEGGEPVYFAVVFQQLQVVGDVCDNGCGLW
              190     200     210     220     230     240

              250     260     270     280     290     300
m209.pep    AGVEVDGGFGFAPFWMAAKGTLTLVLYSLRLRLMSMLHSPAAQTLCLPLGWRIQVDMKW
              |||
a209         AGVEVDGGFGFAPFWIAAKGTLTLVLYSLRLRLMSIRQSPAAQTLCPPLGWRIQVDMKW
              250     260     270     280     290     300

              310     320     330     340
m209.pep    CSIMPSQPVGVLRMYSASDLPDLASSSKSEKLTFWKLPSGVX

```

```

          |||||
a209      CSIMPSQPVGVLRMYSASDLPDLASSKSEKLTFWKLP SGVX
          310      320      330      340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 727>:

```

g211.seq
  1  atgttgcgga ttgctgctgc caatcagttg ggcggtcgaa atgggtcggc
 51  ggtgggaaac ggggtcgata agtttgggcg tgggtgctgat aatcaggttg
101  agtttttggg aggaaacctg attgtagtcg gcgcgtccgg gcgtgccgct
151  gtaacggtag ccgtggcgca attcgagcgt gcgtttgttg tccttcagcg
201  agaagttacc ttctttggcg aagatgatgt tgtcgccgcc gtttttgtcc
251  tgttcgcgca ggaacagggt tttcatgatg ccggattcgg tgtcaaagggt
301  ttcgacgaaa taaacctgcg cgttgcgctt gcccaagtta ttgaactcgc
351  cggtctccac caaagacaat tcctgcttct gttcaaaaat ttcggcatat
401  tcgcggtcgc gcagctctgc ccacggtatc acccaaagct gcatgacggc
451  aatcaggatg gcaaacggca cggcaaactg catgacgggg cgtatccact
501  gtttcaacgc caatccgcag gatag

```

This corresponds to the amino acid sequence <SEQ ID 728; ORF 211.ng>:

```

g211.pep
  1  MLRIAAANQL GGRNGAAVGN GVDKFRGAD NQVEFLEGNL IVVGASGRAA
 51  VTVAVAQFER AFVVLQREVT FFGEDDVVAA VFVLFAQEQV FHDAGFGVKG
101  FDEINPAVAL AQVIELAGFH QRQFLLLQLN FGIFAAALC PRYHPKLHDG
151  NQDGKRHGKL HDGAYPLFQR QSAG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 729>:

```

m211.seq
  1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGGTACGGC
 51  GGTGGGAAAC GGGGTCGATG AGTTTGGGCG TGGTGTGAT AATCAGGTTG
101  AGTTTTTGGG AGGAAACCTG ATTGTAGTCG GCGCGTCCGG GCGTGCCGCT
151  GTAACGGTAG CCGTGGCGCA ATTCGAGCGT GCGTTTGTG TCGTTCAGCG
201  AGAAGTTACC TTCTTTGGCG AAGATGATGT TGTGCGCGCC GTTTTGTGCC
251  TGTTGCGGCA GGAACAGGTT TTTATGATG CCGGATTCGG TATCGAAGGT
301  TTCGACAAAA TAAACCTGC CGTTGCGCTT GCCCAAAGT TTGAACTCGC
351  CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401  TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451  AACCAAAACG GCAAACGGCA CCGCAAAGT CATCACCGG CGTATCCATT
501  GTTTCATGCA CAATCCGCA GATAG

```

This corresponds to the amino acid sequence <SEQ ID 730; ORF 211>:

```

m211.pep
  1  MLRVAAANQL GGRNGTAVGN GVDEFGRGAD NQVEFLEGNL IVVGASGRAA
 51  VTVAVAQFER AFVVVQREVT FFGEDDVVAA VFVLFAQEQV FHDAGFGIEG
101  FDKINPAVAL AQTVELACLH QRQFLLLQD FSVFAAAXLC PRYHPKLHDG
151  NQNGKRHGKL HHRAYPLFQC QSAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 211 shows 89.1% identity over a 174 aa overlap with a predicted ORF (ORF 211.ng) from *N. gonorrhoeae*:

```

m211/g211
          10      20      30      40      50      60
m211.pep  MLRVAAANQLGGRNGTAVGN GVDKFRGADNQVEFLEGNLIVVGASGRAAVTVVAQFER
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g211      MLRIAAANQLGGRNGAAVGN GVDKFRGADNQVEFLEGNLIVVGASGRAAVTVVAQFER
          10      20      30      40      50      60

          70      80      90      100     110     120
m211.pep  AFVVVQREVTFFGEDDVVAAVFVLFAQEQVFHDAGFGIEGFDKINPAVALAQTVELACLH

```



```

401 tcatcggtgc aggcattgcc ggcgcatcga ccgcccacgc cttagcatca
451 cacggcattt cegtaccgt attggaagcc cgaaaagccg ctcaagccgc
501 cagcggaac cggaagggc tgctttacgc caaatctcg ccgcacgaca
551 ccggacagac cgaactgctg cttgccggct acggctacac caaacgcctg
601 ctccggacaca tctgcccga ctccgacact tggggcggca acggcatcat
651 ccacctcaat tacagccgca ccgaacaaca acgcaatcac gaattgggtt
701 tgcaaaaaca ccataaccac ctctaccgca gcatcacgtc tgcagaagcc
751 gaaaaaatcg ccggcatccc gctgaacacg ccctacgccg aaccattatg
801 cggactctac tggcaacacg gcgtatggct caatccgccc gcattcgtcc
851 gcaccctcct cagccatccg ctgatcgaac tatatgaaaa cacaacgtta
901 accggcattt cccacgacgg agaaaagtgg attgcaagca cgccaaacgg
951 cacatttacc gccacacaca tcatctactg caccggcgcg cacagcccct
1001 gctgcccga aaccaacctc gccgccctac ccctcaggca aatacgcgga
1051 caaaccggcc tcacaccgtc caccocgttt tccgaacaac tgcgttgcg
1101 cgttttcaggc gaaagctaca tcagcccgtc gtggcacgga ctgcaactgt
1151 acggcgcgag ttttattccc aacagcagca ataccggatg gaacgaagcc
1201 gaagaagcct caaaccgcca agcattggca caccttaacc ccgcccttgc
1251 cgaatcattg ttt...

```

This corresponds to the amino acid sequence <SEQ ID 734; ORF 212.ng>:

g212.pep (partial)

```

1 MDNLVWDGIP DIRTLDQIR KHAHPLNLIV CLPDNQIPDF QTAQDASDSE
51 CRLKHLRDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKSDKPWFAL PQTSEKKPE HVLVIGAGIA GASTAHALAS
151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTGQTELL LAGYGYTKRL
201 LGHILPDSDT WGGNGIIHLN YSRTEQQRNH ELGLQKHNNH LYRSITSAEA
251 EKIAGIPLNT PYAEPLCGLY WQHGVLNPP AFVRTLLSHP LIELYENTTL
301 TGISHDGEKW IASTPNGTFT ATHIIYCTGA HSPCLPETNL AALPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSNTGWNEA
401 EEASNRQALA HLNPALAESL F...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 735>:

m212.seq

```

1 ATGGACAATC TCGTATGGGA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AGCATCCGC AAACACGCAC CCCCCTCAA CCTGATTATC TGCCTCCCCG
101 ATAATCAGAT TCCGATTTT CAAACCGCAC AAGATGCTTC GGACGCGGAA
151 TGCCGTCTGA AGCACCGTTT GGATCAGGCA ATGCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTCATCGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCAC CACCTGCACG AACATTTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGCAAGCCCG ACAAACCCTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGCGC GGCATATACC GGC GCGGCAA CCGCCCACGC CTTAGCATCA
451 CACGGCATT TCCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCGC
501 CAGCGGCAAC CGCCAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAGAC CGAACTTTTG CTGCGCGGCT ACGGCTACAC CAAACGCTTG
601 CTCGGACACA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACATC TGCAGAAGCC
751 GAAAAAATCG CCGGTATCCC ACTGTCCGTC CCATACGACC ACCCTTCATG
801 CGGACTCTAC TGGCAACACG GCGTATGGCT CAATCCACCC GCATTCTGTC
851 GCACCCTCCT CAACCATCCG CTCATTGGAC TACACGAAGA CACACCCTTG
901 ACCGACATTT CCCACGACGG GGAAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCCT
1001 ACCTACCGGA AACCAACCTC GCCGCCCTGC CTCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TGC GTTGCGC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCACGGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTCCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CAAAAACAC CAAGGGCACG
1301 CCGCCATACG CTGCGACAGC CCCGACCACC TTCCCCTAGT CGGCGCACTC
1351 GGCGACATTG CCGCCATGCG GCAGACCTAC ACCAAACTCG CGCTGGACAA
1401 AAATAACCGC ATCGACACCC CATGCCATA CCTGCCTAAT GCCTACGTCA
1451 ACACCGCGCA CGGCACCCGC GGA CTGCGCCGCA CCGCCCCCAT CTGCGCCGCC

```

1501 GmCAwTGCAG CCCAAATCsT AGGCyTGCCC CATCCCTTTT yAcAAcGCCT
 1551 gCGCCACGCC cTAcACCCCA ACCGCACCAT CATCCGCGCC ATCGTCAGAA
 1601 GGAAGGATCT AACCCCTTAA

This corresponds to the amino acid sequence <SEQ ID 736; ORF 212>:

m212.pep
 1 MDNLVWDGIP DIRTLDQAIR KHAPPLNLII CLPDNQIPDF QTAQDASDAE
 51 CRLKHRLDQA MQCLQFDSIN LIEHILPDVR FWLVPPSRTH HLHEHFHHIS
 101 WQTEAIPQTE SKPDKPWFAL POTSERQKPE HILVIGAGIS GAATAHALAS
 151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL
 201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA
 251 EKIAGIPLSV PYDHPSCGLY WQHGVLNPP AFVRTLLNHP LIGLHEDTPL
 301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL AALPLRQIRG
 351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSHTGWNEA
 401 EEASNRQALA HLNPALES LFAANPNPQKH QGHAAIRCDS PDHPLVLGAL
 451 GDIAAMRQTY TKLALDKNYR IDTPCPYLPN AYVNTAHGTR GLATAPICAA
 501 XXAAQIXGLP HPFXQRLRHA LHPNRTIIRA IVRRKDLTP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 212 shows 92.9% identity over a 421 aa overlap with a predicted ORF (ORF 212.ng) from *N. gonorrhoeae*:

m212/g212

m212.pep	10	20	30	40	50	60
	MDNLVWDGIPDIRTLDQAIRKHAPPLNLIIICLPDNQIPDFQTAQDASDAECRLKHRLDQA					
g212	MDNLVWDGIPDIRTLDQTIRKHAHPLNLIVCLPDNQIPDFQTAQDASDSECRLKHRLDQA					
	10	20	30	40	50	60
m212.pep	70	80	90	100	110	120
	MQCLQFDSINLIEHILPDVRFWLVPPSRTHHLHEHFHHISWQTEAIPQTESKPDKPWFAL					
g212	TQCLQFDSINLIEHILPDVRFWLVPPSRTRRLHEHFHHISWQTEAIPQTESKSDKPWFAL					
	70	80	90	100	110	120
m212.pep	130	140	150	160	170	180
	POTSERQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
g212	PQTSERKKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	130	140	150	160	170	180
m212.pep	190	200	210	220	230	240
	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIIHLNYSRTEQQRNHELGLQKHHNH					
g212	PHDTGQTELLLAGYGYTKRLLGHILPDSDTWGGNGIIHLNYSRTEQQRNHELGLQKHHNH					
	190	200	210	220	230	240
m212.pep	250	260	270	280	290	300
	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGVLNPPAFVRTLLNHP LIGLHEDTPL					
g212	LYRSITSAEAEKIAGIPLNTPYAEPLCGLYWQHGVLNPPAFVRTLLSHPLIELYENTTL					
	250	260	270	280	290	300
m212.pep	310	320	330	340	350	360
	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPLYLPETNL AALPLRQIRGQTGLTPSTPF					
g212	TGISHDGEKWIASTPNGTFTATHIIYCTGAHSPCLPETNL AALPLRQIRGQTGLTPSTPF					
	310	320	330	340	350	360
m212.pep	370	380	390	400	410	420
	SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSHTGWNEAE EASNRQALAHLPALSES L					

490

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 737>:

a212.seq	1	ATGGACAATC	TCGCATGGAA	CGGCATTCCC	GACATCCGCA	CACTCGACCA
	51	AACCATCCGC	AAACACGCAC	ACCCGCTCAA	CCTGATTGTC	TGCTCCCCG
	101	ATAATCAGAT	TCCCAATTTT	CAAACCGCAC	AAGATGCTTC	GGACGCGGAA
	151	TGCCGTCTGA	AGCACCGTTT	GGATCAGGCA	ACCCAGTGCC	TCCAGTTCGA
	201	CAGCATCAAC	CTGATTGAAC	ACATCCTGCC	CGATGTCCGC	TTCTGGCTGG
	251	TTCCCCCTTC	ACGCACCCGC	CGCCTGCACG	AACACTTCCA	CCACATTTC
	301	TGGCAGACCG	AAGCCATCCC	GCAAACCGAA	AGTAAGCCCG	ACAAACCCTG
	351	GT'TTGCAC'T	CCACAAACAT	CCGAACGGCA	AAAACCCGAA	CACATCCTCG
	401	TTATCGGAGC	GGGCATATCC	GGCGCGGGCA	CCGCCCACGC	CTTAGCATCA
	451	TACGGCATTT	CCGTTACCGT	ATTGGAAGCC	CGAAAGCCCG	CCCAAGCCCG
	501	CAGCGGCAAC	CGCTAAGGGC	TGCTCTACGC	CAAAATCTCG	CCGCACGACA
	551	CCGAACAAAC	CGAACTGCTG	CTTGCCGGCT	ACGGCTACAC	CAAACGCCTG
	601	CTCGGACATA	TCCTGCCCGA	ATCCGAAACC	TGGGGCGGCA	ACGGCATCAT
	651	CCACCTCAAT	TACAGCCGCA	CCGAACAACA	ACGCAATCAC	GAAT'TGGGTT
	701	TGCAAAAACA	CCATAACCAC	CTCTACCGCA	GCATCACGCA	GGCAGAAGCC
	751	GAAAAAATCG	CCGGCATCCC	TCTGAACACG	CCCTACGCCG	AACCATATG
	801	CGGACTGTTT	TGGCAGTACG	CGGTATGGCT	CAATCCTCCC	ACATT'CGTCC
	851	GCGCCTCCT	CAGCCATCCG	CTCATTGGAC	TACACGAAGA	CACACCGTTA
	901	ACCGACATTT	CCCACGACGG	GGAAAAGTGG	ATTGCAAGCA	CGCCAAACGG
	951	CACATTTACC	GCCACACACA	TCATCTACTG	CACCGGTGCG	AACAGCCCCT
	1001	ACCTACCCGA	AACCAACCTC	GCCACCCTGC	CCCTCAGGCA	AATACGCGGA
	1051	CAAACCGGCC	TCACACCGTC	CACCCCGTTT	TCCGAACAAC	TGCGTTGCGC
	1101	CGTTTCAGGC	GAAAGCTACA	TCAGCCCGTC	GTGGCACGGG	CTGCACTGCT
	1151	ACGGCGCGAG	TTTTATTCCC	AACAGCAGCC	ATACCGGATG	GAACGAAGCT
	1201	GAAGAAGCCT	CAAACCGCCA	AGCATTGGCA	CACCTTAACC	CCGCCCTTTC
	1251	CGAATCATTG	TTTGCCGCCA	ACCCAAACCC	CCAAAAACAC	CAAGGGCACG
	1301	CCGCCATACG	CTGCGACAGC	CCCGACCACC	TTCCCTAGT	CGGCGCACTC
	1351	GGCGACATTG	CCGCTATGCA	ACAAACTTAC	GCCAAACTCG	CGCTGGACAA
	1401	AAACTATCGC	ATCGATGCCC	CCTGCCCGTA	CCTGCCCAAT	GCCTACGCCA
	1451	ACACCGCCCC	CGGCACACGC	GGGCTTGCCA	CCGCCCCCAT	CTGCGCCGCG
	1501	GCCGTTGCAG	CCGAAATCCT	AGGCTTGCCC	CATCCCTCT	CAAAACGCCT
	1551	GCGCCACGCC	CTACACCCCA	ACCGCGCCAT	CATCCGCGCC	ATCGTCAGAA
	1601	GGAAGGATCT	AACCCCTTAA			

This corresponds to the amino acid sequence <SEQ ID 738; ORF 212.a>:

a212.pcp					
1	MDNLAWNGIP	DIRTLDQ TIR	KHAHPLN LIV	CLPDNQIPNF	QTAQDASDAE
51	CRLKHLRDQA	TQCLQFDSIN	LIEHILPDVR	FWLVPPSRTR	RLHEHFHHIS
101	WQTEAIPQTE	SKPDKPWFAL	PQTSEKQPE	<u>HILVIGAGIS</u>	<u>GAATAHALAS</u>
151	YGISVTVLEA	RKAAQAASGN	RQGLLYAKIS	PHDTEQTELL	LAGYGYTKRL
201	LGHILPESET	WGGNGIIHLN	YSRTEQQRNH	ELGLQKHHNH	LYRSITQAEA
251	EKIAGIPLNT	PYAEPLCGLF	WQYGVWLNPP	TFVRALLSHP	LIGLHEDTPL
301	TDISHDGEKW	IASTPNGTFT	ATHIITYCTGA	NSPYLPETNL	ATLPLRQIRG
351	QTGLTPSTPF	SEQLRCAVSG	ESYISPSWHG	LHCYGASFIP	NSSHTGWNEA
401	EEASNQQALA	HLNPALESSE	FAANPNPQKH	QGHAARICDS	PDHPLPLVGA
451	GDIAAMQQAT	LYALDKNYSR	IDAPCPYLPN	AYANTAHGTR	<u>GLATAPICAA</u>
501	AVAAEILGLP	HPLSKRLRHA	LHPNRAIIRA	IVRRKDLTP*	

m212/a212 93.7% identity in 539 aa overlap

	10	20	30	40	50	60
m212.pep	MDNLVWDGIPDIRTL	DQAI RKHAPPLNLI	ICLPDNI	PDFQTAQDASDAE	CRLK	HRLDQA
a212	MDNLAWNGIPDIRTL	DQTIRKHAHPLNLIV	CLPDNI	PNFQTAQDASDAE	CRLK	HRLDQA

491

	10	20	30	40	50	60
m212.pep	70	80	90	100	110	120
a212	70	80	90	100	110	120
m212.pep	130	140	150	160	170	180
a212	130	140	150	160	170	180
m212.pep	190	200	210	220	230	240
a212	190	200	210	220	230	240
m212.pep	250	260	270	280	290	300
a212	250	260	270	280	290	300
m212.pep	310	320	330	340	350	360
a212	310	320	330	340	350	360
m212.pep	370	380	390	400	410	420
a212	370	380	390	400	410	420
m212.pep	430	440	450	460	470	480
a212	430	440	450	460	470	480
m212.pep	490	500	510	520	530	540
a212	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 739>:

g214.seq

```

1  atgatacaaa agatatgtaa gctatttgtt ttaattgtaa tttttgcaac
51  ttctcccgtt tttgcccttc aaagcgacag cagacggccc atccaaatcg
101 aagccgacca aggttcgctc gatcaagcca accaaaggac cacatttagc
151 ggcaatgtca tcatcagaca gggtacgctc aacatttccg cctcgtgtgt
201 caacgtcaca cgcggcaggc aaagcgcgcg aatccgtgag ggcggaaggt
251 tcgcccgtcc gcttcagcca aacgttggac gggggcaaaag ggacggtgcg
301 cggtcaggca aacaacgtta cctattcctc cgcaggaagc actgtcgctt
351 tgaccggcaa tgcacaaagt cagcgcggcg gcgacgttgc cgaaggtgcg
401 gtcattacct acaacaccaa aaccgaagtc tataccatca acggcagcac
451 gaaatcgggt gcgaaatccg cttccaaaac cggcagggtc agcgtcgtca
501 tccagccttc aagcacacaa aaaaccgaat aaccccgatg ccgtctgaaa
551 cggaaacgca gttcagacgg catttgccga ccgaaatgcc gagaagagat
601 tattga

```

This corresponds to the amino acid sequence <SEQ ID 740; ORF 214.ng>:

g214.pep

```

1  MIQKICKLFV LIVIFATSPA FALQSDSRP IQIEADQGS L DQANQRTTFS
51  GNVIIROGTL NISASCVNVT RGRQRRRIE GGRFARPLQ NVGRGQRDGA
101 RSGKQRYLFL RRKHCRSDRQ CQSAARRRR RRCGHYLQHQ NRSLYHQRQH
151 EIGCEIRFQN RQGQRRHPAF KHTKNRITPM PSETETQFRR HLPTEPRRD
201 Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 741>:

```

m214.seq (partial)
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTCGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCG CCGCCCGCGT
201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGGCGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATT...

```

This corresponds to the amino acid sequence <SEQ ID 742; ORF 214>:

```

m214.pep (partial)
1  MIQKICKLFV LIAFFSASPA FALQSDSRP IQIEADQGS L DQANQSTTFS
51  GNVVIRQTL NISAARVNVT RGRQRRRIE GGRFASPLQ DIGRRQRHGA
101 RTGKQRCLFI CRQHRSLNR* CQSTARRRCR RRCGDYIQHQ NRSLYHQRQH
151 KI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 214 shows 80.3% identity over a 152 aa overlap with a predicted ORF (ORF 214.ng) from *N. gonorrhoeae*:

```

m214/g214

          10      20      30      40      50      60
m214.pep  MIQKICKLFVLIAFFSASPAFALQSDSRPIQIEADQGS LDQANQSTTFSGNVVIRQTL
          |||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
g214       MIQKICKLFVLIVIFATSPA FALQSDSRPIQIEADQGS LDQANQRTTFSGNVIRQTL
          10      20      30      40      50      60

          70      80      90      100     110     120
m214.pep  NISAARVNVTGRQRRRIREGGRFASPLQPDIGRRQRHGARTGKQRCLFICRQHRSLNRX
          |||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|:|:|:|:|:|:
g214       NISASCVNVTRGRQRRRIREGGRFARPLQPNVGRGQRD GARSQRYLFLRRKHCRSDRQ
          70      80      90      100     110     120

          130     140     150
m214.pep  CQSTARRRCRRRCGDYIQHQNRSLYHQRQHKI
          |||:|||||:|:|:|||||:|:|:|||||:|:|:|:|:|:|:|:|:
g214       CQSAARRRRRCRRCGHYLQHQNRSLYHQRQHEIGCEIRFQNRQQRHPAFKHTKNRITPM
          130     140     150     160     170     180

g214       PSETETQFRRHLPTEPRRDY
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 743>:

```

a214.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTCGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCG CCGCCCGCGT
201 CAATGTTACA CGCGGC.GGC AAAGGCGGCG AATCCGTGAG GCGGAAGGTT
251 TCGCCAGTCC GCTTCAGCCA GACATTGGAC GCGGCAAAG GCACGGTGCG
301 CGGACAGGCA AACAACGTTG CTTATTCATC TGCAGGCAGC ACCGTAGTCT

```

```

351 TAACCGGTAA TGCCAAAGTA CAGCGCGGCG GCGATGTCGC CGAAGGTGCG
401 GTGATTACAT ACAACACCAA AACCGAAGTC TATACCATCA GCGGCAGCAC
451 AAAATCCGGC GCAAAATCCG CTTCCAAATC CGGCAGGGTC AGCGTCGTTA
501 TCCAGCCTTC GAGTACGCAA AAATCCGAAT AATCCCAATG CCGTCTGAAA
551 CATAAACCTG GTTCGGACGG CATTGCGCA CCGAAATATT GAAGAGATAT
601 TTATGA

```

This corresponds to the amino acid sequence <SEQ ID 744; ORF 214.a>:

```

a214.pep
  1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
 51 GNVVIRQGT L NISAARVNVT RGXQRRRIRE GGRFASPLQ P DIGRRQRHGA
101 RTGKQRCFL I CRQHRSLNR* CQSTARRRRC RRCGDYIQH Q NRSLYHQ RQH
151 KIRRKIRFQ I RQGQRRYPAF EYAKIRIIP M PSET*TWFG R HLPTEILKRY
201 L*

```

m214/a214 99.3% identity in 152 aa overlap

```

              10      20      30      40      50      60
m214.pep      MIQKICKLFVLIAFFSASPAFALQSDSRQPIQIEADQGS LDQANQSTTFSGNVVIRQGT L
               |||||||
a214           MIQKICKLFVLIAFFSASPAFALQSDSRQPIQIEADQGS LDQANQSTTFSGNVVIRQGT L
               10      20      30      40      50      60

              70      80      90     100     110     120
m214.pep      NISAARVNVTGRGQRRRIREGGRFASPLQPDIGRRQRHGARTGKQRC L FICRQHRSLNRX
               |||||||
a214           NISAARVNVTGRGQRRRIREGGRFASPLQPDIGRRQRHGARTGKQRC L FICRQHRSLNRX
               70      80      90     100     110     120

              130     140     150
m214.pep      CQSTARRRRCRRRCGDYIQHQNRSLYHQ RQH K I
               |||||||
a214           CQSTARRRRCRRRCGDYIQHQNRSLYHQ RQH K I R R K I R F Q I R Q G Q R R Y P A F E Y A K I R I I P M
               130     140     150     160     170     180

a214           PSETXTWFG R HLPTEILKRY L X
               190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 745>:

```

g214-1.seq
  1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATTGTAA TTTTTCGAAC
 51 TTCTCCCGCT TTTGCCCTTC AAAGCGACAG CAGACGGCCC ATCCAATTCG
101 AAGCCGACCA AGGTTCGCTC GATCAAGCCA ACCAAAGTAC CACATTAGC
151 GGCAATGTCA TCATCAGACA GGTACGCTC AACATTTCG CCTCGCGCGT
201 CAACGTCACA CGCGCGGCGA AAGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCCGTCCG CTTAGCCAA ACGTTGGACG GGGGCAAAGG GACGGTGCGC
301 GGTCAGGCAA ACAACGTTAC CTATTCCTCC GCAGGAAGCA CCGTCGTTCT
351 GACCGGCAAT GCCAAAGTGC AGCGGCGCGG CGACGTTGCC GAAGGTGCGG
401 TCATTACCTA CAACACCAA ACCGAAGTCT ATACCATCAA CGGCAGCACG
451 AAATCGGGTG CGAAATCCGC TTCCAAAACC GGCAGGGTCA GCGTCGTCAT
501 CCAGCCTTCA AGCACACAAA AAACCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 746; ORF 214-1.ng>:

```

g214-1.pep
  1 MIQKICKLFV LIVIFATSPA FALQSDSRRP IQIEADQGS L DQANQSTTFS
 51 GNVVIRQGT L NISASRVNVT RGGKGGESVR AEGSPVRFSQ TLDGGKGTVR
101 GQANNVTYSS AGSTVVL TGN AKVQRGGDVA EGAVITYNTK TEVYTINGST
151 KSGAKSASKT GRVSVVIQPS STQKTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 747>:

```

m214-1.seq
  1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
 51 GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTCGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCG CCGCCGCGT

```

```

201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAAA ACCGAACTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAAATCCGC TTCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 748; ORF 214-1>:

m214-1.pep

```

1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISAARVNV T RGGKGGESV R AEGSPVRF S Q TLDGGKGT V R
101 GQANNVAY S S AGSTVVL T GN AKVQRGDV A EGAVITYN T K TEVYTISG S T
151 KSGAKSAS K S GRVSVVIQ P S STQKSE*

```

m214-1/g214-1 93.8% identity in 176 aa overlap

```

          10      20      30      40      50      60
m214-1.pep MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g214-1      MIQKICKLFV LIVIFATSPAFALQSDSRRP IQIEADQGS L DQANQSTTFS GNVII RQGT L
          10      20      30      40      50      60

          70      80      90     100     110     120
m214-1.pep NISAARVNV TRGGKGGESV R AEGSPVRF S Q TLDGGKGT V R GQANNVAY S S AGSTVVL T GN
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g214-1      NISASRVNV TRGGKGGESV R AEGSPVRF S Q TLDGGKGT V R GQANNV T Y S S AGSTVVL T GN
          70      80      90     100     110     120

          130     140     150     160     170
m214-1.pep AKVQRGDV A EGAVITYN T K TEVYTISG S T KSGAKSAS K S GRVSVVIQ P S STQKSE X
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g214-1      AKVQRGDV A EGAVITYN T K TEVY T ING S T KSGAKSAS K T GRVSVVIQ P S STQKTE X
          130     140     150     160     170

```

g214-1/p38685

sp|P38685|YHBN_ECOLI 17.3 KD PROTEIN IN MURA-RPON INTERGENIC REGION PRECURSOR (ORF185)
>gi|551336 (U12684) orf185 [Escherichia coli] >gi|606139 (U18997) ORF_ol85 [Escherichia coli]
>gi|1789592 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 185
Score = 97.1 bits (238), Expect = 6e-20
Identities = 57/126 (45%), Positives = 74/126 (58%), Gaps = 3/126 (2%)

Query: 19 PAFALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L NISAARVNV TR--GGKGG 76
PAFA+ D+ QPI IE+DQ SLD TF+GNV++ QGT+ I+A +V VTR G +G
Sbjct: 24 PAFAVTGTDTQPIHIESDQQLDMQGNVNVFTGNVIVTQGTIKINADKVVVTRPGGEQ GK 83

Query: 77 ESVRAEGSPVRF S Q TLDGGKGT V R GQANNVAY S S AGSTVVL T GNAKVQRGDV A EGAVIT 136
E + G P F Q D GK V G A+ + Y A VVLTGNA +Q+ +G IT
Sbjct: 84 EVIDGYGKPATFYQM QDN GK -PVEGHASQMHYELAKDFVVL TGNAYLQQVDSNIKGDKIT 142

Query: 137 YNTKTE 142
Y K +
Sbjct: 143 YLVKEQ 148

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 749>:

a214-1.seq

```

1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTCGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCCG CCGCCCGCGT
201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAAA ACCGAACTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAAATCCGC TTCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 750; ORF 214-1.a>:

a214-1.pep

```

1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS

```



```

51  GNVVIRQCTL NISAARVNVT RGGKGGESVR AEGSPVRFSQ TLDGGKGTVR
101  GQANNVAYSS AGSTVVL TGN AKVQRGGDVA EGAVITYNTK TEVYTISGST
151  KSGAKSASKS GRVSVVIQPS STQKSE*

```

a214-1/m214-1 100.0% identity in 176 aa overlap

```

          10      20      30      40      50      60
a214-1.pep  MIQKICKLVLIAFFSASPALQSDSRQPIQIEADQGS LDQANQSTTFSGNVVIRQCTL
          |||||
m214-1      MIQKICKLVLIAFFSASPALQSDSRQPIQIEADQGS LDQANQSTTFSGNVVIRQCTL
          10      20      30      40      50      60

          70      80      90     100     110     120
a214-1.pep  NISAARVNVT RGGKGGESVRAEGSPVRFSQ TLDGGKGTVRGQANNVAYSSAGSTVVL TGN
          |||||
m214-1      NISAARVNVT RGGKGGESVRAEGSPVRFSQ TLDGGKGTVRGQANNVAYSSAGSTVVL TGN
          70      80      90     100     110     120

          130     140     150     160     170
a214-1.pep  AKVQRGGDVAEGAVITYNTKTEVYTISGSTKSGAKSASKSGRVSVVIQPSSTQKSEX
          |||||
m214-1      AKVQRGGDVAEGAVITYNTKTEVYTISGSTKSGAKSASKSGRVSVVIQPSSTQKSEX
          130     140     150     160     170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 751>:

```

g215.seq
1   atgaaagtaa gatggcggtta cgggaattgcg ttccattga tattggcggt
51  tgccttgggc agcctgtcgg catggttggg ccgtatcagc gaagtcgaaa
101 tcgaggaagt caggtcfaat cccgacgaac ctcaatacac aatggacggc
151 ttggacggaa ggcggtttga cgaacagggg tacttgaaag aacatttgag
201 cgcgaaaggt gcgaaacagt ttcccgaaaa cagcgacatc cattttgatt
251 cgccgcatct cgtgttcttc caagaaggca ggctgttga cgaagtcggc
301 agcgatgaag ccgtttacca taccgaaaac aaacaggttc ttttataaaa
351 caacgttgtg ctgacaaaaa ccgccgacgg caggcggcag gcgggtaaag
401 tcgaaaccga aaaactgcac gtcgataccg aatctcaata tgcccaaacc
451 gatacgctg tcagtttcca atatggcgcg tcgcacggtc aggcggcgcg
501 tatgacctac aaccacaaaa caggcatgtt gaacttctca tctaaagtga
551 aagccgcgat ttatgataca aaagatatgt aa

```

This corresponds to the amino acid sequence <SEQ ID 752; ORF 215.ng>:

```

g215.pep
1   MKVRWRYGIA FPLILAVALG SLSAWLGRIS EVEIEEVR LN PDEPQYTM DG
51  LDGRRFDEQ GYLKEHLSAKG AKQFPENSDI HFDSPLVFF QEGRLLYE VG
101 SDEAVYHTEN KQVLFKNNVV LTKTADGRRQ AGKVETELH VDTESQYA QT
151 DTPVSFQYGA SHGQAGGMTY NHKTGMLNFS SKVKAAYD T KDM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 753>:

```

m215.seq (partial)
1   ..AGCCTGTCGG CATGGTTGGG TCGTATCAGC GAAGTCGAGA TTGAAGAAGT
51  CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACAGC TTGGACGGCA
101 GGCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTGAG CGCGAAGGGC
151 GCGAAACAGT TTCCGGAAG CAGCGACATC CATTTTGATT CGCCGCATCT
201 CGTGTCTTTC CAAGAAGGCA GGTGTGTGTA CGAAGTCGGC AGCGACGAAG
251 CCGTTTACCA TACCGAAAAC AAACAGGTTT TTTTAAAAA CAACGTGTG
301 CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG TTGAAGCCGA
351 AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAACC GATACGCCTG
401 CAGTTTCCA ATATGGTGCA TCGCACGGTC AGGCGGGCGG CATGACTTAC
451 GACCACAwWA CAGGCATGTT GAACCTCTCA TCTAAAGTGA AAGCCACGAT
501 TTATGATACA AAAGATATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 754; ORF 215>:

```

m215.pep (partial)
1   ..SLSAWLGRIS EVEIEEVR LN PDEPQYTM DS LDGRRFDEQ GYLKEHLSAKG
51  AKQFPESDI HFDSPLVFF QEGRLLYE VG SDEAVYHTEN KQVLFKNNVV
101 LTKTADGKRQ AGKVEAEKLH VDTESQYA QT DTPVSFQYGA SHGQAGGMTY

```

496

151 DHXTGMLNFS SKVKATIYDT KDM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

m215/g215

		10	20	30	40
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG			
		:			
g215	MKVRWRYGIAFPLILAV	10	20	30	40
		50	60	70	80
m215.pep	YLKEHLSAKGAKQFP	50	60	70	80
		:			
g215	YLKEHLSAKGAKQFP	70	80	90	100
		110	120	130	140
m215.pep	LTKTADGKRQAGKVE	110	120	130	140
		:			
g215	LTKTADGRRQAGKVE	130	140	150	160
		170	180	190	200
m215.pep	SKVKATIYDTKDMX	170	180	190	200
		:			
g215	SKVKAAYIDTKDM	190	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

a215.seq	1	ATGAAAGTAA	GATGGCGGTA	CGGAATTGCG	TTCCCATTGA	TATTGGCGGT
	51	TGCCTTGGGC	AGCCTGTCGG	CATGGTTGGG	ACGCATCAGC	GAAGTCGAGA
	101	TTGAAGAAGT	CAGGCTCAAT	CCCGACGAAC	CGCAATACAC	AATGGACGGA
	151	TTGGATGGCA	GGCGTTTGA	CGAACAGGGA	TACTTGAAAG	AACATTTGAG
	201	TTCGAAGGGC	GCGAAACAGT	TTCCCGAAAG	CAGCGACATT	CATTTGCGACT
	251	CACCGCATCT	CGTGTCTTC	CAAGAAGGCA	GGTGTGTGA	CGAAGTCGGC
	301	AGCGATGAAG	CCGTTTACCA	TACCGAAAAC	AAACAGGTTT	TTTTTAAAAA
	351	CAACGTTGTG	CTGACCAAAA	CCGCCGACGG	CAAACGGCAG	GCGGGTAAAG
	401	TTGAAGCCGA	AAAGCTGCAC	GTCGATACCG	AATCTCAATA	TGCCCCAAACC
	451	GATACGCCTG	TCAGTTTCCA	ATATGGTGCA	TCGCACGGTC	AGGCGGGCGG
	501	CATGACTTAC	GACCACAAA	CAGGCATGTT	GAACTTCTCA	TCTAAAGTGA
	551	AAGCCACGAT	TTATGATACA	AAAGATATGT	AA	

This corresponds to the amino acid sequence <SEQ ID 756; ORF 215.a>:

a215.pep	1	MKVRWRYGIA	FPLILAV	ALG	SLSAWLGRIS	EVEIEEVRLN	PDEPQYTM
	51	LDGRRFDEQG	YLKEHLSSKG	AKQFPSSDI	HFDSPHLVFF	QEGRLLYEVG	
	101	SDEAVYHTEN	KQVLFKNNVV	LTKTADGKRQ	AGKVEAEKLH	VDTESQYAQT	
	151	DTPVSFQYGA	SHGQAGGMTY	DHKTGMLNFS	SKVKATIYDT	KDM*	

m215/a215 98.3% identity in 173 aa overlap

		10	20	30	40
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG			
		:			
a215	MKVRWRYGIAFPLILAV	10	20	30	40
		50	60	70	80
m215.pep	YLKEHLSAKGAKQFP	50	60	70	80
		:			
		90	100	110	120

```

a215      |||||:|||||
          YLKEHLSSKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
          70      80      90      100      110      120

          110      120      130      140      150      160
m215.pep  LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHTGMLNFS
          |||||
a215      LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHTGMLNFS
          130      140      150      160      170      180

          170
m215.pep  SKVKATIYDTKDMX
          |||||
a215      SKVKATIYDTKDMX
          190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 757>:

g216.seq (partial)

```

1  ..atgatatcga tttcgagctc ggtacccagc gacgaaatca ccgccatcat
51  ccccgcactc aaacgcaaag acattaccct cgtctgcatc accgcccgcg
101 ccgattcaac catggcgcg ccatgccgata tccacatcac cgcacgggtt
151 tcgcaagaag cctgcccgtt ggggcttgcc ccgaccacca gcaccaccgc
201 cgttatggct ttgggcgacg cgttggcggt cgtcctgctg cgcgcccgcg
251 cgttcacgcc cgacgacttc gccttgatcc accctgccgg cagcctcggc
301 aaacgcctgc ttttgcgctg tgccgacatt atgcacaaag gcggcggcct
351 gcccgccgct cgactcggca cgcccttgaa aggagccatc gtcagcatga
401 gcgagaaagg tttgggcatg tgggcgggaa cggacgggca aaggctgtct
451 gaaaggcctt tttactga

```

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

g216.pep (partial)

```

1  ..MISISSVPS DEITAIIPAL KRKDITLVC I TARP DSTMAR HADIHITASV
51  SQEACPLGLA PTTSTTAVMA LGDALAVLL RARAFTPDDF ALIHPAGSLG
101 KRLLLRVADI MHKGGGLPAV RLGTPLKGAI VSMSEKGLGM WAGTDGQRLS
151 ERPFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 759>:

m216.seq

```

1  ATGGCAATGG CAGAAAACGG AAAATATCTC GACTGGGCAC GCGAAGTGTT
51  GCACGCCGAA GCGGAAGGCT TGC GCGAAAT TGCAGCGGAA TTGsACAAAA
101 ACTTCGTCCT TGC GGCAGAC GCGTTGTTGC ACTGCAAGGG CAGGGTCGTT
151 ATCACGGGCA TGGTCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 TATGGCCTCG ACCGGCACGC CTGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGgCGA TTGGGGTATG ATTGTGGACA rCGACGTGGT CGTCGCGATT
301 TCCAATTCCG GCGAAAGCGA CGAAATCGCC GCCATCATCC CCGCACTCAA
351 ACGCAAAGAC ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACGCGG TCATGGCTTT
501 GGGCGATGCG TTGGCGGTCG TCctGCTGCG CgcACGCGCG TTCACGCCCC
551 ACGATTTTCG CTTGAGCCAT CCTGCCGGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCCTGC CTGCCGTCGG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGCCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTG CTGGCGGCAC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 760; ORF 216>:

m216.pep

```

1  MAMAENGKYL DWAREVLHAE AEGLREIAAE LXKNFVLAAD ALLHCKGRVV

```

```

51  ITGMVKSGHI GRKMAATMAS TGTPAFFVHP AEAHGDLM IVDXDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAPPTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRLL
201 LRVADIMHKG GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQGRLLKGVF
251 TDGDLRRLFQ ECDNFTGLSI DEVMHHPKT ISAERLATEA LKVMQANHVN
301 GLLVTDADGV LIGALNMHDL LAARIV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 216 shows 91.8% identity over a 147 aa overlap with a predicted ORF (ORF 216.ng) from *N. gonorrhoeae*:

m216/g216

```

              70      80      90      100      110      120
m216.pep      TMASTGTPAFFVHPAEAAHGDLMIVDXDVVVAISNSGESDEIAAIIPALKRKDITLVC
g216                                     :::|||:|||||||
              10      20      30
              130     140     150     160     170     180
m216.pep      TARPDMSTARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPD
g216           |||||||:|||||||
              40      50      60      70      80      90
              190     200     210     220     230     240
m216.pep      ALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVTDGQGR
g216           |||||||:|||||||
              100     110     120     130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 761>:

a216.seq

```

1  ATGGCGATGG CAGGAAACGA AAAATATCTT GATTGGGCAC GCGAAGTGTT
51 GCACACCGAA GCGGAAGGCT TGCGCGAAAT TGCGGCGGAT TTGGACGAAA
101 ACTTCGCCCT TGCGGCGGAC GCGTTGTGTC ACTGCAAAGG CAGGGTCGTT
151 ATCACGGGCA TGGGCAAGTC GGGACATATC GGGCGCAAAA TGCGGCAAC
201 CATGGCCTCG ACCGGCACGC CCGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGGCGA TTTGGGCATG ATTGTGGACA ACGACGTGGT CGTCGCGATT
301 TCCAATTCCG GTGAAAGCGA CGAAATCGCC GCCATCATCC CCGCGCTCAA
351 ACGCAAAGAT ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACGCGCG TTATGGCTTT
501 GGGCGATGCG TTGGCGGTTG TCCTGCTGCG CGCCCGCGCG TTCACGCCCC
551 ACGACTTCGC CTTGAGCCAC CCTGCCGCGA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GCGGCGCTGC CTGCCGTCCG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GGCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGCCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAAGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTT TTGGCGCGCG GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 762; ORF 216.a>:

a216.pep

```

1  MAMAGNEKYL DWAREVLHTE AEGLREIAAD LDENFALAAD ALLHCKGRV
51  ITGMKSGHI GRKMAATMAS TGTPAFFVHP AEAHGDLM IVDNDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAPPTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRLL
201 LRVADIMHKG GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQGRLLKGVF
251 TDGDLRRLFQ ECDNFTGLSI DEVMHHPKT ISAERLATEA LKVMQANHVN

```

151 DHXTGMLNFS SKVKATIYDT KDM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

m215/g215

		10	20	30	40
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG			
		:			
g215	MKVRWRYGIAFPLILAVALG	SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG			
	10	20	30	40	50
	50	60	70	80	90
m215.pep	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQEG	RLLYE	VGSD
	:				
g215	YLKEHLSAKGAKQFP	ENS	DIHFDS	PHLVFFQEG	RLLYE
	70	80	90	100	110
	110	120	130	140	150
m215.pep	LTKTADGKRQAGK	VEAEKLH	VDTESQ	YAQTD	TPV
	: :				
g215	LTKTADGRRQAGK	VET	TEKLH	VDTESQ	YAQTD
	130	140	150	160	170
	170				
m215.pep	SKVKATIYDTKDMX				
	:				
g215	SKVKA	AIYDTKDM			
	190				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

a215.seq

1	ATGAAAGTAA	GATGGCGGTA	CGGAATTGCG	TTCCCATTTGA	TATTGGCGGT
51	TGCCCTTGGGC	AGCCTGTCGG	CATGGTTGGG	ACGCATCAGC	GAAGTCGAGA
101	TTGAAGAAGT	CAGGCTCAAT	CCCGACGAAC	CGCAATACAC	AATGGACGGA
151	TTGGATGGCA	GGCGGTTTGA	CGAACAGGGA	TACTTGAAAG	AACATTTGAG
201	TTCGAAGGGC	GCGAAACAGT	TTCCCGAAAG	CAGCGACATT	CATTTGCACT
251	CACCGCATCT	CGTGTCTCTC	CAAGAAGGCA	GGTTGTGTGA	CGAAGTCGGC
301	AGCGATGAAG	CCGTTTACCA	TACCGAAAAC	AAACAGGTTT	TTTTTAAAAA
351	CAACGTTGTG	CTGACCAAAA	CCGCCGACGG	CAAACGGCAG	GCGGGTAAAG
401	TTGAAGCCGA	AAAGCTGCAC	GTCGATACCG	AATCTCAATA	TGCCCAAACC
451	GATACGCCCTG	TCAGTTTCCA	ATATGGTGCA	TCGCACGGTC	AGGCGGGCGG
501	CATGACTTAC	GACCACAAA	CAGGCATGTT	GAACTTCTCA	TCTAAAGTGA
551	AAGCCACGAT	TTATGATACA	AAAGATATGT	AA	

This corresponds to the amino acid sequence <SEQ ID 756; ORF 215.a>:

a215.pep

1	MKVRWRYGIA	FPLILAVALG	SLSAWLGRIS	EVEIEEVRLN	PDEPQYTM
51	LDGRRFDEQG	YLKEHLSSKG	AKQFPSSDI	HFDS	PHLVFF
101	SDEAVYHTEN	KQVLFKNNVV	LTKTADGKRQ	AGKVEAEKLH	VDTESQY
151	DTPVSFQYGA	SHGQAGGMTY	DHKTGMLNFS	SKVKATIYDT	KDM*

m215/a215 98.3% identity in 173 aa overlap

		10	20	30	40
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG			
		:			
a215	MKVRWRYGIAFPLILAVALG	SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG			
	10	20	30	40	50
	50	60	70	80	90
m215.pep	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQEG	RLLYE	VGSD
	:				

```

|||||:|||||
a215      YLKEHLSSKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
              70      80      90      100      110      120

              110      120      130      140      150      160
m215.pep  LTKTADGKRQAGKVEAEKLVHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHXTGMLNFS
|||||
a215      LTKTADGKRQAGKVEAEKLVHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHXTGMLNFS
              130      140      150      160      170      180

              170
m215.pep  SKVKATIIYDTKDMX
|||||
a215      SKVKATIIYDTKDMX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 757>:

```

g216.seq (partial)
1      ..atgatatcga ttctgagctc ggtaccacgc gacgaaatca ccgccatcat
51     ccccgactc aaacgcgaaag acattaccct cgtctgcatc accgcccgcg
101    ccgattcaac catggcgcgcg catgccgata tccacatcac cgcacgggtt
151    tcgcaagaag cctgcccgtt ggggcttgcc ccgaccacca gcaccaccgc
201    cgttatggct ttgggcgacg cgttggcggt cgtcctgctg cgcgcccgcg
251    cgttcacgcc cgacgacttc gccttgatcc accctgccgg cagcctcggc
301    aaacgcctgc ttttgcgcggt tgccgacatt atgcacaaag gcggcggcct
351    gcccgccgct cgactcggca cgcccttgaa aggagccatc gtcagcatga
401    gcgagaaaagg tttgggcatg tgggcgggaa cggacgggca aaggctgtct
451    gaaaggcctt tttactga

```

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

```

g216.pep (partial)
1      ..MISISSVPS DEITAIIPAL KRKDITLVC I TARPDMAR HADIIHITASV
51     SQEACPLGLA PTTSTTAVMA LGDALAVVLL RARAFTPDDF ALIHPAGSLG
101    KRLLLRVADI MHKGGGLPAV RLGTPLKGAI VSMSEKGLGM WAGTDGQRLS
151    ERPFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 759>:

```

m216.seq
1      ATGGCAATGG CAGAAAACGG AAAATATCTC GACTGGGCAC GCGAAGTGTT
51     GCACGCCGAA GCGGAAGGCT TGCGCGAAAT TGCAGCGGAA TTGsACAAAA
101    ACTTCGTCCT TGCGGCAGAC GCGTTGTTGC ACTGCAAGGG CAGGGTCGTT
151    ATCACGGGCA TGGTCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201    TATGGCCTCG ACCGGCACGC CTGCGTTTTT CGTCCACCCT GCGGAAGCGG
251    CACACGCGA TTTGGGTATG ATTGTGGACA rCGACGTGGT CGTCGCGATT
301    TCCAATTCCG GCGAAAGCGA CGAAATCGCC GCCATCATCC CCGCACTCAA
351    ACGCAAAGAC ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401    TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451    TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACCGCCG TCATGGCTTT
501    GGGCGATGCG TTGGCGGTGCG TCCTGCTGCG CgcACGCGCG TTCACGCCCG
551    ACGATTTTCG CTTGAGCCAT CCTGCCGGA GCTCGGCAA ACGCCTACTT
601    TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCCTGC CTGCCGTCG
651    ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701    TGGGCATGTT GGCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751    ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTTACCGG
801    TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAACC ATCTCCGCCG
851    AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901    GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951    GCACGACCTG CTGGCGGCAC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 760; ORF 216>:

```

m216.pep
1      MAMAENGKYL DWAREVLHAE AEGLREIAAE LXKNFVLAAD ALLHCKGRVV

```

ORF 216 shows 91.8% identity over a 147 aa overlap with a predicted ORF (ORF 216.ng) from *N. gonorrhoeae*:

	70	80	90	100	110	120
m216.pep	TMASTGTPAFFVHPAEAAHGDLGMIVDXDVVVAISNSGESDEIAAIIIPALKRKDITLVC					
	:: : :					
g216	MISISSSVPSDEITAIIPALKRKDITLVC					
	10	20	30			
	130	140	150	160	170	180
m216.pep	TARPDMSTARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPDDF					
	:					
g216	TARPDMSTARHADIHITASVSQEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPDDF					
	40	50	60	70	80	90
	190	200	210	220	230	240
m216.pep	ALSHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLKEAIVSMSEKGLGMLAVTDGQGR					
g216	ALIHAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLKGAIVSMSEKGLGMWAGTDGQRLS					
	100	110	120	130	140	150

1	ATGGCGATGG	CAGGAAACGA	AAAATATCTT	GATTGGGCAC	GCGAAGTGT
51	GCACACCGAA	GCGGAAGGCT	TGCGCGAAAT	TGCGGCGGAT	TTGGACGAAA
101	ACTTCG CCT	TGCGGCGGAC	GCGTTGTTGC	ACTGCAAAGG	CAGGTCGTT
151	ATCACGGGCA	TGGGCAAGTC	GGGACATATC	GGGCGCAAA	TGGCGGCAAC
201	CATGGCCTCG	ACCGGCACGC	CGCGCTTTT	CGTCCACCTT	CGGGAAGCGG
251	CACACGGCGA	TTTGGGATG	ATTGTGTGTA	ACGACGTGGT	CGTCGCGATT
301	TCCAATTCCG	GTGAAAGCGA	CGAAATCGCC	GCCATCATCC	CCGCGCTCAA
351	ACGCAAAGAT	ATCACGCTTG	TCTGCATCAC	CGCCCGCCCC	GATTCAACCA
401	TGGCGCGCCA	TGCCGACATC	CACATCACGG	CGTCGTTTTC	CAAAGAAGCC
451	TGCCCGCTGG	GGCTTGCCCC	GACCACCAGC	ACCACCGCCG	TTATGGCTTT
501	GGGCGATGCG	TTGGCGGTTG	TCCTGCTGCG	CGCCCGCGCG	TTACAGCCCG
551	ACGACTTTCG	CTTGAGCCAC	CCTGCCGGCA	GCGTCGGCAA	ACGCTTACTT
601	TTGCGCGTTG	CCGACATTAT	GCACAAAGGC	GGCCGCTGCT	CTCCGCTCCG
651	ACTCGGCACG	CCCTTGAAAG	AAGCCATCGT	CAGCATGAGT	GAAAAAGGGC
701	TGGGCATGTT	GGCGGTAACG	GACGGGCAAG	GCCGCTGAA	AGGCGTATTC
751	ACCGACGCG	ATTTGCGCG	CCTGTTTCAA	GAATGCGACA	ATTTTACCGG
801	TCTTTCGATA	GACGAAGTCA	TGCATACGCA	TCCTAAAAAC	ATCTCCGCCG
851	AACGTCCTCG	CACCGAAGCG	CTGAAAGTCA	TGCAGGCAAA	CCATGTGAAC
901	GGGCTTCTGG	TTACCGATGC	AGATGGCGTG	CTGATCGGCG	CGCTGAATAT
951	GCACGACCTT	TTGGCGGCGC	GGATTGTATA	G	

1	MAMAGNEKYL	DWAREVLHTE	AEGLREIAAD	LDEFNLAAD	ALLHCKGRVV
51	ITGMGKSGHI	GRKMAATMAS	TGTPAFFVHP	AEAAHGDLGM	IVDNDVVVAI
101	SNSGESEDEIA	AIIPALKRKD	ITLVCITARP	DSTMARHADI	HITASVSKEA
151	CPLGLAPTTS	<u>TTAVMALGDA</u>	LAVVLLRARA	FTPDDFALSH	PAGSLGKRLL
201	LRVADIMHKG	GGLPAVRGLT	PLKEAIVSMS	EKGLGMLAVT	DGQGRKGVF
251	TDGDLRLRFO	ECNDNETGLSI	DEVHMTHPKT	ISAERLATEA	LKVMQANHVN

301 GLLVTDADGV LIGALNMHDL LAARIV*

m216/a216 97.2% identity in 326 aa overlap

	10	20	30	40	50	60
m216.pep	MAMAENKYL	DWAREVLHAE	AEGLREIAAE	LXKNFVLAAD	ALLHCKGRVV	ITGMVKS
a216	MAMAGNEKYL	DWAREVLHTE	AEGLREIAAD	LDENFALAAD	ALLHCKGRVV	ITGMGKS
	10	20	30	40	50	60
	70	80	90	100	110	120
m216.pep	GRKMAATMA	STGTPAFFV	HPAEAAHGD	LGMIVDXDV	VVAISNSGE	SDEIAAII
a216	GRKMAATMA	STGTPAFFV	HPAEAAHGD	LGMIVDNDV	VVAISNSGE	SDEIAAII
	70	80	90	100	110	120
	130	140	150	160	170	180
m216.pep	ITLVCITAR	PDSTMARHA	DIHITASVS	KEACPLGLA	PTTSTTAV	MALGDALAV
a216	ITLVCITAR	PDSTMARHA	DIHITASVS	KEACPLGLA	PTTSTTAV	MALGDALAV
	130	140	150	160	170	180
	190	200	210	220	230	240
m216.pep	FTPDDFALS	HPAGSLGKR	LLLRVADIM	HKGGGLPAV	RLGTPLKEA	IVSMSEKGL
a216	FTPDDFALS	HPAGSLGKR	LLLRVADIM	HKGGGLPAV	RLGTPLKEA	IVSMSEKGL
	190	200	210	220	230	240
	250	260	270	280	290	300
m216.pep	DGQGRCLK	GVFTDGD	LRLRFQEC	DNFTGLSI	DEVMTHTPK	TISAERLATE
a216	DGQGRCLK	GVFTDGD	LRLRFQEC	DNFTGLSI	DEVMTHTPK	TISAERLATE
	250	260	270	280	290	300
	310	320				
m216.pep	GLLVTDADG	VLIGALNMH	DLLAARIVX			
a216	GLLVTDADG	VLIGALNMH	DLLAARIVX			
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 763>:

g217.seq

```

1  atggcgatg acggtttgtt gcggaactg tccgaaaaac ccagccaaag
51  tgcctctctt ctgccatttg acccattcgt ttctgaggtt ttggactgcc
101 ttttggtcat cgggcccggc ttgaaacaat gtttcaagca aatcccggca
151 acgcgccacc cattcgccga ccgtcgagg ttgccgcat atccgggcaa
201 tatccgacag ggtttcgagg aaggcgcaa aacgtccgaa catggcggtt
251 tgattcacgt cggcatacca cgcgctgaca tcctgccaca tcgggttgcc
301 gccttcgggc agcatccagc ccaatatcat acggtctgcc gcctgcttcc
351 aggtaaacag ctgatccgtg ccgccgcgca tttctccgtc caatccccaa
401 tggacgttca aatcggcaac catatcgtgc aaaagcggca aatcgtcccc
451 ggtcagtcgc aaacggcgca acacggggcg ggtttccaaa agcgcgagca
501 ctttgccgac ttcaaaacgg ctttccagca agtcggacac gactccaac
551 gcataaaaaa acggttgccg gcggtgatt ttcacgtccg aaacggaata
601 cggcaatgcc tgcgcgccgg gttgcgcctg tccgaacacg gcttccataa
651 aaggcgata gggttcgata ttcgggggta a

```

This corresponds to the amino acid sequence <SEQ ID 764; ORF 217.ng>:

g217.pep..

```

1  MADDGLLRQL SEKPSQSALF LPFDPFVFEV LDCLLVIGPG LKQCFKQIPA
51  TRHPFADRRR LPPYPGNIRQ GFEEGGKTSE HGGLIHVGIP RADILPHRVA
101 AFGQHPAQYH TVCRLLPGKQ LIRAAAHFSV QSPMDVQIGN HIVQKRQIVP
151 QQSETAQHGR GFQKREHFAD FKTAFAQVGH ALQRIKKRLP AADFHVNRGI

```


201 RQCLRAGLRL SEHGFKRRI GFDIRG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 765>:

m217.seq

```

1  ATGGCGGATG ACGGTGTGCG GCGGCAACTG TCCGAAAAAT TGCGCCAATT
51  CGGTTTCCGC CTrCCATTG ACCCATTCGT TTTCAAGGTT TTGGACTGAC
101 TTTTGGTCAT CGGCTTCAGC TTGGAACAAT GTTTCAAGCA AATCCCGGCA
151 ACGCGCCACC CATTGCGCGA CCGTTGCGGG CTGCGGCCAT ATCCGTACAA
201 TATCCGTCAG GGTTCGAGG AAGGCGGCAA AACGTCCGAA CATGGCGGTT
251 TGATTACAGT CGGCATACCA CGCGCTGACA TCCTGCCACA TCGGATTGCC
301 GCCTTTGGGC AGCATCCAGC CCAATATCAT GCGTCTACC GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCCGCGCA TTTCTCCGTC CAAACCCAG
401 TGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGTA AATCGTCCTC
451 AGTCAGTCCG AAACGGCGCA ACACGGGCGC GGTTTCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA GCGGTGGCG GCGGCTGATT TTCACGTCTG ACACGGAATA
601 CGGCAATGCC TGCGACCgG GctGCGCCTG TCCGAACACG GCTTCGATAA
651 AAGCGGTATA GGATTCGATA TTCGGGGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 766; ORF 217>:

m217.pep

```

1  MADDGVRRL SGKLRQFGR LPFDPFVFKV LDXLLVIGFS LEQCFKQIPA
51  TRHPFADRCG LPPYPYNIQ GFEEGGKTSE HGGLIHVGIP RADILPHRIA
101 AFGQHPAQYH AFYRLPGEQ LIRAAHFSV QTPVDVQIGN HVVQKRXIVL
151 SQSETAQHGR GFXXKHKFID FKSAFQQVEQ AXQSMKQRLA AADFHVXHGI
201 RQCLRTGLRL SEHGFKRRI GFDIRG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 217 shows 80.5% identity over a 226 aa overlap with a predicted ORF (ORF 217.ng) from *N. gonorrhoeae*:

m217/g217

	10	20	30	40	50	60
m217.pep	MADDGVRRLSGKLRQFGFRLPFDPFVFKVLDXLLVIGFSLEQCFKQIPATRHFPADRCG					
	: : : :					
g217	MADDGLLRQLSEKPSQSALFLPFDPFVFEVLDCLLVIGPGLKQCFKQIPATRHFPADRRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m217.pep	LPPYPYNIQGFEEGGKTSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLPGEQ					
	: : :					
g217	LPPYPGNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRVA AFGQHPAQYHTVCRLLPQKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m217.pep	LIRAAAHFSVQTPVDVQIGNHVQKRXIVLSQSETAQHGRGFXXKHKFIDFKSAFQQVEQ					
	: : : : : :					
g217	LIRAAAHFSVQSPMDVQIGNHIVQKQIVPGQSETAQHGRGFQKREHFADFKTAFQQVGH					
	130	140	150	160	170	180
	190	200	210	220		
m217.pep	AXQSMKQRLAAADFHVXHGI RQCLRTGLRLSEHGFKRRI GFDIRGX					
	: : :					
g217	ALQRIKKRLPAADFHVRNGIRQCLRAGLRLSEHGFKRRI GFDIRG					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 767>:

a217.seq

```

1  GTGGCGGATG ACGGTGTGCA GCGGCAACTG TCCGAAAAAT TGCGCCAATT
51  CGGTTTCCGC CTGCCATTG ACCCATTCGT TTTGAGGCT TTGGACTGCC
101 TTTTGGTCAT CGCCTTCGAC TTGGAACAAT GTTTCAAGCA AATCCCGGCA
151 ACGCGCCACC CATTGTCGCA CCGTCGAGG TTGCGGCCAT ATCCGTACAA

```

201	TATCCGTCAG	GGTTTCGAGG	AAGGCGGCAA	AACGTCGGAA	CAGGGCGGTT
251	TGGTTCACGT	CGGCATACCA	CGCGCTGACC	CCCTGCCACA	TCGGATTGCC
301	GCCTTCGGGC	AGCATCCAGC	CCAATATCAT	GCGTTCTACC	GCCTGCTTCC
351	AGGTGAACAG	CTGATCCGTG	CCGCCGCGCA	TTTCTCCGTC	CAAACCCAG
401	CGGACGTTCA	AATCGGCAAC	CATGTCGTGC	AAAAGCGGCA	AATCGTCCTC
451	AGTCAGTCCG	AAATGGCGCA	ACACGGGGCG	GGTTTCTAA	AGCACAAGCA
501	CTTTATCGCA	TTCAAAATCGG	CTTTCCAACA	AGTCGAACAG	GCATGACAAA
551	GCATGAAACA	CGCGTTGTGC	CGCGGTGATT	TTCCATCCG	AAACGGAATA
601	CGGCAATGCC	TGCGCGCCGG	GCTGCGCTG	TCCGAACACG	GCTTCGATAA
651	AAGGCGTATA	GGATTCGATA	TTCGGGGTTA	A	

a217.pcp

[illegible]

g218.seq

g218.pep

1 MVAVDPYTAK VVNTMPRNQG WYHTMDEIHG DMMLGAAGDY LLETAASLTI

```

51  IMVVSGLYLW WAKQRGIKAM LLPPKSRARS WWRNLHGAFG TWVSLILLLF
101 CLSGIAWAGI WGGKFVQAWN QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK
151 EVPWILELMP MPVSGTTVGE NGINPTEPNN IGNRRPFRAG NRFQALSVE
201 FAQRRGRGMD FVAGFYEL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 771>:

```

m218.seq
1  ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG
51  CAATCAGGGT TGGTATTACA CGATGGATGA AATCCACAGC GATATGATGC
101 TCGGTGCGGC AGGCGATTAT CTTTGGAAA CGGCAGCTTC ACTGACCATT
151 ATTATGGTTG TCAGCGGCTT GTACCTTTGG TGGGTGAAAC GGCGCGGCAT
201 CAAGGCGATG CTGCTGCCGT CAAAAGGCAR GGCGCGTTCT TGGTGGCGGA
251 ATCTGCACGG CACGTTTGGG ACTTGGGTGT CGTTGATTTT GCTGTTGTTT
301 TGCCTGTCGG GTATTGCTTG GCGGGGTATT TGGGGCGGCA AGTTCGTACA
351 GGCTTGGAGT CAGTTCCTTG CCGGTAAATG GGGTGTGCGA CCGAACCCCG
401 TTTCAGTCGT GCCGACCCAC GCGGAGGTAT TGAATGACGG CAAGGTTAAG
451 GAAGTGCCGT GGGTTTTGGA GCTTACGCCT ATGCCTGTTT CAGGGACGAC
501 yGtgGGCAA GACGGCATT ACCCTGACGA GCCGATGACA TTGGAAACCG
551 TCGACCGCTT TCGCGGnGA AATCGGTTT AAAGGGCGTT ATCAGTTGAA
601 TTTGCCCAA GCGGAGGACG GCGTATGGAC TTTGTCGAG GATTCTATGA
651 GTTA

```

This corresponds to the amino acid sequence <SEQ ID 772; ORF 218>:

```

m218.pep
1  MVAVDPYTAK VVSTMPRNQG WYYTMDEIHS DMMLGAAGDY LLETAASLTI
51  IMVVSGLYLW WVKRRGIKAM LLPSKXARS WWRNLHGTFG TWVSLILLLF
101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK
151 EVPWLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQALSVE
201 FAQRRGRMD FVAGFYEL

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 218 shows 87.2% identity over a 218 aa overlap with a predicted ORF (ORF 218.ng) from *N. gonorrhoeae*:

```

m218/g218

      10      20      30      40      50      60
m218.pep  MVAVDPYTAKVVSTMPRNQGWWYTMDEIHS DMMLGAAGDY LLETAASLTI IMVVSGLYLW
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g218      MVAVDPYTAKVVNTMPRNQGWWYHTMDEIHGDMMLGAAGDY LLETAASLTI IMVVSGLYLW
          10      20      30      40      50      60

      70      80      90      100     110     120
m218.pep  WVKRRGIKAMLLPSKXARSWWRNLHGTFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS
          |:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g218      WAKQRGIKAMLLPPKSRARSWWRNLHGAFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWN
          70      80      90      100     110     120

      130     140     150     160     170     180
m218.pep  QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKEVPWVLELTPMPVSGTTVGKDGINPDEPMT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g218      QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKEVPWVLELTPMPVSGTTVGGENGINPTEPNN
          130     140     150     160     170     180

      190     200     210
m218.pep  LETVDRFARXNRFQALSVEFAQRRGRMD FVAGFYEL
          : : |||||:|||||:|||||:|||||:|||||:
g218      IGNRRPFRAGNRFQALSVEFAQRRGRMD FVAGFYEL
          190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 773>:

a218.seq

```

1  ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG
51  CAATCAGGGT TGGTATTACG CGATGGATGA AATCCACAGC GATATGATGC
101 TCGGTTTCGAC AGGTGATTAT CTTTGGAAA CGGCTGCATC GCTGACGATT
151 ATCATGATAA TCAGCGGTTT GTACCTTTGG TGGGTGAAAC GGCGCGGCAT
201 CAAGGCGATG CTGCTGCCGC CAAAAGGCAG GGCGCGTTCT TGGTGGCGGA
251 ATCTGCACGG CGCGTTTGA ACTTGGGTGT CGTTGATTTT ACTGTTGTTT
301 TGCCTGTCGG GTATTGCTTG GGCAGGTATT TGGGGCGGCA AGTTCGTGCA
351 GGCTTGGAGT CAGTTCCCGG CAGGCAAATG GGGTGTGCAA CCGAACCTTG
401 TTTCAGTCGT GCCGACCCAC GGCAGGTAT TGAATGACGG CAAGGTTAAG
451 GAAGTGCCGT GGGTTTGA GCTTACGCCT ATGCCTGTTT CAGGGACGAC
501 TGTGGGCAAA GACGGTATTA ACCCTGACGA GCCGATGACA TTGGAAACCG
551 TCGACCGTTT TGC GCGG.GA AATCGGTTTC AAAGGCGTT ATCAGCTGAA
601 TTTGCCCAAA GGCGAGGACG GCGTATGGAC TTTGTCGCAG GATTCTATGA
651 GTTA

```

This corresponds to the amino acid sequence <SEQ ID 774; ORF 218.a>:

a218.pep

```

1  MVAVDPYTAK VVSTMPRNQG WYYAMDEIHS DMMLGSTGDY LLETAASLTI
51  IMIISGLYLW WVKRRGIKAM LLPPKGRARS WWRNLHGAFG TWVSLILLFL
101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSVVPTH GEVLNDGKVK
151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQRLSAE
201 FAQRRGRMD FVAGFYEL

```

m218/a218 95.9% identity in 218 aa overlap

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQGWYYTMDIEHSDMMLGAAGDYLLETAASLTIIMVVSGLYLW					
a218	MVAVDPYTAKVVSTMPRNQGWYYAMDEIHSMDMLGSTGDYLLETAASLTIIMIISGLYLW					
	10	20	30	40	50	60
m218.pep	WVKRRGIKAMLLPSKGXARSWWRNLHGTFTWVSLILLFLCLSGIAWAGIWGGKFVQAWS					
a218	WVKRRGIKAMLLPPKGRARSWWRNLHGAFGTWVSLILLFLCLSGIAWAGIWGGKFVQAWS					
	70	80	90	100	110	120
m218.pep	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVKVPWVLELTPMPVSGTTVGKDGINPDEPMT					
a218	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVKVPWVLELTPMPVSGTTVGKDGINPDEPMT					
	130	140	150	160	170	180
m218.pep	LETVDRFARXNRFQRLSAEFAQRRGRMDFVAGFYEL					
a218	LETVDRFARXNRFQRLSAEFAQRRGRMDFVAGFYEL					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 775>:

```
g219.seq
  1  atgacggcaa ggtaaggaa gtgccgtgga ttttgagct tatgcctatg
 51  cctgtctcag ggacgactgt gggtgaaaac ggcattaacc ccaccgagcc
101  caataacatt ggaaaccgtc gaccgtttcg cgcgggaaat cggtttcaaa
151  gggcggtatc agttgaattt gcccaaaggc gaggacgggg tatggacttt
201  gtgcgaggat tctatgagtt atgacatgat cagcccgttt gccgaccgca
251  cgggtacatat cgaccagtac agcggcgaga ttcttgccga catccgtttt
301  gacgattaca acccgttcgg caaatattatg gcggcaagca ttgcgctgca
351  tatggggact ttgggctggt ggagcgtggt ggcaacgtc gtgttctgcc
401  ttgccgtgat ttttatcggc atcagcggct gcgtgatgtg gtggaaacgc
451  cgtccgtccg gcgtggcggg cattgttccct ccggcgcaaa aaatcaaact
501  gcccgctctg tgggcgatgg cattgccgct gctgttgatt gcactgcttt
551  tcccgaccgc gctgcttgcc attgccgtga tttggctggt ggataccttg
601  ctgctgtcgc ggattcctgt gttgaggaaa tggtttaaat ga
```

This corresponds to the amino acid sequence <SEQ ID 776; ORF 219.ng>:

```
g219.pep
  1  MTARLRKCRG FWSLCLCLSQ GRLWVKALT PPSPITLETV DRFAREIGFK
 51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGEILADIRF
101  DDYNPFGKFM AASIALHMG T LGWWSVLANV VFCLAVIFIG ISGCVMWKR
151  RPSGVAGIVP PAQKIKLPVW WAMALPLLLI ALLFPTALLA IAVIWLLDTL
201  LLSRIPVLRK WFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 777>:

```
m219.seq
  1  ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTTGAGCT TACGCCTATG
 51  CCTGTTTCAG GGACGACyGt gGGCAAAGAC GGCATTAACC CTGACGAGCC
101  GATGACATTG GAAACCGTCG ACCGCTTTGC GCGGnGAAAT CGGTTTCAAA
151  GGGCGTTATC AGTTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201  GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCCGACCGCA
251  CCGTACATAT CGACCAGTAC AGCGGCAAAA TCCTTGCCGA CATCCGTTTT
301  GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351  TATGGGGACT CTGGGCTGGT GGAGCGTGTT GGCGAACGTC TTGTTCTGCC
401  TTGCCGTCAT TTTTATCGGT ATCAGCGGCT GCGTGATGTG GTGAAACGC
451  CGTCCGACCG GAGCGGTGGG CATCGTTCCG CCGGCGCAGA AAGTCAAGCT
501  GCGCGTTTGG TGGATGATGG CATTGCCGCT ATTGGCAATC GCACTGCTCT
551  TCCCGACCTC ACTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601  CTGTTGTGCG GGATTCTGT TTTGAGGAGA TGGTTTAAAT GA
```

This corresponds to the amino acid sequence <SEQ ID 778; ORF 219>:

```
m219.pep
  1  MTARLRKCRG FWSLRLCLFQ GRXWAKTALT LTRXHWKPS TALRGEIGFK
 51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101  DDYNPFGKFM AASIALHMG T LGWWSVLANV LFCLAVIFIG ISGCVMWKR
151  RPTGAVGIVP PAQKVLPVW WMMALPLLLI ALLFPTSLLA IAVIWLLDTL
201  LLSRIPVLRK WFK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 219 shows 86.9% identity over a 213 aa overlap with a predicted ORF (ORF 219.ng) from *N. gonorrhoeae*:

```
m219/g219

          10          20          30          40          50          60
m219.pep  MTARLRKCRGFWSLRLCLFQGRXWAKTALTLSRXHWKPS TALRGEIGFKGRYQLNLPKG
          |||||
g219       MTARLRKCRGFWSLCLCLSQGRLWVKALTTPSPITLETVDRFAREIGFKGRYQLNLPKG
          10          20          30          40          50          60

          70          80          90          100         110         120
m219.pep  EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG T
          |||||
g219       EDGVWTLSDSMSYDMISPFADRTVHIDQYSGEILADIRFDDYNPFGKFMAASIALHMG T
```

505

	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCMWWKRRPTGAVGIVPPAQKVKLPVWMMALPLLAI					
	: : : : :					
g219	LGWWSVLANVVFCLAVIFIGISGCMWWKRRPSGVAGIVPPAQKIKLPVWAMALPLLII					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	: : : :					
g219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRKWKFK					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 779>:

```

a219.seq
1  ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACTGT GGGCAAAGAC GGTATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGTTTTCG GCGG.GAAAT CGGTTTCAAA
151 GGGCGTTATC AGCTGAATT GCCCAAAGGC GAGGACGCGG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCTGACCGCA
251 CGGTGACATAT CGACAGTAC AGCGGCAAGA TTCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT TTGGGCTGGT GGAGCGTGTG GCGGAACGTT TTGTTCTGCC
401 TTGCCGTGAT TTTTATCGCG ATCAGCGGCT GCGTGATGTG GTGGAACGCG
451 CGTCCGTCCG GCGCGGTGGG CATGGTTCCG CCGGCGCAAA AAATCAAGCT
501 GCGCGTCTGG TGGGCAATGG CCGTGCCGCT GCTGCTGATT GCATTGCTTT
551 TCCCGACCGC GTTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 780; ORF 219.a>:

```

a219.pep
1  MTARLRKCRG FWSLRCLCFQ GRLWAKTVLT LTSR*HWKPS TVLRXEIGFK
51  GRYQLNLPKG EDGVWTLSDQ SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMGT LGWWSVLANV LFCLAVIFIG ISGCMWWKR
151 RPSGAVGMVP PAQKIKLPVW WAMAVPLLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRW WFK*

```

m219/a219 94.8% identity in 213 aa overlap

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRCLCFQGRXWAKTALTLSRXHWKPSTALRGEIGFKGRYQLNLPKG					
	: : : :					
a219	MTARLRKCRGFWSLRCLCFQGRVWAKTVLTLSRXHWKPSTVLRXEIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSDQSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMGT					
	: : : :					
a219	EDGVWTLSDQSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMGT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCMWWKRRPTGAVGIVPPAQKVKLPVWMMALPLLAI					
	: : : :					
a219	LGWWSVLANVLFCLAVIFIGISGCMWWKRRPSGAVGMVPPAQKIKLPVWAMAVPLLLI					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	: : :					
a219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRWFKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 781>:

```
g221.seq
1  atgcacgacc acggcgccat ggatcgccgc ctccccgctt tcggaagtct
51  gatcgggcga gccgtaaatac adatcgagcg tgacggattt gaaccctgcc
101 tcacggggcgg catcgatgac ttctttggtt tcttcgtagc tttggatgcg
151 gttgactgcc gcctgcactt tggggtcgaa atcctgaatg ccgacgctca
201 tgcggttgaa gccgagtcctg ccgagcatga ggacggtgct gcggctgact
251 ttgcgcgggt cgatttcgat ggaatattcg ccggacggta tcagttcgaa
301 atgtttgcgg atcatgcgga agacacgttc gatctgttcg tcgctcaaaa
351 aggtcggcgt gccgccgccg aagtgcagtt gggcaagctg gtgccgtccg
401 ttcagatgtg gagcgagcag ttccatttct ttttcaagat attcgatgta
451 ggtatcgggc cggtttttgt ctttggatgat gattttgttg cagccgcagt
501 agtagcagat ggtgttgcaa aacggaatgt gaatgtaaag ggaaagcggg
551 ttgtttaa
```

This corresponds to the amino acid sequence <SEQ ID 782; ORF 221.ng>:

```
g221.pep
1  MHDHGAMDRR LPAFGSLMRR AVNXIDADGF EPCLTGGIDD FFGFFVALDA
51  VDCRLHFGVE ILNADAHAVE AESAEHEDGV AADFARVDFD GIFAGRYQFE
101 MFADHAEDTF DLFVAQKGRR AAAEVQLGKL VPSVQMWSEQ FHFFFKIFDV
151 GIGAAFVFGD DFVAAAVVAD GVAKRNVNVK GKRFV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 783>:

```
m221.seq
1  ATGGyGGTTT TGATGcwcmg AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51  CGACGCTGAC GGATTGTAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACCTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTGCGCG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCCGCCG TGGGGATTAA CTCGAAATGT TTGCGTATCA TCGGGAAGAC
301 ACGTTCGATC TGTTCTGTCG TCAAAAAGGt GCGTGCcCCG CCGAAGTGCA
351 GTTGGGCAAG CTGGTGCCGT CCGTTCAGAT GTGGAGCGAG CAGTTCCATT
401 TCTTTTTCAA GATATTCGAT GTAGGCATCG GCGCGGCTT TGTCTTTGGT
451 GATGATTTTG TTGCAGCCGC AGTAGTAGCA GATGGTGTG CAGAACGGAA
501 TGTGAATGTA AAGGGAAAGC GGTGTGTTA A
```

This corresponds to the amino acid sequence <SEQ ID 784; ORF 221>:

```
m221.pep
1  MXVLMXRSLV RQAVNQIDAD GFEPFRFARRI DDFGFFVTL DAVDRRLHFG
51  VEILNADAHAVEAESAEHED GVAADFARVD FDGVFAGGDx LEMFAYHAED
101 TFDLFVAQKG ACPAEVQLGK LVPSVQMWSE QFHFFFKIFD VGIGAAFVFG
151 DDFVAAAVVA DGVAERNVNV KGKRFV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 221 shows 87.6% identity over a 170 aa overlap with a predicted ORF (ORF 221.ng) from *N. gonorrhoeae*:

```
m221/g221

          10      20      30      40      50
m221.pep      MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDDFGFFVTLDAVDRRLHFGVE
                ||::||| ||||| |:: ||||| |::||| |||||
g221           MHDHGAMDRRLPAFGSLMRRAVNXIDADGFEPCLTGGIDDFFGFFVALDAVDCRLHFGVE
                10      20      30      40      50      60

          60      70      80      90     100     110
m221.pep      ILNADAHAVEAESAEHEDGVAADFARVDFDGVFAGGDxLEMFAYHAEDTFDLFVAQKGA-
                ||||| |::||| ||||| |::||| ||||| |::||| |||||
g221           ILNADAHAVEAESAEHEDGVAADFARVDFDGI FAGRYQFEMFADHAEDTFDLFVAQKGRR
                70      80      90     100     110     120

          120     130     140     150     160     170
```

507

```

m221.pep    CPAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAFVFGDDFVAAAVVADGVAERNVNVK
            |||||
g221        AAAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAFVFGDDFVAAAVVADGVAKRNVNVK
            130      140      150      160      170      180

m221.pep    GKRFVX
            |||||
g221        GKRFVX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 785>:

```

a221.seq
1  ATGGTGGTTT TGATGCTCCG AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51 CGACGCTGAC GGATTTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TGCGGAAGAC
301 ACGTTCGATT TGGTCGTCGC TCAAAAAGGT CGGCGTGCCG CCGCCGAAGT
351 GCGTTGGGCG AAGCTGGTGC CGTCCGTTCA GATGTGGAGC GAGCAGTTCC
401 ATTTCTTTTT CAAGAAATTC GATGTAGGCA TCGGCGCGGC TTTTGTCTTT
451 GGTGATGATT TTGTTGCAGC CGCAGTAGTA GCAGATGGTG TTGCAGAACG
501 GAATGTGAAT GTAAAGGGAA AGCGGTTTGT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 786; ORF 221.a>:

```

a221.pep
1  MVVLMRLSLV RQAVNQIDAD GFEPRFARRI DDFGFFVTL DAVDRRLHFG
51 VEILNADAHA VEAESAHEHD GVAADFARVD FDGVFAGGD* LEMFAYHAED
101 TFDLVVAQKG RRAAAEVQLG KLVPSVQMW S EQFHFFFKF DVGIGAAFV
151 GDDEFVAAAVV ADGVAERNVN VKGKRFV*

```

m221/a221 95.5% identity in 177 aa overlap

```

m221.pep    10      20      30      40      50      60
            MXVLMXRSLVRQAVNQIDADGFEPRFARRIDDFGFFVTLDAVDRRLHFGVEILNADAHA
            | | | | |
a221        10      20      30      40      50      60
            MVVLMRLSLVRQAVNQIDADGFEPRFARRIDDFGFFVTLDAVDRRLHFGVEILNADAHA

m221.pep    70      80      90      100     110     119
            VEAESAHEHDGVAADFARVDFDGVFAGGD*LEMFAHYAEDTFDLFVAQKGA-CPAEVQLG
            | | | | |
a221        70      80      90      100     110     120
            VEAESAHEHDGVAADFARVDFDGVFAGGD*LEMFAHYAEDTFDLVVAQKGRRAAAEVQLG

m221.pep    120     130     140     150     160     170
            KLVPSVQMWSEQFHFFFKIFDVGIGAAFVFGDDFVAAAVVADGVAERNVNVKGKRFVX
            | | | | |
a221        130     140     150     160     170
            KLVPSVQMWSEQFHFFFKIFDVGIGAAFVFGDDFVAAAVVADGVAERNVNVKGKRFVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 787>:

```

g223.seq
1  atggaattca ggcaccaggt agtggtagtt ggtgtcgaa catttggtca
51 tttcgatggc gaattggtct ttgttgccgc gcgccagttg gaagaattgt
101 tccaaaggca ggttttggtc atcgaagccg aaacgggcgg gaatcgcgcc
151 cgtggatact tgcaggctga ggatgtgatg gtagaaagtg aaatcacgta
201 cagcaacgta atcagcgtaa ggagcagctt ggtgtttcca gtttttctcg
251 cgcaggctct tggcaacgtc gaggcagctt tgttcactga tctctttgcg
301 ccagtatttt tcttgggcga atttcaattc acggaaggcg ccgacacgcg
351 ggaagcctga

```

This corresponds to the amino acid sequence <SEQ ID 788; ORF 223.ng>:

g223.pep..

m223.seq

m223.pcp

m223/g223

a223.seq

a223.pep

	10	20	30	40	50	60
m223.pep	VEFRHQVVVVGVPEFGHFDSELVFTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDVV					
a223	VEFRHQVVVVGVPEFGHFDSELVFTARQLEELFQRXVLAVEAEAGGNRAGGDLQVEDVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m223.pep	VESEIXYGNIEIGVGSDDLVPFVFLAQVFSNSQQFLLADFFAPVFFLCEFFQFAEGADTREAX					
a223	VESEIAYGNVIGVGSGLVPFVFLAQVFSNSQQFLLADFFAPVFFLCEFFQFAEGGDTREAX					

70 80 90 100 110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 793>:

```
g225.seq
1   atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgcgcgtccg cccgcccctt cgcagcaggt gaccaacctg ctcagcagcc
101 gcgagcagat tctcagacag tttgccgaag acgaacagcc cgttttaccc
151 gtcaaccgag cccccgcccg gcgggcgggc aatgccgacg aactcatcgg
201 cggcgcgatg gggcttaacg aacagcccgt tgtacgcgtc aaccgagccn
251 ccgcccggcg ggcgggcaat gccgacaaac tcatcggcag cgcgatgcgg
301 cttttgggta ttgcctaccg ctacggcggc acatcggtgt ctaccggttt
351 tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401 acctgccgcg cagtcggcg gaacaggcgc ggatggcgcg acccgttgcc
451 cgaagcgaat tgcagcccgg ggatatggtg tttttccgca cgctcggcgg
501 cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatcc
551 acgcgccgcg cagggggaaa aatatcgaaa tcaccagcct gagccacaaa
601 tattggagcg gcaaatatgc gttcgcccgc cgggtcaaga aaaacgaccc
651 gtcacgcttt ctgaactga
```

This corresponds to the amino acid sequence <SEQ ID 794; ORF 225.ng>:

```
g225.pep
1   MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101 LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151 RSELQPGDMV FFRTLGSRI SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201 YWSGKYAFAR RVKKNPSRF LN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 795>:

```
m225.seq (partial)
1   ..TTTTCAAACC CGGCAGTTTG GGCGGTTTGT TGGCTGAWGT TTGCCGTCCG
51  CCCC GCCCTT GCCGACGAGT TGACCAACCT GCTCAGCAGC CGCGAGCAGA
101 TTCTCAGACA GTTTGCCGAA GACGAACAGC CCGTTTACC CATCAACCGA
151 GCCCCGCCCG GGCGGGCGGG CAATGCCGAC GAACTCATCG GCAGCGCGAT
201 GGGGCTTAAC GAACAGCCCG TTTTACCCGT CAACCGAGTC CCCGCCCGGC
251 GGGCGGGCAA TGCCGACGAA CTCATCGGCA ACGCGATGGG GCTTAACGAA
301 CAGCCCGTTT TACCCGTCAA CCGAGCCCCC GCCCGGCGGG CGGGCAATGC
351 CGACGAACTC ATCGGCAACG CGATGGGACT TTTGGGTATT GCCTACCGCT
401 ACGGCGGCAC ATCGGTTTCT ACCGGTTTTG ACTGCAGCGG CTTCATGCAG
451 CACATCTTCA AACGCGCCAT GGGCATCAAC CTGCCGCGCA CGTCGGCAGA
501 ACAGGCACGG ATGGGTACGC CGGTTGCCCC AAGCGAATTG CAGCCCCGAG
551 ATATGGTGTT TTTCCGCACG CTCGGCGGCA GCCGCATTTC CCATGTCGGA
601 CTTTATATCG GCAACAACCG CTTTATCCAC GCGCCGCGCA CGGGGAAAAA
651 TATCGAAATC ACCAGCCTGA GCCACAAATA TTGGAGCGGC AAATACGCGT
701 TCGCCCGCCG GGTCAAGAAA AACGACCCGT CCCGCTTCTT GAACTGA
```

This corresponds to the amino acid sequence <SEQ ID 796; ORF 225>:

```
m225.pep (partial)
1   ..FSNPAVWAVL WLXFAVRPAL ADELTNLLSS REQILRQFAE DEQVLPINR
51  APARRAGNAD ELIGSAMGLN EQVLPVNRV PARRAGNADE LIGNAMGLNE
101 QVLPVNRAP ARRAGNADEL IGNAMGLLGI AYRYGGTSVS TGFDCSGFMQ
151 HIFKRAMGIN LPRTSAEQAR MGTPVARSEL QPGDMVFFRT LGGSRISHVG
201 LYIGNNRFIH APRTGKNIEI TSLSHKYWSG KYAFARRVKK NDPSRFLN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 225 shows 83.5% identity over a 248 aa overlap with a predicted ORF (ORF 225.ng) from *N. gonorrhoeae*:

```
m225/g225
10 20 30 40 50
m225.pep FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
      | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
g225     MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPVNRAPARRAG
```

510

	10	20	30	40	50	60
m225.pep	60	70	80	90	100	110
	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA					
g225	NADELIG-----GAMGLNEQPVVRVNRAXARRAGNA					
		70	80	90		
m225.pep	120	130	140	150	160	170
	DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR					
	: : :					
g225	DKLIGSAMRLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
m225.pep	180	190	200	210	220	230
	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
g225	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
	160	170	180	190	200	210
m225.pep	240	249				
	VKKN DPSRFLNX					
g225	VKKN DPSRFLN					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 797>:

```

a225.seq
1  ATGGATTCTT TTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTGCGCAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCC GCCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGCGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCCG CCCGGCGGGC
351 GGGCAATGCC GACGAACCTA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCGCCCGCCC GCGGGCGGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CGGCACATCG ATTTCTACCG GTTTTGACTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 CCGCGGATGG GTACGCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTC CAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATCACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAT ACGCGTTCGC
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 798; ORF 225.a>:

```

a225.pep
1  MDSFFKPAV AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVAR ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKN DPSRFLN *

```

m225/a225 87.4% identity in 277 aa overlap

	10	20	30	40	50
m225.pep	FSNPAVWAVLWLXFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG				
	: : :				
a225	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRXPARRAG				
	10	20	30	40	50
	60	70	79	80	
m225.pep	NADELIGSAMGLNEQPVLPVNR-----VPARRAGNA				

This corresponds to the amino acid sequence <SEQ ID 802; ORF 217>:

m225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRAPARRAG NADELIGSAM GLNEQPVLPV NRVPARRAGN ADELIGNAMG
101 LNEQPVLPVN RAPARRAGNA DELIGNAMGL LGIAYRYGGT SVSTGFDCSG
151 FMQHIFKRAM GINLPRTSAE QARMGTPVAR SELQPGDMVF FRTLGGSRIS
201 HVGLYIGNNR FIHAPRTGKN IEITSLSHKY WSGKYAFARR VKKNDPSRFL
251 N*
```

m225-1/g225-1 84.9% identity in 251 aa overlap

	10	20	30	40	50	60
m225-1.pep	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG					
g225-1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m225-1.pep	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA					
g225-1	NADE-----LIGGAMGLNEQPVVRVNRAXARRAGNA					
		70	80	90		
	130	140	150	160	170	180
m225-1.pep	DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR					
g225-1	DKLIGSAMRLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
	190	200	210	220	230	240
m225-1.pep	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPARTGKNIETISLSHKYWSGKYAFARR					
g225-1	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPARTGKNIETISLSHKYWSGKYAFARR					
	160	170	180	190	200	210
	250					
m225-1.pep	VKKNDPSRFLNX					
g225-1	VKKNDPSRFLNX					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 803>:

a225-1.seq

```

1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCC CGCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGGC GCGCGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCCG CCCGCGGGGC
351 GGGCAATGCC GACGAACCTCA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCGCCCGCCC GCGGGGCGGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CGGCACATCG ATTTCTACCG GTTTTACTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTT CGCAGGCTCG GCGGCAGCGC CATTTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAT ACGCGTTCGC
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA
```

This corresponds to the amino acid sequence <SEQ ID 804; ORF 225-1.a>:

a225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAIYRYGGTS ISTGFDCSGF MQHIFKRAM INLPRTSAEQ
201 ARMGTPVARS ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNNDPSRFLN *
```

a225-1/m225-1 88.6% identity in 280 aa overlap

	10	20	30	40	50	60
a225-1.pep	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG					
m225-1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG					
	10	20	30	40	50	60
	70	80	90	100	110	120
a225-1.pep	NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA					
m225-1	NADELIGSAMGLNEQ-----VLPVNRVPARRAGNA					
	70				80	90
	130	140	150	160	170	180
a225-1.pep	DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLGIAIRYGGTSISTGFDCSGF					
m225-1	DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLGIAIRYGGTSVSTGFDCSGF					
	100	110	120	130	140	150
	190	200	210	220	230	240
a225-1.pep	MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF					
m225-1	MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF					
	160	170	180	190	200	210
	250	260	270	280		
a225-1.pep	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLNX					
m225-1	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLNX					
	220	230	240	250		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 805>:

g226.seq

```

1  ATGAGCGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TCGGCTGAAA cccGccgtCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC GCAGCTTGCG
301 GGCAGCGTTA cggGCATTGT tacggggATG TATTTTgccc cttggctcgg
351 gccggatacc caattctcct tcccgcctcg tcttcaatat ctgttattta
401 caccctctgg aatcccaatt cacaccctgt atgcgcgggt tctcccgcc
451 tttctgttgc ctccgcctct cctgccgcgc ctccggccgc atacattgcg
501 ccggttcaca atacttccaa aaaaactacg gccgtttaag cccctcctcc
551 cagttgtggt cttttctcct Cggggcctcg cccctcccct cttataa

```

This corresponds to the amino acid sequence <SEQ ID 806; ORF 226.ng>:

g226.pep

```

1  MSEILRQPSV LLFLTLAVYA LAIIVRTRTG NIFCNPLVLS TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFRLK PAVVVLAVPL YQNRRIKFNQ WLPVIVSCLA
101 GSVTGIVTGM YFAAWLGPDT QFSFPPRLQY LLFTPSGIPI HTLYARVLPP
151 FLLPPPLLPR LGPHTLRRFT ILPKKLRFK PLLPVVVLSP PGLAPPLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 807>:

m226.seq

```

1  ATGAACGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TTGGCTGAAA CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC ACAGCTTGCG
301 GGCAGCGTTA CGGGCATTGT TACAGGGATG TATTTTGCCA AATGGCTGGG
351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAACC
401 CCATCGCTAT TGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
451 GCCGCCACCG TCATCATTGC CGGTCTGGTC GGACAGATTG CCGGTTACAA

```

514

501 AATGCTGAAG AACACGGTCG TCATGCCCTC GTCCGTGGGT ATGTCGCTCG
 551 GCACGGCTTC GCACGCGATG GGGATTGCCG CCTCGCTCGA ACGCAGCCGC
 601 CGTATGGCGG CATA CGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC
 651 CGCGCTGATT GCGCCGCTGC TCATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 808; ORF 226>:

m226.pep
 1 MNEILRQPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT
 151 AATVIIAGLV GQIAGYKMLK NTVVMPSSVG MSLGTASHAM GIAASLERSR
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 226 shows 94.2% identity over a 121 aa overlap with a predicted ORF (ORF 226.ng) from *N. gonorrhoeae*:

m226/g226

	10	20	30	40	50	60
m226.pep	MNEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKLIGIDYAVYHN					
	:					
g226	MSEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKLIGIDYAVYHN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m226.pep	AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSOLAGSVTGIVTGM YFAKWLGAER					
g226	AAQFIDFRLKPAVVVLAVPLYQNRKIFNQWLPVIVSOLAGSVTGIVTGM YFAAWLGPDT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m226.pep	EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSSVG					
	:					
g226	QFSFPRLQYLLFTPSGIPHTLYARVLPPFLLPPPLPRLGPHTLRRFTILPKKL RPFK					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 809>:

a226.seq
 1 ATGAACGAAA TCCTCAGGCA GCCGAGCATC CTGCTTTTCC TCACGCTTGC
 51 CGTGTACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGT AATATCTTCT
 101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCA CCTGAAATC
 151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAGT TTATCGATTT
 201 CTGGCTCAAG CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAACC
 251 GCGTAAAT CTTCAACCA TGGCTGCCG TCATCGTTTC GCAGCTTGC
 301 GGCAGCGTTA CGGGCATTGT TACGGGGATG TATTTTGCCA AATGGCTGGG
 351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAATC
 401 CTATCGCCAT CGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
 451 GCGGCCACCG TCATCATTGC CGGCCTGGTC GGACAGATTG CCGTTACAA
 501 AATGTTGAAA AACACGGTCG TTATGCCCTC ATCTGTCGGA ATGTCGCTCG
 551 GCACGGCTTC GCACGCGATG GGCATTGCCG CCTCGCTCGA ACGCAGCCGC
 601 CGCATGGCGG CATA CGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC
 651 CGCGCTGATT GCGCCGCTGC TTATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 810; ORF 226.a>:

a226.pep
 1 MNEILRQPSI LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT
 151 AATVIIAGLV GQIAGYKMLK NTVVMPSSVG MSLGTASHAM GIAASLERSR
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF *

m226/a226 99.6% identity in 230 aa overlap

10 20 30 40 50 60

515

```

m226.pep      MNEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
|||||:|||||
a226          MNEILRQPSILLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
              10      20      30      40      50      60

              70      80      90      100     110     120
m226.pep      AAQFIDFWLKPAVVVLAVPLYQNRRIKFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
|||||
a226          AAQFIDFWLKPAVVVLAVPLYQNRRIKFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
              70      80      90      100     110     120

              130     140     150     160     170     180
m226.pep      EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSVVG
|||||
a226          EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSVVG
              130     140     150     160     170     180

              190     200     210     220     230
m226.pep      MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
|||||
a226          MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 811>:

```

g227.seq
1   atgaacatca tccgcgcgct cctcatcatc ctcggtgcc tcgccgccgg
51  cgaaaccgcc gttttcctag caggcatcaa actgcccgcc agcatcgctg
101 gcatggcgct gctgtttgcg cttttgcagg cgggttggtc caaaacgtct
151 tggctgcaac agcttaccga cgcgctgatg gcaaactga cgctgttcct
201 cgtgccgccc tgcgtggcgg tcatcagcta tttggatttg attgccgacg
251 attggtttcc gatactggtt tccgcctccg ccagcacttt gtgcgtactg
301 ctggttacgg gcaagggtca ccgctggata cggagcatta tctga

```

This corresponds to the amino acid sequence <SEQ ID 812; ORF 227.ng>:

```

g227.pep
1   MNIIRALLII LGCLAAGETA VFLAGIKLPG SIVGMGVLEA LLQAGWLKTS
51  WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 813>:

```

m227.seq (partial)
1   ..ACGCTCTkGC TGCAACAGCT TACCGACGCG CTGATGTCGA ACCTGACGCT
51  GTtCCTCGTG CCgCC.TGCG TGGCGGTCAT CAGCTATTTG GATTTGATTG
101 CCGACGATTG GTTTTCGATA CTGGTTCCG CCTCCGCCAG cACTTTGTGC
151 GTACTGCTGG TTACGGGCAA AGTCCACCGG TGGATACGGG GTATTATCCG
201 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 814; ORF 227>:

```

m227.pep (partial)
1   ..TSXLQQLTDA LMSNLTLFLV PPCVAVISYL DLIADDWFSI LVSASASTLC
51  VLLVTGKVHR WIRGIIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 227 shows 95.5% identity over a 66 aa overlap with a predicted ORF (ORF 227.ng) from *N. gonorrhoeae*:

```

m227/g227

              10      20      30
m227.pep      TSXLQQLTDALMSNLTLFLVPPCVAVISYL
              || |||||:|||||
g227          TAVFLAGIKLPGSIVGMGVLFALLQAGWLKTSWLQQLTDALMANLTLFLVPPCVAVISYL
              20      30      40      50      60      70

              40      50      60

```


516

```

m227.pep      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
               |||||||||||||||||||||||||||||:|
g227          DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSII
               80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 815>:

```

a227.seq
1  ATGAACATCA TCCGCGCGCT CCTCATCATC CTCGGCTGCC TCGCCACCGG
51 CGAAACCGCC GTTTCCTAG CAGGCATCAA ACTGCCCGGC AGCATCGTCG
101 GCATGGGCGT ACTGTTTGGC CTTTTCAGG CGGGTTGGGT CAAAACGTCT
151 TGGCTGCAAC AGCTTACCGA CGCGCTGATG GCGAATCTGA CGTTGTTTCT
201 CGTGCCGCCC TCGGTGGCGG TCATCAGCTA TTTGGATTG ATTGCCGACG
251 ATTGTTTTTC GATACTGGTT TCCGCCTCCG CCAGCACTTT GTGCGTACTG
301 CTGTTTACAG GCAAGGTTCA CCGCTGGATA CGGAGCATTA TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 816; ORF 227.a>:

```

a227.pep
1  MNIIRALLII LGCLATGETA VFLAGIKLPG SIVGMGVLEA LLQAGWVKTS
51 WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

m227/a227 95.5% identity in 66 aa overlap

```

m227.pep      TSXLQQLTDALMSNLTFLVPPCVAVISYL
               || |||||||||||:|||||||||||||
a227          TAVFLAGIKLPGSIVGMGVLFALLQAGWVKTSWLQQLTDALMANLTLFLVPPCVAVISYL
               20      30      40      50      60      70

               40      50      60
m227.pep      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
               |||||||||||||||||||||||||||||:|
a227          DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSII
               80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 817>:

```

m228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 818; ORF 228>:

```

m228.pep
1  MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAD
101 KMKDAAK*

```

Computer analysis of this amino acid sequence gave the following results:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 819>:

```

a228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 820; ORF 228.a>:

517

```

a228.pep
  1  MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
 51  VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
101  KMKDAAK*

```

m228/a228 100.0% identity in 107 aa overlap

	10	20	30	40	50	60
m228.pep	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
a228	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
	10	20	30	40	50	60
	70	80	90	100		
m228.pep	AAADAKASAEAEVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
a228	AAADAKASAEAEVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 821>:

```

g229.seq
  1  atggctgccg tatcgggcgg cgggtgcggtc ttcctgataa tgcttcacaa
 51  tattgcccgc gttcagcgtc agccgccagc gttcgcccaa gcgtcgggag
101  aaatcggcat tgaagccgcc ggcgaaattg tatcggctgc cgcccaagag
151  gttttgcccg acaaacggca cgggtgccga cgagcgcgtt accgaacggt
201  tttgatggcc gaacgacagg cgcaggttct gttcgtgtaa atctttgtta
251  tcccaataat gcacgccgcg gctgatgccg ccgtagagga aatgatgccc
301  gcccgcattg atttcgcgcg acacgcccga gccgtagcgc aaaccgtgtg
351  ccttttgccg caggctgtcg gcggttttcg tccagcttct gcccgaat
401  tcaatcgttt tttcggacga agcgttggtt atagcggatt aacaaaaatc
451  aggacaaggc ggcgggcccgc aggcagtacg gatggtacgg aaccggttcg
501  cccggtgctt ggacgcctta gggaaccggt ccctttgagc cggggcgggg
551  caaccgtac cggtttttgt tcatccgcca tattgtgttg a

```

This corresponds to the amino acid sequence <SEQ ID 822; ORF 229.ng>:

```

g229.pep
  1  MAAVSGGGAV FLIMLPHIAR VQRQPPAFAQ ASGEIGIEAA GEIVSAAAQE
 51  VLPDKRHGAE RARYRTLMA ERQAQVLFAE IFVIPIMHAA ADAAVEEMMP
101  ARIDFARHAQ AVAQTVCLLR QAVGGFRPAS ARKFNRFGR SVVYSGLTKI
151  RTRRRAAGST DGTEPVRPVL GRLREPFPLS RGGATRTGFC SSAILC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 823>:

```

m229.seq (partial)
  1  ..GCTCAAGCGT TGGGAGAAAT CGGCATTGAA GCCGCCGACG AAATTGTATC
 51  GGCTGCCGCC TAAGAGGTTT TGCTCGACAA ACGGCACGAT GCCGAACGAG
101  CGCGTTACCG AACGGTTTTT ATAGCCGAAC GACAGGCGCA GGCTCTGTTC
151  GCTGAAATCT TTGTTATCCC AATAATGCAC GCCGCCGCGG CTGATGCCGC
201  CGTAGAGGAA ATGATGCCTG CCCGCATTGA TTTCGCGCGA CACGCCTAAG
251  CCTAGCGCA AACCGTGTGC CTTTGCAGC AGGCTGTCGG CGGTTTTCGT
301  CCAGCTTCTG CCCGCAAATT CAATCGTTTT TCGGACGAA GCGTTGTTTA
351  TAGCGGATTA AAAAAATCA GGACAAGGCA ACGAAGCCGC AGACAGTACA
401  AATAGTACGG AACCGATTCA CTTGGTGCTT CAGCACCTTA GAGAATCGTT
451  CTCTTTTTTG TTCATCCGCT ATATTGTGTT GA

```

This corresponds to the amino acid sequence <SEQ ID 824; ORF 229>:

```

m229.pep (partial)
  1  ..AQALGEIGIE AADEIVSAAA XEVLLDKRHD AERARYRTVF IAERQAQALF
 51  AEIFVIPIMH AAAADA AVEE MPPARIDFAR HAXALAQTVC LLRQAVGGFR
101  PASARKFNRF FGSRVVYSGL TKIRTRQRSA DSTNSTEPIH LVLQHLRESR
151  SLFCSAILC *

```

Computer analysis of this amino acid sequence gave the following results:

m229/g209

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 825>:

This corresponds to the amino acid sequence <SEQ ID 826; ORF 229.a>:

m229/a229 85.6% identity in 167 aa overlap

```

                                     10      20      30
m229.pep                        A QALGEIGIEAADEIVSAAAXEVLLDKRHD AE
                               ||| | ||||| ||||| ||||| ||||| |||||
a229    MAVVSGGGAVFLITLPHIAHVQRQPPXFAQASGEIGIEAADEIVSAAAXEVLLDKRHD AE
                    10       20       30       40       50       60

                                40      50      60      70      80      90
m229.pep    RARYRTVFIAERQAQALFAE I FVIPI MHAAAADA AVEEMMPARIDF ARHAXALAQT VCLL
            ||| | ||||| ||||| ||||| |: :|||:::|| ||||| |: |||||
a229        XARYXTVFIAERQAQALFAE I FVILIV HAAAADVS VEEMMPARIDF ARHAQAVAQT VCLL
                70      80      90      100     110     120
```

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	100	110	120	130	140	149
m229.pep	RQAVGGFRPASARKFNRFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRES---					
a229	RQAVGGFRPASACKFNRFGRSVVYSGLTKIRTRRRSADSTDSTEPIHLVLQHLRESSLX					
	130	140	150	160	170	180
	150	160				
m229.pep	-----RSLFCSSAILCX					
a229	AKARQRRTGFCSSSTI					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 827>:

```

g230.seq
1  atgttccatt ccatcgaaaa atacagaaca cccgccaag tcttattagg
51  cctgattgca ttaacttttg tcggcttcgg cgtcagcacg gtttcccatc
101 cgggcgccga ctacatcgtc caagtggcg acgaaaaat cagcgagcac
151 tcaatcaaca acgccatgca gaacgagcag gcggacggcg gcagcccttg
201 gcgcgacgcg gtgttccaat ccctgctgca acgcgcctac ctgaaacagg
251 gcgcgaagct gatgggcatt tcggtttctt ccgaacaaat caagcagatg
301 attgtggacg atcccaattt ccacgacgca aacggcaaat tcagtacgc
351 gcttttgagt caatacctgt cgcaacgcca tatgtctgaa gaccagtgtg
401 tcgaagaaat ccgcgatcag tttgccttgc agaatttggg aagcctcgtc
451 caaaacggcg tattggtcgg cgacgcgcag gcggaacagc tgatcaggct
501 gacgcaggtc aaccgcacca tccgttcgca cactttcaac cccgacgagt
551 tcatcgccca agtcaaagcg tctgaagccg atttgcagaa attttataat
601 gcgaacaaaa aagactatct gctgccgcag gcggtcaaat tggaaatatgt
651 cgcttgaaat ctgaaggatt ttgcagacaa gcagaccgtc agtgaaacgg
701 aagtgaaaaa tgcgtttgaa gagcgcgtgg cgcgtttgcc ggcacatgaa
751 gccaaacctt ctttcgagca ggaaaaagcc gccgtcgaaa acgaattgaa
801 aatgaaaaag gcggttgccg acttcaacaa ggcaaaagaa aagctgggcg
851 acgatgcgtt caatcatccc tctcgttg ccgaagccgc caaaacagc
901 ggtttgaaag tggaaaccca agaaacttgg ctgagcaggc aggacgcaca
951 aatgtccggc atgcccgaac acctaataca tgccgtattc agcgacgacg
1001 tattgaagaa aaaacacaat tccgaagtgc tgaccatcaa cagcgaaacc
1051 gcgtgggctg tccgcgccaa agaagtccgc gaagaaaaaa acctactgtt
1101 tgaagaagcc aaagatgcgg tcgctcaggc ctatatccgt accgaagccg
1151 ccaaactttt gaaaacaatg taa

```

This corresponds to the amino acid sequence <SEQ ID 828; ORF 230.ng>:

```

g230.pep
1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGA KLMI SVSSEQIKQM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHMSE DQFVEEIRDQ FALQNLVSLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELMKKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVL TINSET
351 AWVVRakeVR EEKNLLFEEA KDAVRQAYIR TEAAKLLKTM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 829>:

```

m230.seq (partial)
1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAaT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGTTT AAACCTCGTC

```

520

```

451 CAAACGCGC TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTGCGA CACTTTC AAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGAG GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGg
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGC.GT cAACCATCCT TCyTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT.. ...

```

This corresponds to the amino acid sequence <SEQ ID 830; ORF 230>:

```

m230.pep (partial)
  1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
  51 SINNAIQNEQ ADGGGSPDA VFQSLQRAY LKQGAklmgi SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEK AAVENELKMK AVADFNKAKE KLGDDAVNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWWVRAKEVR EEKTLPF AEA KDAVRQAYIR TEAKL....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 230 shows 95.9% identity over a 386 aa overlap with a predicted ORF (ORF 230.ng)

from *N. gonorrhoeae*:

m230/g230

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
m230.pep	70	80	90	100	110	120
	ADGGGSPDAVFQSLQRAYLKQGAklmgiSVSSEQIKQIIVDDPNFHDANGKFDHALLN					
g230	ADGGSPWRDAVFQSLQRAYLKQGAklmgiSVSSEQIKQMIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
m230.pep	130	140	150	160	170	180
	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN					
g230	QYLSQRHMSEDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN					
	130	140	150	160	170	180
m230.pep	190	200	210	220	230	240
	PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNKLKDFADKQTVSETEVKNAFE					
g230	PDEFIAQVKASEADLQKFYNANKKDYLLPQAVKLEYVALNKLKDFADKQTVSETEVKNAFE					
	190	200	210	220	230	240
m230.pep	250	260	270	280	290	300
	ERVARLPANEAKPSFEQEKAAVENELKMKKAVADFNKAKEKLGDDAVNHPSSLAEAAKNS					
g230	ERVARLPAHEAKPSFEQEKAAVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m230.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRAKEVR					
g230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRAKEVR					
	310	320	330	340	350	360
	370	380				
m230.pep	EEKTLPF AEAKDAVRQAYIRTEAAKL					
	:					
g230	EEKNLLFEEAKDAVRQAYIRTEAAKLKTM					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 831>:

a230.seq	(partial)	
1	ATGTTCCATT	CCATCGAAAA ATACAGAACG CCCGCCAAG TCCTTTTGGG
51	CCTGATTGCA	TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCATC
101	CGGGTGCCGA	CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151	TCCATCAACA	ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201	GCGCGACGCG	GTGTTCCAAT CCCTGCTACA ACGCGCCTAC CTGAAACAGG
251	GCGCGAAGCT	GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301	ATCGTGGACG	ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351	GCTTTTAAAC	CGCTACCTTT CCCAACGTCA TATGTCTGAA GACCAGTTTG
401	TCGAAGAAAT	CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC
451	CAAAACGGCG	TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501	GACGCAGGTC	AACCGCACCA TCCGTTTCGCA CACTTTC AAC CCCGACGAAT
551	TCATCGCCCA	AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601	GCAAACAAAA	AAGACTACCT GCTTCCCAA GCGGTCAAAT TGGAATATGT
651	CGCCTTGAAT	CTGAAAGACT TTGCAGACAA ACAGACCGTC AGCGAAACAG
701	AAGTGAAAAA	TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751	GCCAAACCTT	CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801	AATGAAAAAG	GCGGTTGCCG ACTTCAATAA GGCAAAAGAA AAGCTGGGCG
851	ATGACGCGTT	CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901	GGTTTGAAAG	TCGAAACCCA AGAACTTGG CTGAGCAGGC AGGATGCCCA
951	AATGTCCGGT	ATGCCCAGAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001	TATTGAAGAA	AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051	GCGTGGGTTC	TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101	TGCCGAAGCC	AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151	CCAAACTT	

This corresponds to the amino acid sequence <SEQ ID 832; ORF 230.a>:

a230.pep	(partial)	
1	MFHSIEKYRT	PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51	SINNAIQNEQ	ADGGGPSRDA VFQSLQRAY LKQGAQLMGI SVSSEIQIKQI
101	IVDDPNFHDA	NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151	QNGVLVGDAQ	AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201	ANKKDYLLPK	AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251	AKPSFEQEKA	AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301	GLKVETQETW	LSRQDAQMSG MPENLINAVF SDDVLKKKHNSVLTINSET
351	AWVVRAKEVR	EEKTLPF AEAKDAVRQAYIR TEAAKL

m230/a230 99.2% identity in 386 aa overlap

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230.pep	ADGGGPSRDAVFQSLQRAYLKQGAQLMGISVSSEIQIKQIIVDDPNFHDANGKFDHALLN					
a230	ADGGGPSRDAVFQSLQRAYLKQGAQLMGISVSSEIQIKQIIVDDPNFHDANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180

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m230.pep	RYLSQRHMS	EDQFVEE	IRDQFAL	QNLVNLV	QNGVLVG	DAQAEQL	LIRLTQVN	RTIRSH	TFTN
a230	RYLSQRHMS	EDQFVEE	IRDQFAL	QNLVNLV	QNGVLVG	DAQAEQL	LIRLTQVN	RTIRSH	TFTN
	130	140	150	160	170	180			
m230.pep	PDEFIAQVK	VSEADLQ	KFYNN	ANKKDYLL	PQAVKLE	YVALNLK	DFADKQ	TVSETE	VKNAFE
a230	PDEFIAQVK	VSEADLQ	KFYNN	ANKKDYLL	PKAVKLE	YVALNLK	DFADKQ	TVSETE	VKNAFE
	190	200	210	220	230	240			
m230.pep	ERVARLPAN	EAKPSFE	QEKAAVE	NELKMKK	AVADFNK	AKEKLG	DDAVNHP	SSLAEE	AAKNS
a230	ERVARLPAN	EAKPSFE	QEKAAVE	NELKMKK	AVADFNK	AKEKLG	DDAFNHP	SSLAEE	AAKNS
	250	260	270	280	290	300			
m230.pep	GLKVETQET	WLSRQDA	QMSGMP	ENLINAV	FSDDVLK	KKHNS	EVLTIN	SETAWV	VRAKEVR
a230	GLKVETQET	WLSRQDA	QMSGMP	ENLINAV	FSDDVLK	KKHNS	EVLTIN	SETAWV	VRAKEVR
	310	320	330	340	350	360			
m230.pep	EEKTLPFAE	AKDAVRQ	AYIRTEA	AKL					
a230	EEKTLPFAE	AKDAVRQ	AYIRTEA	AKL					
	370	380							

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 833>:

g230-1.seq

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACA CCCGCCCAAG TCTTATTAGG
51  CCTGATTGCA TTAACCTTTG TCGGCTTCGG CGTCAGCACG GTTTCCCATC
101 CGGGCGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGAGCAC
151 TCAATCAACA ACGCCATGCA GAACGAGCAG GCGGACGGCG GCAGCCCTTG
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATG
301 ATTGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCAGTCACGC
351 GCTTTTGAGT CAATACCTGT CGCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTGCTTGC AGAATTGGT AAGCCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCGCACCA TCCGTTGCGA CACTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGCG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAATA AAGACTATCT GCTGCCGAG GCGGTCAAAT TGGAAATATG
651 CGCCTTGAAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACCGG
701 AAGTGAAAAA TGCCTTTGAA GAGCGCGTGG CGCGTTTGCC GGCACATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAGAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAGAGAA AAGCTGGGCG
851 ACGATGCGTT CAATCATCCC TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TGGAAACCCA AGAAACTTGG CTGAGCAGGC AGGACGCACA
951 AATGTCCGGC ATGCCCGAAA ACCTAATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAAAAAA ACCTACTGTT
1101 TGAAGAAGCC AAAGATGCGG TCGCTCAGGC CTATATCCGT ACCGAAGCCG
1151 CCAAACCTGC CGAAAACAAG GCAAAAGAAG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCGA TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCGCA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCCGCCTATG TCAGACTGAC CGGTCTGCCG
1351 GCACCCGTGA TTGTCGAGGC GCAGGCAGTC ACGCCTCCGG AGGATATTGC
1401 CGCACAGCTT CCTCCTGCGA AACAGGCTTT GGCGCAACAG CAGTCTGCCA
1451 ATACTTTCGA CCTGCTGATC CGCTATTTCA ACGGAAAAAT CAAACAGACT
1501 AAAGGAGCAC AATCGGTTGA CAACGCGGAT GGTAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 834; ORF 230-1.ng>:

g230-1.pep

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGVGVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGAKLMGI SVSSEQIKQM
101  IVDDPNFHDA NGKFSHALLS QYLSQRHMSE DQFVEEIRDQ FALQNLVSLV

```

```

151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINA VF SDDVLKKKHN SEVL TINSET
351 AWWVRRAKEVR EEKNLLFEEA KDAVRQAYIR TEAAKLAENK AKEVLTQLNG
401 GKAVDVKWE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLTGLP
451 APVIVEAQAV TPEIDIAAQL PPAKQALAQQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDGD GQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 835>:

m230-1.seq

```

1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51 CCGTATTGCA TTAACCTTCG TCGGCTTCGG GGTGAGCAGC GTATCCCATC
101 CCGGTGCGCA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCCTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTGCGA CACTTTCAAC CCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGC GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACGG
701 AAGTGAAAAA TGCATTGAA GAGCGCGTGG CGCGTTTGCC GGCAATATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCGGGT ATGCCCAGAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTACGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTGC CGAAAACAAG GCAAAAGACG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCGGTTT TGGGCGCACA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCCGCTACG TCAGGCTGAT CGGTCTGCCG
1351 GCACCCGTA TTGTGGAAGT ACAGGCTGTA ACCCCGCCGG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GGCGCAACAG CAGTCTGCCA
1451 ATACTTTCGA CTTGTTGATA CGTTATTTCA ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTCGA CAACGCGGAC GGTACGTAA

```

This corresponds to the amino acid sequence <SEQ ID 836; ORF 230-1>:

m230-1.pep

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPSRDA VFQSLQRAY LKQGA KLMI SVSSEQIKQI
101 IVDDPNFHD NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINA VF SDDVLKKKHN SEVL TINSET
351 AWWVRRAKEVR EEKTLPFEEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPDIDIAAQL PLAKQALAQQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDGD GQ*

```

m230-1/g230-1 96.3% identity in 512 aa overlap

```

          10      20      30      40      50      60
m230-1.pep MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ
          |||||
g230-1      MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ
          10      20      30      40      50      60

          70      80      90      100     110     120
m230-1.pep ADGGGSPSRDAVFQSLQRAYLKQGA KLMI SVSSEQIKQIIVDDPNFHDANGKFDHALLN
          |||||
g230-1      ADGGSPWRDAVFQSLQRAYLKQGA KLMI SVSSEQIKQMIVDDPNFHDANGKFSHALLS
          70      80      90      100     110     120

          130     140     150     160     170     180
m230-1.pep RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN

```


	130	140	150	160	170	180
g230-1	QYLSQRHMSEDOQFVEEIR	DQFALQNLVSLVQNGVL	VGDAQAEQLIRLTQVNR	TI	RSHTFN	
m230-1.pep	190	200	210	220	230	240
g230-1	PDEFIAQVKVSEADLQKF	YNANKKDYLLPQAVKLEY	VALNLKDFADKQTVSE	TEVKNAFE		
	190	200	210	220	230	240
m230-1.pep	250	260	270	280	290	300
g230-1	ERVARLPANEAKPSFEQ	EKAAVENELKMKKAVAD	FNKAKEKLGDDAFNHP	SSLAEEAKNS		
	250	260	270	280	290	300
m230-1.pep	310	320	330	340	350	360
g230-1	GLKVETQETWLSRQDAQ	MSGMPENLINAVFSD	VDLKKKHNSVLTIN	SETAWVVRAKEVR		
	310	320	330	340	350	360
m230-1.pep	370	380	390	400	410	420
g230-1	EEKTLFPFAEAKDAVRQ	AYIRTEAAKLAENKA	KDVLTLQNGGKA	VDVKWSEVSVLGA	QQAAR	
	370	380	390	400	410	420
m230-1.pep	430	440	450	460	470	480
g230-1	QSMPPPEAYAEELLKAK	PANGKPAYVRLIGLPA	PVIVEQAVTPPDDIA	AQLPLAKQALAAQ		
	430	440	450	460	470	480
m230-1.pep	490	500	510			
g230-1	QSANTFDLLIRYFNGKI	KQTKGAQSVNDG	GDGQX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 837>:

a230-1.seq

1	ATGTTCCATT	CCATCGAAAA	ATACAGAACG	CCCGCCCAAG	TCCTTTTGGG
51	CCTGATTGCA	TTAACCTTCG	TCGGCTTCGG	GGTCAGCAGC	GTATCCCATC
101	CGGGTGCCGA	CTACATCGTC	CAAGTGGGGC	ACGAAAAAAT	CAGCGCACAC
151	TCCATCAACA	ACGCCATACA	GAACGAACAG	CGCGACGGCG	GCGGCCCTTC
201	GCGCGACGCG	GTGTTCCAAT	CCCTGCTACA	ACGGCGCTAC	CTGAAACAGG
251	GCGCGAAGCT	GATGGGCATT	TCGGTTTCTT	CCGAACAAAT	CAAGCAGAT
301	ATCGTGGACG	ATCCCAAATT	CCACGACGCA	AACGGCAAAAT	TCGCACACGC
351	GCTTTTAAAC	CGCTACCTTT	CCCCACGTCA	TATGTTCTGA	GACCCAGTTG
401	TCGAGAAGAT	CCGCGATCAG	TTTGCTTTGC	AGAATTTGGT	AAACCTCGTC
451	CAAACGCGCG	TATTGGTCGG	CGACGCGCAG	GCGGAACAGC	TGATCAGGCT
501	GACGCAAGTG	AACCGCAATG	TCCGTTTCGA	CACTTTCAAC	CCCGACGAAT
551	TCATCGCCCA	AGTCAAAAGT	TCGTAAGCCG	ATTTGCGAAG	GTTTATAAAC
601	GCAACAAAAA	AGACTACTCT	GCTTCCCAAA	GCGGTCAAAAT	TGGAATATGT
651	CGCCTTGAAT	CTGAAAGACT	TTGCAGACAA	ACAGACCGTC	AGCGAAACAG
701	AAGTAAAAAA	TGCGTTTGAA	GAGCGCGTGG	CGCGTTTGCC	GGCAAATGAA
751	GCCAAACCTT	CTTTCGAGCA	GGAAAAAGCC	GCCGTCGAAA	ACGAATTGAA
801	AATGAAAAAG	CGGGTTGCGC	ACTTCAATGA	GGCAAAAGAA	AAAGTCGGCG
851	ATGACGCGTT	CAACCATCCT	TCTCGGTTG	CCGAAGCCGC	CAAAAACAGC
901	GGTTTGAAAG	TCGAAACCCA	AGAAACTTGG	CTGAGCAGGC	AGGATGCGCA
951	AATGTCCGGT	ATGCCCGAAA	ACCTGATCAA	TGCCGTATTCT	AGCGACGACG
1001	TATTGAAGAA	AAAAACAAT	TCCGAAGTGC	TGACCATCAA	CAGCGAAACC
1051	GCTGTGGGTC	TCGCGGCCAA	AGAAGTCCGC	GAAGAGAAAA	CCCTGCCGTT
1101	TGCCGAAGCC	AAAGACGCGG	TACGTCAGGC	TTATATCCGT	ACCGAAGCCG
1151	CCAAACTTGC	CGAAAAACAG	GCAAAAGACG	TGCTTACCCA	ACTGAACGGC
1201	GGCAAGGCTG	TTGACGTGAA	ATGGTCGGAA	GTGTCCGTTT	TGGGCGCACA
1251	GAGGCAAGG	CAGTCCATGC	CGCCCGAGAA	TTATGCGGAA	CTGCTGAAG
1301	CAAACCGGC	AAACGGCAAA	CCCGCTACG	TCAGGCTGAT	CGGTCTGCCG
1351	GCACCCGTGA	TTGTCGAAGT	ACAGGCTGTA	ACCCGCGCCG	ATGATATCGC
1401	CGCAGACGTT	CCGCTTGCAA	AACAGGCTTT	GGCGCAACAG	CAGTCTGCCA
1451	ATACTTTTCA	CTTGTGTGTA	CGTTATTTCA	ACGGCAAAAT	CAAACAGACC
1501	AAAGGAGCGC	AATCGGTCGA	CACCGCGCAC	GGTCAGTAA	

This corresponds to the amino acid sequence <SEQ ID 838; ORF 230-1.a>:

a230-1.pep

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPPSRDA VFQSLQRAY LKQGAKLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRakeVR EEKTLPFMEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWE VSVLGAQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPPDDIAAQL PLAKQALAQQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNGD GQ*

```

a230-1/m230-1 99.8% identity in 512 aa overlap

a230-1.pep	10	20	30	40	50	60
m230-1	10	20	30	40	50	60
a230-1.pep	70	80	90	100	110	120
m230-1	70	80	90	100	110	120
a230-1.pep	130	140	150	160	170	180
m230-1	130	140	150	160	170	180
a230-1.pep	190	200	210	220	230	240
m230-1	190	200	210	220	230	240
a230-1.pep	250	260	270	280	290	300
m230-1	250	260	270	280	290	300
a230-1.pep	310	320	330	340	350	360
m230-1	310	320	330	340	350	360
a230-1.pep	370	380	390	400	410	420
m230-1	370	380	390	400	410	420
a230-1.pep	430	440	450	460	470	480
m230-1	430	440	450	460	470	480
a230-1.pep	490	500	510			
m230-1	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 839>:

g231.seq

```

1  atgtcaaaac gaaaatccat aaaccgtccg tatcaaaaac cggcggaact
51  gccgccgttg caaaataatc cgccatttta ccgtaaaaac cgccgcctga
101 acttttttat cgcggcagac ggcggttgcg cgtctccgca aaaatgcagg
151 gcgcgcgggtt ttcagacggc atttgccgtt caaggccgtg cgggtgtcttt
201 accaaatgcc caaccattcg cccacggaat ccatccaatc cttattgccc
251 ccgccgctcc tgcctgcccg gcggtacgcc cacggcgctt gcggattttt
301 agctttccac aatcctttgc gtcccttttc cgctgaatt tgagcgctcg
351 catagtcggc aaaatccgcc ttatcctgct gttcttttagc ataactttta
401 taatgccacg ccgccccgtc ctgcacctgc atcagggttca aatcggtttt
451 gccggcggat acctgcgcca cttcgcgctg atagcggctg gtttcaaca
501 cacgtacact gactttccta ccctccgcgc ccgcgcgcag gttgtcgcgc
551 gaacgtgtac cgtaacgctg tttcatctcc ggtgcgtcga tatacgccat
601 ccgaatttta tgtttcgcgc cgtcgccgtc gatgacgtga agggatcgc
651 cgtcatagac tttggacacc gtgcctgtgt agctgtggcc ggatttcgcc
701 gatgcccgtc ggcgaacggg cgcgtcgaaa cccacgtccc ctgcagtgcc
751 gagtacgtcg agtacggcaa ccgccgtccg caccgcctca ctgtcatatc
801 ccgtataacc caacgcgcc aaaagcgaca gggcgacggg aagccatttc
851 atgatttttt taatctgcat atttttcaaa tgccgatgcc gtctgaacat
901 ctctga

```

This corresponds to the amino acid sequence <SEQ ID 840; ORF 231.ng>:

g231.pep

```

1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFV  QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNL SVGIVG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 AGGYLRHFAL IAVGFKHTYT DFPTLRRRAQ VVARTCTVSL FHLRCVDIRH
201 PNFMFRAVAV DDVKGI AVID FGHRACVAVA GFRRCP SANG RVETHVPCSA
251 EYVEYGNRRP HRLTVISRIT QRAQKRQGDG KPFHDFNLH IFQMPMPSEH
301 L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 841>:

m231.seq (partial)

```

1  ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51  GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG GC...

```

This corresponds to the amino acid sequence <SEQ ID 842; ORF 231>:

m231.pep (partial)

```

1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFV  QGRAVSLPNA QPFG.....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 231 shows 98.6% identity over a 73 aa overlap with a predicted ORF (ORF 231.ng) from *N. gonorrhoeae*:

m231/g231

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
g231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
	70					
m231.pep	QGRAVSLPNAQPFG					
	: :					
g231	QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFQSFAPFRLNL SVGIVG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 843>:

527

a231.seq (partial)

```

1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGNGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGGTGCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTAA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTC AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTCG GTGTGCAACA
501 CCGGACGCT GACTTTCCTG CCTTCCGCG CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GGCGCGTCGA TATACGCCAT
601 CCGGATTTTG TGTTTCGCGC CGTCGCCGTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GGCGGGCGGG CGCGTCGGAA CCCGCTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCGTCCG CACCGCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACC AAAAGCGACA AGGCGACGGG AAGCCATTT
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATC

```

This corresponds to the amino acid sequence <SEQ ID 844; ORF 217.a>:

a231.pep (partial)

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPQKCR
51 ARGFQTAFAV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFF RLNLVGIIG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRHEAL VAVGVEHADA DFPAFRRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRAVAV DNVKGVAVID FGHRACVAVA GFRRC SAAG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMMPSEH
301 I

```

m231/a231 98.6% identity in 73 aa overlap

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFAV					
a231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPQKCRARGFQTAFAV					
	10	20	30	40	50	60
	70					
m231.pep	QSRVSLPNAQPFG					
a231	QSRVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPRLNLVGIIG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 845>:

g231-1.seq

```

1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGGTGCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGAAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAGTCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTAA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTC AATCGGTTTT
451 GCCGGCGGAT ACCTGCGCCA CTTGCGCTG ATAGCGGTCG GTTTCAAACA
501 CaCgTaCaat gagtttcgta ccctccGCCG ccgcgcgCAG GTTGTcgcGC
551 GAACgTGTAC CGTAagcgtg TTtcatctcc GGTGCgtcGA TATACGCCaT
601 cCgAATTTta tGTttcgcgc cgtcgcCgtc gATGACGTGA AGGGtatcGC
651 CgtcATAGAC TTTGGACACC Gtgctgcgt AGctGTGGCC GGATttcgc

```

This corresponds to the amino acid sequence <SEQ ID 846; ORF 231-1.ng>:

g231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFQTAFAV QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF

```

101 SFPQSFAFPF RLNLVGVIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
 151 AGGYLRHFAL IAVGFKHTYN EFRTLRRRAQ VVARTCTVSV FHLRCVDIRH
 201 PNFMFRAVAV DDVKGIIVID FGHRACVAVA GFR

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 847>:

m231-1.seq

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAAC CGCGGGAAC
 51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
 101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
 151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
 201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
 251 CCGCGCTCC TGCTGCTCG GCGGTACGCC CACGCGCTT GCGGATTTT
 301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
 351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
 401 TAATGCCACG CGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
 451 GCCGACAGAA ACCTGCGCCA CTCGCGCTG GTAGCGGTCG GTATCGAACA
 501 CCGCACGCT GACTTTTCTG CCTTCCGCCG CCGCGCGCAG GTTGTGCGCG
 551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GGCGCGTCGA TATACGCCAT
 601 CCGGATTTTG TGTTCGCGC CGTCGCGCTC GATAACGTGA AGGGTGTGCG
 651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
 701 GATGCTCGGC GCGGGGCGGG CCGCTCGGAA CCCGCTCC CTGCCGCGCC
 751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACCGCTCG CTGCCGTACC
 801 CCGTATAACC CAACGCACCC AAAAGCGACA GGGCGACGGG AAGCCATTTT
 851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
 901 ATCGGAATCG GATTTAGAC GGCATCTTAA

This corresponds to the amino acid sequence <SEQ ID 848; ORF 231-1>:

m231-1.pep

1 MSKRKSINRP YQKPAELPPL QNPPFYRKN RRLNFFIAAD GGCASPQKCR
 51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACS AVRPRRLRIF
 101 SFPQSFAFPF RLNLVGVIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
 151 ADRNLRHFAL VAVGIEHAHA DFPFRRAQ VVARTRAVSL FHLRRVDIRH
 201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRCSAAG RVGTRVPCRA
 251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
 301 IGIGFQTAS*

g231-1/m231-1 87.0% identity in 262 aa overlap

	10	20	30	40	50	60
g231-1.pep	MSKRKSINRPYQKPAELPPLQNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
g231-1.pep	QGRAVSLPNAQPFAHGIHPILIAPAACPAPVRPRRLRIFSFPQSFAFPFRLNLVGVIG					
m231-1	QSRVSLPNAQPFAHGIHPILIAPAACPASAVRPRRLRIFSFPQSFAFPFRLNLVGVIG					
	70	80	90	100	110	120
g231-1.pep	KIRLILFFSITFIMPRRPVLHLHQVQIGFAGGYLRHFALIAVGFKHTYNEFRTLRRRAQ					
m231-1	KIRLILFFSITFIMPRRPVLHLHQVQIGFADNLRHFALVAVGIEHAHADFPFRRAQ					
	130	140	150	160	170	180
g231-1.pep	VVARTCTVSVFHLRCVDIRHPNFMFRAVAVDDVKGIIVIDFGHRACVAVAGFRXCPSANG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNDVKGVAVIDFGHRACVAVAGFRRCSAAGG					
	190	200	210	220	230	240
g231-1.pep	CVETHVPCSAEYVVXGNRRPHR					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 849>:

a231-1.seq

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAAC CGCGGGAAC
 51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
 101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG

529

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151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCTGCCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTAA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTC AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTCG GTGTGGAACA
501 CGCGGACGCT GACTTTCCTG CCTCCGCGC CGCGCGCAG GTTGTGCGGC
551 GAACGCGTGC CGTAAGCCTG TTTTCATCTC GCGCGCTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCGCTC GATAACGTGA AGGGTGTCGC
651 CGTCATAGAC TTTGGACACC GTGCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GCGGGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 850; ORF 231-1.a>:

a231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAACP AVRPRLRIF
101 SFPQSFAFF RLNLVGIIG KIRLILLEFS ITFIMPRRPV LHLHQVIGF
151 ADRNLRHFAL VAVGVEHADA DFPAFRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRAVAV DNVKGVAVID FGHRACVAVA GFRRC SAAG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 IGIGFQTAS*

```

a231-1/m231-1 99.0% identity in 309 aa overlap

	10	20	30	40	50	60
a231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a231-1.pep	QSRVSLPNAQPFPAHGIHPILIAPAACPAPVPRRLRIFSFQSFAPFRLNLVGIIG					
m231-1	QSRVSLPNAQPFPAHGIHPILIAPAACPASAVRPRRLRIFSFQSFAPFRLNLVGIIG					
	70	80	90	100	110	120
	130	140	150	160	170	180
a231-1.pep	KIRLILLEFSITFIMPRRPVLHLHQVIGFADRNLRFHFAVAVGVEHADDFPAFRRAQ					
m231-1	KIRLILLEFSITFIMPRRPVLHLHQVIGFADRNLRFHFAVAVGIEHAHADDFPAFRRAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
a231-1.pep	VVARTRAVSLFHLRRVDIRHPDFVFRAVAVDNVKGVAVIDFGHRACVAVAGFRRC SAAGG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRAVAVDNVKGVAVIDFGHRACVAVAGFRRC SAAGG					
	190	200	210	220	230	240
	250	260	270	280	290	300
a231-1.pep	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300
	310					
a231-1.pep	IGIGFQTASX					
m231-1	IGIGFQTASX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 851>:

g232.seq

```

1 atgatgggca acagcctgat tgaatccggt acgtttgtcg ccatacctgtt
51 tggtcagatt ttgggaacgg cggttgccgg cgcgccgcct tatattgtcg
101 ggatactggt tttgctggtc gccgtcggag gaacggccgg cagcctgttt

```

```

151 atgccgtccg taccgcgcaa ggctgccgat acccaaatcg agtgggaatat
201 tgtccgtggg acaaaatccc tgctgctga aacgggtgcg cacaatcccc
251 tttttaccgc cattatcggc atctcgtggg tttggtttgt cggcgcggtt
301 tataccacgc aactgccgac ctttacccaa atccatttgg gcggcaacga
351 taatgttttt aacctgatgc ttgctttgtt ttccatcggg attgccgcgg
401 gttcgggtact gtgtgccaag ttcggcaggg aacgggtgat gttggcttgg
451 gtaacggttg gtgcgttggg ttcgacgggt tgcggcctgg ttttgggtgtg
501 gctgacgcac ggacaccgtt ttgaagggtt gaacggcatt ttttggtttt
551 tatcgcaagg atgggcatac cccgtgatgg cgggtgatgac gctgatcggc
601 tttttcggcg gatttttctc cgttccgctc tatacctggc tgcaaacgcg
651 cagcagcgag actttccgcg cccgcgccgt tgccgccaac aatatcgtaa
701 acggcatctt tatggtttcc gccgccgtt tgagcgcggt attgctgttt
751 ttgtttgaca gcatttccct gctgtatctg attgtcgcct tgggcaatat
801 tccgttggcg gtatttttga ttaagcgca aaggcggtt ttaggcgcgg
851 cggcaatcag gaaaaaacct tga

```

This corresponds to the amino acid sequence <SEQ ID 852; ORF 232.ng>:

g232.pep

```

1  MMGNSLIESG TFVAILFGQI LGTAVAGAPP YIVGILVLLV AVGGTAGSLF
51  MPSVPAKAAD TQIEWNIVRG TKSLRETIVR HNPVFTAIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FGRERLMLAW
151 VTVGALGSTV CGLVLVWLTH GHRFEGLNGI FWFLSQWAY PMAVMTLIG
201 FFGGFFSVPL YTWLQTASSE TFRARAVAN NIVNGIFMVS AAVLSAVLLF
251 LFDSISLLYL IVALGNIPLA VFLIKRERRF LGAAAIRKKP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 853>:

m232.seq

```

1  ATGATGGGCA ACAGCCTGAT TGAATCGGGT ACGTTTGTCTG CCATCCTGTT
51  CGGTCAGATT TTGGGAACGG CGGTGGCAGG TGTACCGCCT TATATTGTCTG
101 GGATACTGGT TTTGCTGGTC GCCGTCGGAG GCACGGTCGG CAGCCTGTTT
151 ATGCCGTCCG TACCCGCCAA GGCTGCCGAT ACACAAATTG AGTGGAAATAT
201 TGTCCGTGGC ACAAATCCC TGCTGCGTGA AACGGTGCGG CACAAGCCCC
251 TTTTACC GC CATTATCGGT ATTTCTGTTG TTTGGTTTGT CGGCGCGGTT
301 TATACCACGC AACTGCCGAC CTTTACCCAA ATCCATCTGG GCGGCAACGA
351 CAATGTTTTC AACCTGATGC TTGCTCTGTT TTCCATCGGT ATTGCCCGCG
401 GTTCGGTACT GTGTGCCAAG TTCAGCAKGG AACGCCTGAT GTTGCTTGG
451 GTAACGGTTG GTGCGTTGGG TTTGACGGTT TGC GGCTTGG TTTTGGTGTG
501 GCTGACGCAC GGACACCGTT TTGAAGGGCT GAACGGCATT TTTTGTGTTT
551 TATCGCAAGG ATGGGCATAT CCCGTGATGG CGGTGATGAC GCTGATCGGC
601 TTTTTCGGCG GATTTTCTC CGTTCGCTC TATACCT (g) TG CAAACCGCCA
651 TAGCGAGATT TCCGCGCCCg GCCGTGCGG CCAACAATAT CGTTAACGGT
701 ATTTTATGGA TTTCCGCTGC CGTTTGTGAG CGGGTGTGTC GTTTTGTGTT
751 TGACAGCATT TCCTTGTGTT ATCTGATTGT CGCTTTGGGC AATATTCCGT
801 TGTCGGTATT TTTGATTAG CGCGAAAGGC GTTTGTAGG CGCGCGCGCA
851 ATCAGGAAAA AACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 854; ORF 232>:

m232.pep

```

1  MMGNSLIESG TFVAILFGQI LGTAVAGVPP YIVGILVLLV AVGGTVGSLF
51  MPSVPAKAAD TQIEWNIVRG TKSLRETIVR HKPVFTAIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FSXERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGLNGI FXFLSQWAY PMAVMTLIG
201 FFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLLYLIV ALGNIPLSVF LIKRERRFLG AAIRKKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 232 shows 94.1% identity over a 290 aa overlap with a predicted ORF (ORF 232.ng) from *N. gonorrhoeae*:

m232/g232

```

              10      20      30      40      50      60
m232.pep      MMGNSLIESGTFVAILFGQILGTAVAGVPPYIVGILVLLVAVGGTVGSLFMPSVPAKAAD
              |||||:|||||:|||||:|||||:|||||:
g232          MMGNSLIESGTFVAILFGQILGTAVAGAPPYIVGILVLLVAVGGTAGSLFMPSVPAKAAD

```


531

	10	20	30	40	50	60
	70	80	90	100	110	120
m232 . pep	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
g232	TQIEWNIVRGTKSLLRETVRHNPFVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
	130	140	150	160	170	180
m232 . pep	NLMLALFSIGIAAGSVLCAKFSXERLMLAWVTVGALGLTVCGLVLVWLTHGHRFEGLNGI					
g232	NLMLALFSIGIAAGSVLCAKFRERLMLAWVTVGALGSTVCGLVLVWLTHGHRFEGLNGI					
	190	200	210	220	230	
m232 . pep	FXFLSQGWAYPVMAMVMTLIGFFGGFFSVPLYT-VQTAIARFPRP-AVAANNIVNGIFMVS					
g232	FWFLSQGWAYPVMAMVMTLIGFFGGFFSVPLYTWLQTASSETFRARAVAANNIVNGIFMVS					
	240	250	260	270	280	289
m232 . pep	AAVLSAVLLFLFDSISLLYLIALGNIPLSVFLIKRERRFLGAAAIRKKPX					
g232	AAVLSAVLLFLFDSISLLYLIALGNIPLAFLIKRERRFLGAAAIRKKP					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 855>:

```

a232 . seq
1  ATGTACGCTA AAAAAGGCGG TTTGGGACTG GTTAAAAGCC GCCGTTTCGC
51  ACCTCTTTTC GCTACGCAGT TTCTCGGCGC GTTCAACGAC AATGTGTTCA
101 AAACCGCGCT GTTTGTGATG ATTGGGTTTT ACGGTTTGGG GCAAAACGGC
151 TTCCTGCCTG CCGGACAGAT GTTGAACCTG GGCGCGTTGC TGTATTATTT
201 GCCGTATFTC CTGTTTTCCCT CGCTGTCGGG GCAGTTGGGT AACAAATTCG
251 ACAAGGCCGT TTTGGCGCGT TGGGCCAAGG TGCTGGAAAT GATCATTATG
301 GCGGTGGCGG CATACGGGTT TTATATCCGG TCTGCCCGC TGCTTTTGGC
351 GTGTCTGTTT TGCATGGGCG CGCAATCGAC GCTGTTTCGG CCGCTGAAAT
401 ACGCCATCCT GCCCGATTAT CTCGACGACA AAGAGTTGAT GATGGGCAAC
451 AGCCTGATTG AATCGGGTAC GTTTGTGCGC ATCCTGTTCT GTCAGATACT
501 GGGGACTGCG GTGGCAGGTG TACCGCCTTA TATTGTCGGG ATACTGGTTT
551 TGCTGGTTCG CGTAGGAGGC ACGGTCGGCA GCCTGTTTAT GCCGTCCGTA
601 CCCGCCAAGG CTGCCGATAC ACAAAATTGAG TGGAATATTG TCCGGGGTAC
651 AAAATCCCTG CTGCGTGAAA CCGTGCGGCA CAAGCCCGTT TTTACCGCCA
701 TTATCGGTAT TTCGTGGTTT TGGTTTGTCT GCGCGGTTTA TACCACGCAA
751 CTGCCGACCT TTACCCAAAT CCATCTAGGC GGCAACGACA ATGTTTTCAA
801 CCTGATGCTT GCCCTGTTT CCATCGGTAT TGCCGCCGGT TCGGTACTGT
851 GTGCCAAGTT CAGCAGGGA CCGCTGAGGT TGGCTTGGGT AACGTTGGT
901 GCGTTGGGTT TGACGGTTTG CCGCTTGGT TTGGTGTGGC TGACGCACGG
951 ACACCGTTTT GAAGGGCTGA ACGGCATTTT TTGGTTTTTA TCGCAAGGAT
1001 GGGCATATCC CGTGATGGCG GTGATGACGC TGATCGGCTT TTTCCGCGGA
1051 TTTTCTCCG TTCCGCTCTA TACCTGGCTG CAAACCGCCA GTAGCGAGAC
1101 TTTCCGCGCC CGCGCGTTG CCGCCAACA TATCGTTAAC GGTATTTTTA
1151 TGGTTTCCGC TGCCGTTTG AGCGCGGTG TGCTGTTTTT GTTTGACAGC
1201 ATTTCTTGT TGTATCTGAT TGTCGCTTTG GGCAATATTC CGTTGTCGGT
1251 ATTTTGTATT AAGCGCGAAA GCGGTTTTT AGGCGCGGCG GCAATCAGGA
1301 AAAAACCTTG A

```

This corresponds to the amino acid sequence <SEQ ID 856; ORF 232.a>:

```

a232 . pep
1  MYAKKGLGL VKSRRFAPLF ATQFLGAFND NVFKTALFVM IGFYGLGQNG
51  FLPAGQMLNL GALLFILPYF LFSSLSGQLG NKFDKAVLAR WAKVLEMIIM
101 AVAAYGFYIR SAPLLLACLF CMGAQSTLFG PLKYAILPDY LDDKELMMGN
151 SLIESGTFVA ILFGQILGTA VAGVPPYIVG ILVLLVAVGG TVGSLEMPVS
201 PAKAADTQIE WNIVRGTKSL LRETVRHKPV FTAIGISWF WFGAVYTTQ
251 LPTFTQIHLG GNDNVFNLM ALFSIGIAAG SVLCAKFSRE RLRLAWVTVG

```

532

301 ALGLTVCGLV LVWLTHGHRF EGINGIFWFL SQGWAYPVMA VMTLIGFFGG
 351 FFSVPLYTWL QTASSETFRA RAVAANNIVN GIFMVSAAVL SAVLLFLFDS
 401 ISLLYLIVAL GNIPLSVFLI KRERRFLGAA AIRKKP*

m232/a232 95.9% identity in 290 aa overlap

m232.pep					10	20	30
					MMGNSLIESGTFVAILFGQILGTAVAGVPP		
a232	ACLFCMGAQSTLFGPLKYAILPDYLDKELMMGNSLIESGTFVAILFGQILGTAVAGVPP						
	120	130	140	150	160	170	
m232.pep		40	50	60	70	80	90
		YIVGILVLLVAVGGTVGSLEMPSPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
a232	YIVGILVLLVAVGGTVGSLEMPSPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG						
	180	190	200	210	220	230	
m232.pep		100	110	120	130	140	150
		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMALFSIGIAAGSVLCAKFSXERLMLAW					
a232	ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMALFSIGIAAGSVLCAKFSRERLRLAW						
	240	250	260	270	280	290	
m232.pep		160	170	180	190	200	210
		VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFXFLSQGWAYPVMAMVTLIGFFGGFFSVPL					
a232	VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFWFLSQGWAYPVMAMVTLIGFFGGFFSVPL						
	300	310	320	330	340	350	
m232.pep		220	230	240	250	260	
		YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
a232	YTWLQTASSETFRARAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS						
	360	370	380	390	400	410	
m232.pep		270	280	289			
		VFLIKRERRFLGAAAIRKKPX					
a232	VFLIKRERRFLGAAAIRKKPX						
	420	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 857>:

g233.seq

1	atgaaacgca	aaaatatcgc	gctgattccc	gccgccggca	tccgggtgcg
51	tttcggtgcg	gacaaaccca	agcaatatgt	cgaaatcgga	agcaaaaccg
101	ttttagaaca	tgtacttggg	atttttgaac	ggcatgaggc	cgctgatattg
151	accgtcgttg	tcgtctcgcc	cgaagacacg	tttgccgata	aggttcagac
201	ggcatttcca	caggttcggg	tgtggaaaaa	cggtggacag	acccgcgccg
251	aaactgtccg	caacggtgtg	gcaaaactgt	tggaaaccgg	tttggcggcg
301	gaaaccgaca	atattctggt	acacgatgcc	gcccgcgtgct	gcctgccgtc
351	tgaagctctg	gcgcggttga	tagaacaggc	gggcaacgcc	gccgaaggcg
401	ggattttggc	agttcccgtt	gccgatacgc	tcaagcgcgc	agaaagcgga
451	caaatcagtg	caactgtcga	ccgttcgggg	ctttggcagg	cgcaaacgcc
501	gcagcttttt	caagcgggtt	tgctgcaccg	cgcattggct	gcggaaaact
551	tgggcggcat	taccgatgaa	gcgtccgccg	tggaaaaact	gggtgtgcgt
601	ccgtactga	tacagggcga	cgcgcgcaat	ttgaaactga	cgcagccgca
651	ggacgcatac	atcgtcaggc	tgctgctcaa	tgccgtctga	

This corresponds to the amino acid sequence <SEQ ID 858; ORF 233.ng>:

g233.pep

1	MKRKNIALIP	AAGIGVREFA	DKPKQYVEIG	SKTVLEHVLG	IFERHEAVDL
51	TVVVVSPEDT	FADKVQTAFP	QVRVWKNNGQ	TRAETVRNGV	AKLLETGLAA
101	ETDNILVHDA	ARCCLPSEAL	ARLIEQAGNA	AEGGILAVPV	ADTLKRAESG

151 QISATVDRSG LWQAQTPQLF QAGLLHRLA AENLGGITDE ASAVEKLGVR
201 PLLIQGDARN LKLTQPDAY IVRLLLLNAV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 859>:

m233.seq (partial)
1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG
51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG
101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTTG
151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC
201 GGCATTCCA CAGGTTCTGGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG
251 AAACCGTCCG CAACGGTGTG GCAAACTGT TGGAAACCGG TTTGGCGGCG
301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCC GCCGAAGGCG
401 GGATTTTGGC AATTCCCAT TCCGATACGC TCAAGTGCGC GGACGGTGGG
451 AACATT....

This corresponds to the amino acid sequence <SEQ ID 860; ORF 233>:

m233.pep (partial)
1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51 TVVVVSPEDT FADKVQTAFP QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAIPI ADTLKCADGG
151 NI....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 233 shows 93.4% identity over a 152 aa overlap with a predicted ORF (ORF 233.ng) from *N. gonorrhoeae*:

m233/g233

	10	20	30	40	50	60
m233 .pep	MKRKNIALIPAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
	: : : : :					
g233	MKRKNIALIPAAGIGVRFGADKPKQYVEIGSKTVLEHVLGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m233 .pep	FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	: : : : :					
g233	FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	70	80	90	100	110	120
	130	140	150			
m233 .pep	TRLIEQAGNAEGGILAIPIADTLKCADGGNI					
	: : : :					
g233	ARLIEQAGNAEGGILAVPVADTLKRAESGQISATVDRSGLWQAQTPQLFQAGLLHRLA					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 861>:

a233.seq
1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG
51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG
101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTTG
151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC
201 GGCATTCCA CAGGTTCTGGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG
251 AAACGTCCG CAACGGTGTG GCAAAATTGT TGGAAACCGG TTTGGCGGCG
301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCT GCCGAAGGTG
401 GGATTTTGGC AATTCCCGT TCCGATACGC TCAAGTGCGC GGACGGTGGG
451 AACATTAGTG CAACCGTCGA GCGGACGAGC CTTTGGCAGG CGCAAACGCC
501 GCAGCTTTTC CGCGCCGGGCG TGCTGCACCG CGCATTGGCT GCGGAAAACCT
551 TGGACGGCAT TACCGATGAA GCGTCCGCGG TGGAAAAATT GGGCATCCGC
601 CCTTTGCTGG TGCAGGGCGA CGCGCGCAAT TTGAAACTGA CGCAGCCGCA
651 GGACGCATAC ATCGTCAGGC TGCTGCTCGA TGCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 862; ORF 233.a>:

```
a233.pep
  1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
 51 TVVVVSPEDT FADKVQTAFF QVRVWKNNGGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAI PV ADTLKCADGG
151 NISATVERTS LWQAQTPQLF RAGLLHRLA AENLDGITDE ASAVEKLGIR
201 PLLVQGDARN LKLTQPQDAY IVRLLLDVAV*
```

m233/a233 99.3% identity in 152 aa overlap

```

      10      20      30      40      50      60
m233.pep MKRKNIALIPAAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
|||||
a233      MKRKNIALIPAAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
      10      20      30      40      50      60

      70      80      90     100     110     120
m233.pep FADKVQTAFFQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
|||||
a233      FADKVQTAFFQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
      70      80      90     100     110     120

      130     140     150
m233.pep TRLIEQAGNA AEGGILAIPIADTLKCADGGNI
|||||
a233      TRLIEQAGNA AEGGILAI PVADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA
      130     140     150     160     170     180

a233      AENLDGITDEASAVEKLGIRPLLQGDARNLKLTQPQDAYIVRLLLDVAVX
      190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 863>:

```
g234.seq
  1 atgaaaaccg tttccgccgc catcgctttt gccgccgctg ccgtttcact
 51 gaccggctgt gcgaccgagt cctcacgcag cctcgagggt gcaaaagtcg
101 cctcctgcaa tacgcaatat cacggtgttc gcaccccgat ttccgtcgga
151 acattcgaca accgctccag cttccaaaaa ggcattttct ccgacagtga
201 agaccgtctg ggcagccagg caaaaacat cctggtaaca cacctgcaac
251 aaaccaaccg cttcaacgta ctgaaccgca ccaaccttag cgcattgaaa
301 caggaatccg gcatttcgag caaagcgag aacctgaaag gcgcagatta
351 tgctgttacc ggcgatgtaa ccgaattcgg acgcagagat gtcggcgatc
401 atcagctctt cggcattttg ggtcgcggca aatcgcaaat cgcctatgca
451 aaagtggctc tgaatatcgt caacgtcaat acttccgaaa tcgtctattc
501 cacacagggc gcgggcgaat acgcactttc caaccgcgaa atcatcggtt
551 tcggcggcac ttccggctac gatgcgactt tgaacggcaa agtttttagac
601 ttggcaatcc gcgaagccgt cgacaacttg gttcaggctg tcgacaaccg
651 cgcattggcaa tccaaccgtt aa
```

This corresponds to the amino acid sequence <SEQ ID 864; ORF 234.ng>:

```
g234.pep
  1 MKTVSAAIAF AAAAVSLTGC ATESSRSLEV AKVASCNTQY HGVRTPISVG
 51 TFDNRSSFQK GIFSDSEDRL GSQAKTILVT HLQQTNRNVN LNRTNLSALK
101 QESGISGKAQ NLKGADYVVT GDVTEFGRRD VGDHQLFGIL GRGKSQIAYA
151 KVALNIVNVN TSEIVYSTQG AGEYALSRE IIGFGTSGY DATLNGKVLD
201 LAIREAVDNL VQAVDNGAWQ SNR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 865>:

```
m234.seq (partial)
  1 ...GGCGCGGGCG AATACGCACT TTCCAACCGt GAAATCATCG GTTTCGGCGG
 51 CACTTCCGGC TACGATGCGA CTTTGAACGG CAAAGTTTTA GACTTGGCAA
101 TCCGCGAAGC .gTCAACAGC CTGGTTCAGG CTGTTGACAA CGGCGCATGG
151 CAACCAACC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 866; ORF 234>:

535

m234.pep (partial)
 1 ..GAGEYALSNR EIIGFGGTSG YDATLNGKVL DLAIREAVNS LVQAVDNGAW
 51 QPNR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 234 shows 94.4% identity over a 54 aa overlap with a predicted ORF (ORF 234.ng)
 from *N. gonorrhoeae*:

m234/g234

					10	20	30
m234.pep					GAGEYALSNREIIGFGGTSGYDATLNGKVL		
g234	LGRGKSQIAYAKVALNIVNVNTSEIVYSTQ	GAGEYALSNREIIGFGGTSGYDATLNGKVL					
	140	150	160	170	180	190	
		40	50				
m234.pep		DLAIREAVNSLVQAVDNGAWQPNRX					
g234		DLAIREAVDNLVQAVDNGAWQSNRX					
	200	210	220				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 867>:

a234.seq (partial)
 1 AACCGCACCT ATTTGAACGC ATTAAAACAG GAATCCGGCA TTTCCGGCAA
 51 AGCGCATAAC CTGAAAGGCG CAAATTATGT CGNNACCGGC GATGTAACCG
 101 AATTCGGACG CANAGATGTC GGCGATCATC AGCTCTTCGG CATTTTGGGT
 151 CGCGGCAAAT CGCAAATCGC CTATGCAAAA GTGGCTCTGA ATATCGTCAA
 201 CGTCAATACT TCCGAAATCG TCTATTCCGC ACAGGGCGCG GCGGAATACG
 251 CACTTTCCAA CCGTGAAATC ATCGGTTTCG GCGGCACTTC CGGCTACGAT
 301 GCGACTTTGA ACGGCAAAGT TTTAGACTTG GCAATCCGCG AAGCCGTCAA
 351 CAGCCTGGTT CAGGCTGTTG ACAACGGCGC ATGGCAACCC AACCGTTAA

This corresponds to the amino acid sequence <SEQ ID 868; ORF 234.a>:

a234.pep (partial)
 1 NRTYLNALKQ ESGISKAHN LKGANYVXTG DVTEFGRXDV GDHQLFGILG
 51 RGKSQIAYAK VALNIVNVNT SEIVYSAQGA GEYALSNREI IGFGGTSGYD
 101 ATLNGKVL DL AIREAVNSLV QAVDNGAWQP NR*

m234/a234 100.0% identity in 54 aa overlap

					10	20
30						
m234.pep					GAGEYALSNREIIGFGGTSGYDATLNGKVL	
a234	LGRGKSQIAYAKVALNIVNVNTSEIVYSAQ	GAGEYALSNREIIGFGGTSGYDATLNGKVL				
	50	60	70	80	90	100
		40	50			
m234.pep		DLAIREAVNSLVQAVDNGAWQPNRX				
a234		DLAIREAVNSLVQAVDNGAWQPNRX				
	110	120	130			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 869>:

g235.seq

q235.pep

1	<u>MKPLILGLAA</u>	VLALSACQVR	KAPDLDYTSF	KESKPASILV	VPPLNESPDV
51	NGTWGMLAST	AAPISEAGYY	VFPAAVVEET	FKENGLTNAA	DIHAVRPEKL
101	HQIFGNDAVL	YITVTEYGTS	YQILDSVTTV	SAKARLVDSR	NGKELWSGSA
151	SIREGSNNNS	SGLLGALVGA	VVNQIANSLT	DRGYQVSKTA	AYNLLSPYSR
201	NGILKGPRFV	EEQPK*			

m235.seq

1	ATGAAACCTT	TGATTTTAGG	GCTTGCCGCC	GTGTGGCGC	TGCTGCGCTG
51	CCAAGTTCAA	AAAGCGCCCG	ATTTCTACTA	CACGTCATTC	AAGGAAAGCA
101	AACCGGCTTC	AATTTTGGTG	GTTCGCGCGC	TGAACGAATC	GCCCGATGTC
151	AACGGAACAT	GGGGTGACT	GGCTTCGAC	GCCGCGCCGC	TTTCCGAAGC
201	CGGCTATTAC	GTCTTCCCCT	CCGAGTCGT	GGAGAAAC	TTCAAACAA
251	ACGGCTTGAC	CAATGCGCCG	GATATTACG	CCGTCCGGCC	GGAACAACTG
301	CATCAGATTT	TCGGCAATGA	TGCGGTTTTG	TACATTACGG	TTACCGAATA
351	CGGCACTTCA	TATCAAATTT	TAGACAGCGT	GACGACCGTA	TCCGCCAAG
401	CACGGCTGGT	CGATTCCCGC	AACGGAAG	AGTTGTGGTC	GGGTTCCGCC
451	AGCATCCGCG	AAGGCAGCAA	CAACAGCAAC	AGCGCCTGT	TGGGGGCTTT
501	GGTCAGCGCA	GTGGTCAATC	AGATTGCCAA	GACGCTGAC	GACCCCGGTT
551	ATCAGGTTTC	CAAAACCGCC	GCATAACAAC	TGCTGTCGCC	CTATTCTCAC
601	AACGGCATCT	TGAAAGGTCC	GAGATTGTT	GAAGAGCAGC	CCAAATAA

m235 . pep

1	<u>MKPLILGLAA</u>	VLALSACQVQ	KAPDFDYTSF	KESKPASILV	VPPLNESPDV
51	NGTWGVLAST	AAPLSEAGYY	VFPAAVEET	FKQNGLTNAA	DIHAVRPEKL
101	HQIFGNDAVL	YITVTEYGTS	YQILDSVTTV	SAKARLVDSR	NGKELWSGSA
151	SIREGSNNSN	SGLLGALVSA	VVNQIANSLT	DRGYQVSKTA	AYNLLSPYSH
201	NGILGKPRFV	EEOPK*			

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 235 shows 96.7% identity over a 215 aa overlap with a predicted ORF (ORF 235.ng) from *N. gonorrhoeae*:

m235/q235

	10	20	30	40	50	60	
m235.pep	MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST						
		:		:		:	
g235	MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST						
	10	20	30	40	50	60	
	70	80	90	100	110	120	
m235.pep	AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS						
	:	:		:		:	
g235	AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS						
	70	80	90	100	110	120	
	130	140	150	160	170	180	

537

```

m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||
g235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
          130      140      150      160      170      180

          190      200      210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||
g235      DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPKX
          190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 873>:

```

a235.seq
1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTTCGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAACTG
301 CATCAGATTT TCGGCAATGA TCGGTTTTTG TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAAG
401 CACGGCTGGT CGATTCCCGC AACGGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTCAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC TAAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAAGGTCC GAGATTCGTC GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 874; ORF 235.a>:

```

a235.pep
1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

m235/a235 100.0% identity in 215 aa overlap

```

          10      20      30      40      50      60
m235.pep  MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
          |||
a235      MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
          10      20      30      40      50      60

          70      80      90      100     110     120
m235.pep  AAPLSEAGYYVFPAAVVEETFQKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
          |||
a235      AAPLSEAGYYVFPAAVVEETFQKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
          70      80      90      100     110     120

          130     140     150     160     170     180
m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||
a235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          130     140     150     160     170     180

          190     200     210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||
a235      DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 875>:

g236.seq

```

1 ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCCGCACAG CGTTTGCAGA
51 CGGTTTCATA ACCTGCAACC GCGCCACAT CCGGGTGTA ATGCCAGCAG
101 CGTTCGCATT TTTCGCCGTC GCTGGCTTTG GCGGCAACGG CAAGTTCATC
151 ACCGACTTTC ACTTCTGCTT TAGACACCAG CAGGGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT CTTCCGGCGC GGTAATTTCG
251 GCTTCCGCCT GCAAggacga accgacagTT TTGTcggcGC GCAAAGGCTC
301 GAtagcggcg gTTACTGCTT CGCGCGCTTC GCGGATTGCC GTCCATTTT
351 TCACCAGTTC GGCTTCGGCT TTTTCGTTGA TGGCCGGGAA CTCGTGCCAA
401 GTATGGAAGA GGACGCTGTC TTCTTCGCCG CCGCCGATGA TGTCCCACGC
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTGCGCGC TGCGGCGGGC GCGGCTGTCTG
551 GCTTTGGTGG TGTAAGGGCG GTCTTTCAGG ATGTCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACAATGTC TTTACGGCG AAGTGAAGG
651 CATAGCGCG ATAGTAACCG CCTGCCAAAC GCTCTGCAG CCGCCGCGCC
701 AATACCAAGG CGTAGCGGTC GATTTCCACC ATATCCGCCT GTTGACGGC
751 ATCTTCAATC GGATTAAAGT CGCTCAAATT GGCAAacagG AAGCTCAAGG
801 TATTGCGGAT GCGGCGGTAG CTTTCGGTAA CGCGTTTGAG GATTTCTTTG
851 GAAatcgCCA ATtcgcccgt gTAATCGGTG GATGCCGCC ACAGGCGCAG
901 GATGTCCGCG CCGAATTCTG TATAGACTTC CTGCGGCGCG ACGACGTTGC
951 CGATGGATT TCGACATTTT CCGCCGTTT GGTCAACCAC GAAACCGTGG
1001 GTCAGCAGCT GTTTATACGG TCGCGTCCC ATGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 876; ORF 236.ng>:

g236.pep

```

1 MARFAFSADI LRTAFADGFI TCNRAHIAGV MPAFAFFAV AGFGNGKFI
51 TDFHFCFRHQ QGKAQFFAQ IQIAGHFFRR GNFGFRLQGR TDSFVGAQRL
101 DSGGYCFARF ADCRPFFHQF GFGFFVDGRE LVPSMEEDAV FFAAADDVPR
151 FFAGEAQNRC NQENQAARDV VQGGRLAAAG AAVGFGGVEA VFQDVEVERA
201 QVFRAERNV FHGEVEGIAR IVTACQTLQ PPRQYQGVAV DFHHIRLLHG
251 IFNRIKVAQI GKQEAQGIAD AAVAFGNAFE DFFGNRQFAA VIGGCRPQAG
301 DVRAEFVIDF LRRDDVADGF RHFAAVLVNH ETVGQQLFIR CASHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 877>:

m236.seq (partial)

```

1 ..TTGCACGGAC GAACCGACGG TTTTGTGCGC GCGCAAAGGC TCGATGGCGG
51 CGGTACCGC TTCGCGGGCT TCGCGGATTG CCGTCCATTT TTCACCACT
101 TCGGCTTCGG TTTTTCGTT GATGGTCGGG AACTCGTGCC AAGTATGGAA
151 GAGGACGCTG TCKTCTTCGC CGCCGCCGWT GAYGTCCAC GCTTCTTCGC
201 CGGTGAAGCA CAAATCGGT GCAATCAAGA GAACCAAAC GCGTGTGATG
251 TGATACAGGG CAGTTGTGC GCTGCGGCGT GCATGGCTGT CTGCTTTGGT
301 GGTGTAGAGG CGTCTTTCA GGATGTCGAG GTAGAACGCA CCCAAGTCTT
351 CCGAGCAGAA AGAAACAATG TCTTTACGG CAAAGTGGaA kGCATAACGC
401 GGATAGTAAT CGCCTGCCAG AACTCTTGC AGCTGACGTG CCAATACCAC
451 GCGTAGCGG TCGATTTCCA CCATATCCGC CTGTTGCACG GCATCTTCAA
501 TCGGATTAAA GTCGCTCAAG TTGGCAAACA AAAAGCTCAA GGTATTGCGG
551 ATACGGCGGT AgCTTTCGGT TACGCGTTT AGGATTTCTT TGGAAATCGC
601 CAATTCGCCG CTGTAATCGG TAGATGCCG CCACAGGCG AGGATGTCTG
651 CGCCGAATTC GTTATAAACC TCTTGCGGT CAACGACGTT GCCGATGGAT
701 TTCGACATTT TTTTGCTTC GCCGTCGACA ACGAAACCAT GGGTCAGCAG
751 CTGTTTATAC GCGCGCGAC CCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 878; ORF 236>:

m236.pep (partial)

```

1 ..LHGRTDGFVG AQRLDGGGYR FAGFADCRPF FHQFGFGFFV DGRELVSME
51 EDAVXFAXAX DVPRFFAGEA QNRCNQENQT ACDVIQSLC AAACMAVCFG
101 GVEAVFQDVE VERTQVFRAE RNXFYQKVE XITRIVIAQ TLLQLTCQYH
151 GVAVDFFHIR LLHGIFNRIK VAQVGKQKAQ GIADTAVAFG YAFEDFFGNR
201 QFAAVIGRCR PQAQDVCAEF VINLLRCNDV ADGFRHFFAF AVDNETMGQQ
251 LFIRRATH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 236 shows 82.9% identity over a 258 aa overlap with a predicted ORF (ORF 236.ng) from *N. gonorrhoeae*:

m236/g236


```
m236.pep                               LHGRTDGFVGAQRLDGGGYRFAGFADCRPF
                                         |:|:|:|:|:|:|:|:|:|:|:|:|:|
g236    FRHQQGKAQFFAQSIQIAGHFFRRGNFGFRLQGRTDSFVGAQRLDSSGGYCFARFADCRPF
          60      70      80      90      100     110

          40      50      60      70      80      90
m236.pep FHQFGFGFFVDGRELVPSMEEDAVXFAAAXDVPRFFAGEAQNRCNQENQTACDVIQGS LC
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|:||:|:|
g236    FHQFGFGFFVDGRELVPSMEEDAVFFAAADDVPRFFAGEAQNRCNQENQAARDVVQGLR
          120     130     140     150     160     170

          100     110     120     130     140     150
m236.pep AAACMAVC FGGVEAVFQDVEVERTQVFRAERNXVFYGK VEXITRIV IACQTLLQL TCQYH
          ||| | :|||||:|||||:|||||:|:|:| |:|:|:| |||:|:|
g236    AAAGA AVGGVEAVFQDVEVERAQVFRAERNNVFHGEVEGIARIVTACQTLLQP PRQYQ
          180     190     200     210     220     230

          160     170     180     190     200     210
m236.pep GVAVD FHHIRLLHGIFNRIKVAQVGKQKAQGIADTA VAFGYAFEDFFGN RQFAAVIGRCR
          |||||:|||||:|||||:|||||:|:|:| |:|:|:| |||:|:|
g236    GVAVD FHHIRLLHGIFNRIKVAQIGKQE AQGIADA AAVAFGNA FEDFFGN RQFAAVIGGC R
          240     250     260     270     280     290

          220     230     240     250     259
m236.pep PQAQDVCAEFVINLLRCNDVADGFRHFFAFVDNETMGQQLFIRRATHX
          |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g236    PQAQDVRAEFVIDFLRDDVADGFRHF AAVLVNHETV GQQLFIRCASHG
          300     310     320     330     340
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 879>:

```

a236.seq
1  ATGGCGCGTT TCGCCTTCTC CGCGACATT CTCTGCACAG CGTTTGCAGA
51  CGGTTTCATG GCTTGCAACC GCGCCACAT CGCGGGTGTA GTGCCAGCAG
101 CGTTCGCATT TTTCCACCAT ACTGGCTTTA GCGGCAACGG CAAGTTCGCT
151 GCTACTTTTC ATTCTTGCTT TAGACACCA GAAAGCAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATT CTTCGCGCGC GGTAAATTTCG
251 GCTTCGGCTT GCAAGGACGA ACCGACGGTT TTGTCGCGCG GCAAAGGCTC
301 GATGGCGGCG GTTACCGCTT CGCGGGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAAGTT CGGCTTCGGCT TTTTCGTTGA TGGTCGGGAA CTCGTGCCAA
401 GTATGGA AAA GCACGTGTC TTCTGCGCCG CCGCCGATGA TGTCCCACGC
451 TTCTTCGCGG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTGCGCGC TCGCGCGGGC GCGGCTGTCTG
551 GCTTTGGTGG TATAGAGGCG GTCTTTCAGG ATATCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACCATTTT TTTACGCGCA AAGTGAAGG
651 CATAACGCGG ATAAAAATCA CCGGCAACGC GTTCTTGCAG CCGCCTTGCC
701 AACACCAAGG CATAGCGGTG GATTTCCACC ATATCGCGCT GTTGACAGCG
751 ATCTTCAATA GGATTGAAGT CGCTCAAGTT GGCAAAACAA AAGCTCAAGG
801 TATTGCGGAT ACGGCGGTAG CTTTCGGTTA CGCGCTTGAG GATTTCCTTTG
851 GAAATCGCCA ATTCGCGCGT GTAATCGGTG GATGCGGCCC ACAGGCGCAG
901 GATGTCGCGC CCGAACTCGT TATACACTTC TTGCGGCGCG ACGACGTTGC
951 CGATGGATTT CGACAATTTT GCCCGTTTTT GATCCACCAC GAAACCATGG
1001 GTCAGCAGCT GTTTGTACGG CGCGCGACCC ATTAGA

```

This corresponds to the amino acid sequence <SEQ ID 880; ORF 236.a>:

a236.pep	1	MARFAFSADI	LCTAFADGFM	ACNRAHIAGV	VPAFAFFTTI	TGFSGNKKA
	51	AYFHCFCRHQ	QSKAQFFAQS	IQIAGHFFRR	GNFGFGLQGR	TDGFVGAQRL
	101	DGGGYRFAGF	ADCRPFFHQF	GFGFFVDGRE	LVPSMEKHAV	FCAAADDVPR
	151	FFAGEAQNRC	NQENQAARDV	VQGGRLAAAG	AAVGFGGIEA	VFQDIEVERA
	201	QVFRAERNHF	FHGKVEGIVR	IKITGNAFLQ	PPCQHQGIAV	DFHHIRLLHG
	251	IFNRIEVAQV	GKQAKQGIAD	TAVAFGYALE	DFFGNRQFAA	VIGGCRPQAG
	301	DVRAELVIHF	LRRDDVDADG	RHFAPVLIHH	ETMGQQLFVR	RATH*


```

101 AFQRPEYRVQ TDISIDGIDH IFTLDAAFGR VNQPTVLIRF DARHRGLEN
151 LRAGFGSGAG NTQRVIERMK MPQGQIELCA LVHIAVKLLF QLGFIKPLIM
201 TRTVMPLGVF MPLLQLFPML RTDGNRGITA LPIAIDGMFA DAFVHQFDRL
251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPAGRAEA DTCGFQNDGF
301 MSVFRQRCG TOTAQTAADN AGFGFQTALE FRINSMRINR TKIIRQIFL
351 KIRANHCVCF IGYIFGRNDT DCRAISSXQK IG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 883>:

m237.seq

```

1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCCC CACGAATATT
51 CGATTTTGAC ATCGGCAAGC TCGGGAAGAA CTTTAAGCAT ATCTTGCGCG
101 ACAAGCTCGG TCATaCGCTC AGGATTGTCG ATAAACTCGT TATCCTTACC
151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAAATAT
201 GGCGGTTGTC GCATACTGCC ATATTGTAC GGATAAGCCC TTTTGCGCGC
251 GCGGCAAGG GTTCGGTGC AATAATAAAG GTGCTGACAG CAATCGCCTT
301 GCGTTCCAAA GGCCGGAATA TCGGGTCAA ACCTGCATAA GTATTGACAG
351 CATAGACCAC ATTTTTCAC TCGACGTGC CTTGGGCGT GTAAACCAGC
401 CAACCGTTT GATGCGGTC GATGCAGTC ATCGGGGATT GCTCGAAAAT
451 CTGCGCACCG GCTTCGGCAG CGGCACGAG GATGCCCAA GTGTAAGTGA
501 GCGGATGCAG GTGTCCGGAT AAGGGGTCGA ATTGTGCCCC TTGGTACATA
551 TCGCTGTCAA GCTGCTGTT CAACTCGGCT TTATCCCAA GTTGATAATG
601 ACTCGCACCG TAATGCCGTT GGGCGTGTT ATGCCACTGC TGCAACTCTT
651 CCAATGCTG CGGACGAGC GCAACCGTG CATAACCGCG CTGCCAATCA
701 CAATCGACGG CATGTTGCG GACGCGTTC TCCACAGTT CGACGCCTG
751 CAAAGACTGT TGCCAAAACC ATTGCGCCTG CTCCAAGCCG ACCTGTTTTT
801 CAATTTCCCC CATAACCGAG nCGTAATCG TGATAACCTG CCCGCCACTC
851 CGTCCCGACG CGCCGAAACC GATACGCGG GCTTCCAACA CAACCGTTTC
901 ATGTCCCTGC TCCGCCAAG GCAATGCAGT GCACAAACCA CCCAATCCGC
951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTtCGGATAA
1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
1051 AAAATCAGGG CGAATCATTG TGTTCGCTT ATCAGGTGTA TTTTCGGACG
1101 GAATGATACA GGCTGTCGGG CCATATCGTC CAwACAGAA ATCGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 884; ORF 237>:

m237.pep

```

1 MRDKVGGNVA LPAPRIFDFD IGKLRKNFKH ILADKLGH TL RIVDKLVILT
51 AEKQSAVRAE AVIIQNMAVV AYCHIVTDKP FCARPQGFR NNGGADSNRL
101 AFQRPEYRVQ TCISIDSIDH IFALDAAFGR VNQPTVLMRF DARHRGLEN
151 LRTGFGSGTS DAQSVSERMQ VSGXGVELCP LVHIAVKLLF QLGFIKPLIM
201 TRTVMPLGVF MPLLQLFPML RTDGNRGITA LPITIDGMFA DAFVHQFDRL
251 QRLLPKPLRL LQADLFFNFP HTAXVIADNL PATPSRAET DTRGFQHNRF
301 MSLRQGCQS AQTQSAADD TGIGFQTALK FRINSMRINR TEIIRQIFL
351 KIRANHCVCF IRCIFGRNDT GCRAISSXQK IG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 237 shows 86.1% identity over a 382 aa overlap with a predicted ORF (ORF 237.ng) from *N. gonorrhoeae*:

m237/g237

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGH TL RIVDKLVILTAEKQSAVRAE					
g237	MRDKVGGNIALPAPRIFDSNIGKLRKNFKHILADKLGH TR RIVDKFVILTAEKQPAVRAE					
	10	20	30	40	50	60
m237.pep	AVIIQNMAVVAYCHIVTDKPF CARPQGFRNNGGADSNRLAFQRPEYRVQTCISIDSIDH					
g237	AVIIQNMAVVAYCHIVADKPF CARAQFGGNNKGADGNRLAFQRPEYRVQTDISIDGIDH					
	70	80	90	100	110	120
m237.pep	IFALDAAFGRVNQPTVLMRFDARHRGLENLRTGFGSGTS DAQSVSERMQVSGXGVELCP					
g237	IFALDAAFGRVNQPTVLMRFDARHRGLENLRTGFGSGTS DAQSVSERMQVSGXGVELCP					
	130	140	150	160	170	180

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 885>:

```
a237.seq
1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCCC CACGAATATT
51 CGATTTTGTAC ATCGGCAAGC TCGGAAAAA CTTTAAGCAT ATCTTGGCGG
101 ACAAGCTCGG TCATACGCGC GGGATTGTCG ATAAACTCGT TATCCTTACC
151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG CGGTAACGTA TCCAAAATAT
201 GACGGTTGTG GCATACTGCC ATATTGTTGC GGATAAGCCC TTTTGCACGC
251 GCGCCCAAGG GTTCTGTGGC AATAATAAAG GTGCTGACAG CAATCGCCTT
301 GCGCTCCAAA GGCTTGAATA TCGGATTCAA ACCGGCATAA GTATTGACGG
351 CGTACACCAG ATTTTTGCAT TCGACGCTGC CTTCGGGGGT GTAAACCAGC
401 CAACCGTTTT GATAAGGTTT AATGCGTATC ATGGGAGAAT GCTCAAAAA
451 CTTCGTACCA GCTTCGGCAG CGGCGCGGGC GATGCCAAC TGTAATTGA
501 CGGGATGGAG ATGCCCGGAC AAGGGATCGA ACTGTGCGCC TTGTGTACATA
551 TCGCTGTCAA GCTGCTGCTT CAGTTCAGTG TTATCCCAGA GTTGATAATG
601 AGTTGCACCG TAATATTTTT GGGCGTGCTC ATGCCATTGT TGCAATTCTT
651 CCCAATGCTG CGAACGGATG GCAACCGTGG CATAACCGCG CTGCCAATCG
701 CAATCAATGG CATGTTTGCG GACGCGTTTG TCCACCAGT TCGACCGCTG
751 CAAAGACTGT TGCCAAAACC ATTGCGCTTG CTCCAAACCG ACCTGTTTTT
801 CAATTTCTCT CATAACCGCAG CGGTAATCGC TGATAACCTG CCGCGCACTC
851 CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC
901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CTCAATCCGC
951 CGCCGATGAT ACAGGTATCG GTTTTCAGAG GGCATTGAAG TTTTCGATAA
1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
1051 AAAATCAGGG CGAATCATTG TGTTTGCTTT ATCGGGTATA TTTTCGGACG
1101 GAATGATACA GGCTGTGCGG CCATATCGTC CAAACAGAAA ATCGGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 886; ORF 237.a>:

a237.pep	1	MRDKVGGNVA	LPAPRIFDFD	IGKLRKNFKH	ILADKLGHTR	GIVDKLVILT
	51	AEKQSAVRAE	<u>AVIIQNMTTV</u>	AYCHIVADKP	FCTRAQGFCG	NNKGADSNRL
	101	ALQRLEYRIQ	TGISIDGVHQ	IFAFDAAFEGG	VNQPTVLIRF	NAYHGRMLKN
	151	LRTSFGSGAG	DAQRVIERME	MPGQGIELCA	<u>LVHIAVKLLL</u>	<u>QFSVIPELIM</u>
	201	<u>SCTVIFLGLV</u>	<u>MPLLQFFPML</u>	RTDGNRGITA	LPIANGMFA	DAFVHQFDRL
	251	<u>QRLLPKPLRL</u>	<u>LQTDLFFNFL</u>	HTAGVIADNL	PATPSRAET	DTRGFQHNRF
	301	MSLLRQGQCS	AQTTQSAADD	TGIGFQTALK	FRNSMRNRN	TEIIRRQIFL
	351	KIRANHCVCF	IGYIFGRNDT	GCRAISSKOK	IG*	

m237/a237 85.6% identity in 382 aa overlap

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRIFDFDIGKLRNFKHILADKLGHTRIVDKLVILTAEKQSAVRAE					
a237	MRDKVGGNVALPAPRIFDFDIGKLRNFKHILADKLGHTRGIVDKLVILTAEKQSAVRAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m237.pep	AVIIQNMVAVYCHIVTDKPFPCARPQGFGRNNKGADSNRLAFQRPYRVQTCISIDSIDH					
	: : : : : ::					
a237	AVIIQNMVAVYCHIVADKPFCTRAQGFGRNNKGADSNRLALQRLYRIQTGISIDGVHQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m237.pep	IFALDAAFGRVNQPTVLMRFDARHRGLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP					
	: : : : : : : : :					
a237	IFAFDAAFGGVNQPTVLIRFNAYHGRMLKNLRTSFGSGAGDAQRVIERMEMPGQGIELCA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m237.pep	LVHIAVKLLFQLGFIPKLIMTRTVMPPLGVFMPPLLQLFPMRLTDGNGRGTALPITIDGMFA					
	: : : : : : : : : :					
a237	LVHIAVKLLQLFSVIPELIMSCTVIFLGVLMPLLQFFPMRLTDGNGRGTALPIAINGMFA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m237.pep	DAFVHQFDRLQRLLPKPLRLQLADLFFNFPHXTAXVIADNLPATPSRAETDTRGFQHNRF					
	: : : : : :					
a237	DAFVHQFDRLQRLLPKPLRLQLTDLFFNFLHTAGVIADNLPATPSRAETDTRGFQHNRF					
	250	260	270	280	290	300
	310	320	330	340	350	360
m237.pep	MSLLRQGCQAQTTSAAADDTGIGFQTALKFRINSMRINRTEIIRRQIFLKIRANHCVCVF					
	: : : : : : : :					
a237	MSLLRQGCQAQTTSAAADDTGIGFQTALKFRINSMRINRTEIIRRQIFLKIRANHCVCVF					
	310	320	330	340	350	360
	370	380				
m237.pep	IRCIIFGRNDTGCRAISSXQKIGX					
a237	IGYIFGRNDTGCRAISSKQKIGX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 887>:

g238.seq

```

1  atgaatttgc ctattcaaaa attcatgatg ctgttggcag cggcaatata
51  gatgctgcat atccccatta gtcatgcgaa cggtttggat gcccgtttgc
101 gcgatgatat gcaggcaaaa cactacgaac cgggtggcaa ataccatctg
151 tttggtaatg ctgcgcgcag tgttaaaaat cgggtttgcg ccgtccaaac
201 atttgatgca actgcggtcg gccccatact gcctattaca cacgaacgga
251 caggatttga aggtgttatc ggctatgaaa cccatttttc aggacacgga
301 cacgaagtac acagtcctgt cgataatcat gattcaaaaa gcacttctga
351 tttcagcggc ggcgtagacg gcggttttac cgtttaccaa cttcatcgga
401 cagggtcgga aatacatccc gcagacggat atgacgggcc tcaaggcggc
451 ggttatccgg aaccacaagg ggcaagggat atatacagct accatatcaa
501 aggaacttca accaaaacaa agataaacac tgttccgcaa gccccctttt
551 cagaccgctg gctaaaagaa aatgccggtg ccgcttccgg ttttctcagc
601 cgtgcggatg aagcaggaaa actgatattg gaaaacgacc ccgataaaaa
651 ttggcgggct aaccgtatgg atgatattcg cggcatcgcc caaggtgcgg
701 ttaatccttt tttaacgggt tttcaagggg tagggattgg ggcaattaca
751 gacagtgcgg taagcccggc cacagataca gccgctcagc agactctaca
801 aggtattaat gatttaggaa atttaagtc ggaagcacia cttgcccgcc

```

544

```

851 cgagcctatt acaggacagt gcctttgcgg taaaagacgg catcaattcc
901 gccagacaat gggctgatgc ccatccgaat ataacagcaa cagcccaaac
951 tgcccttgcc gtagcagagg ccgcaggtag ggtttggcgc ggtaaaaaag
1001 tagaacttaa cccgaccaaa tgggattggg ttaaaaaatac cggctataaa
1051 aaacctgctg cccgccatat gcagactgta gatggggaga tggcaggggg
1101 gaatagaccg cctaaatcta taacgtcggg aggaaaagct aatgctgcaa
1151 cctatcctaa gttggttaat cagctaaatg agcaaaactt aaataacatt
1201 gcggctcaag atccaagatt gagtctagct attcatgagg gtaaaaaaaa
1251 ttttccaata ggaactgcaa cttatgaaga ggcagataga ctaggtaaaa
1301 tttgggttgg tgaggggtgca agacaaacta gtggaggcgg atggttaagt
1351 agagatggca ctcgacaata tcggccacca acagaaaaaa aatcacaatt
1401 tgcaactaca ggtattcaag caaattttga aacttatact attgattcaa
1451 atgaaaaaag aaataaaatt aaaaatggac atttaaatat taggtaa

```

This corresponds to the amino acid sequence <SEQ ID 888; ORF 238.ng>:

g238.pep

```

1 MNLPIQKFMM LLAAISM L H IPISHANGLD ARLRDDMQAK HYPEGGKYHL
51 FGNARGSVKN RVCVQTFDA TAVGPILPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP ADGYDGPQGG
151 GYPEPQGARD IYSYHIK GTS TKT KINTVPQ APFSDRWLKE NAGAA SGFLS
201 RADEAGKLIW ENDPDKNWRA NRMDDIRGIV QGAVNPFLTG FQGVGIGAIT
251 DSAVSPVTD T AAQQT LQGIN DLGNLSPEAQ LAAASLLQDS AFAVKDGIN S
301 ARQWADAHPN ITATAQTALA VAEAAGTVWR GKKVELNPTK WDWVKNTGYK
351 KPAARHMQTV DGEMAGGNRP PKSITSEGKA NAATYPKLVN QLNEQNLNNI
401 AAQDPRLSLA IHEGKKNFPI GTATYEEADR LGKIWVGEGA RQTSGGGWLS
451 RDGTRQYRPP TEKKSQFATT GIQANFETYT IDSNEKRNKI KNHGLNIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 889>:

m238.seq

```

1 ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CAC TACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGG CAG TGT TAAAAAG CGGGTTTACG CCGTCCAGAC
201 ATTTGATGCA ACTGCGGTCA GTCCTGTACT GCCTATTACA CACGAACGGA
251 CAGGGTTTGA AGGTGTTATC GGT TATGAAA CCCATTTTTC AGGGCACGGA
301 CATGAAGTAC ACAGTCCGTT CGATCATCAT GATTCAAAAA GCACTTCTGA
351 TTT CAGCGGC GGTGTAGACG GCGGTTT TAC TGT TACCAA CTT CATCGAA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCCGGAGG AGCAAGGGAT ATATACAGCT ATTATGTCAA
501 AGGAAC T TCA AAAAAACAA AGACTAATAT TGTCCCTCAA GCCCATTTT
551 CAGACCGTTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCGGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATGTT CG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT GATTTAGGAA AATTAAGTCC GGAAGCACAA CTTGCTGCCG
851 CGAGCCTATT ACAGGACAGT GCTTTTGCGG TAAAAGACGG TATCAACTCT
901 GCCAAACAAT GGGCTGATGC CCATCCAAAT ATAACAGCTA CTGCCCAAAC
951 TGCCCTTTCC GCAGCAGAGG CCGCAGGTAC GGT T TGGAGA GGTAAAAAAG
1001 TAGAACTTAA CCCGACTAAA TGGGATTGGG TTAAAAATAC CGGTTATAAA
1051 AAACCTGCTG CCCGCCATAT GCAGACTTTA GATGGGGAGA TGGCAGGTGG
1101 GAATAAACCT ATTAAATCTT TACCAAACAG TGCCGCTGAA AAAAGAAAAC
1151 AAAATTTTGA GAAGTTTAA T AGTAACTGGA GTTCAGCAAG TTTTGATTCA
1201 GTGCACAAAA CACTAACTCC CAATGCACCT GGTATTTTAA GTCCTGATAA
1251 AGTTAAACT CGATACACTA GTTTAGATGG AAAAATTACA ATTATAAAAG
1301 ATAACGAAAA CAACTATTTT AGAATCCATG ATAATTCACG AAAACAGTAT
1351 CTTGATTCAA ATGGTAATGC TGTGAAAACC GGTAAATTAC AAGGTAAGCA
1401 AGCAAAAGAT TATTTACAAC AACAACTCA TATCAGGAAC TTAGACAAAT
1451 GA

```

This corresponds to the amino acid sequence <SEQ ID 890; ORF 238>:

m238.pep

```

1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYPEGGKYHL
51 FGNARGSVKK RVYAVQTFDA TAVSPVLPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDHH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS

```

Homology with a predicted ORF from *N. gonorrhoeae*

m238/g238

	10	20	30	40	50	60
m238.pep	MNLPIQKFMMFLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK					
g238	MNLPIQKFMMLLAAAISMLHIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
	10	20	30	40	50	60
m238.pep	RVYAVQTFDATAVSPVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHSDSKSTSDFSG					
g238	RVCAVQTFDATAVGPILPITHERTGFEGVIGYETHFSGHGHEVHSPFDNHSDSKSTSDFSG					
	70	80	90	100	110	120
m238.pep	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYVKGSTSTKTNTNIVPQ					
g238	GVDGGFTVYQLHRTGSEIHPADGYDGPQGGGYPEPQGARDIYSYHIKGTSTKTNTNIVPQ					
	130	140	150	160	170	180
m238.pep	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWVANRMD DVGIGVQAVNPFLMG					
g238	APFSDRWLKENAGAASGFLSRADEAGKLIWENDPDKNWRANRMD DIRGIGVQAVNPFLTG					
	190	200	210	220	230	240
m238.pep	FQGVGIGAITDSAVSPVTD TAAQQT LQGINDLGKLSPEAQLAAASLLQDSAFV KDGINS					
g238	FQGVGIGAITDSAVSPVTD TAAQQT LQGINDLGNL SPEAQLAAASLLQDSAFV KDGINS					
	250	260	270	280	290	300
m238.pep	AKQWADAHPNITATAQTALSAAEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTL					
g238	ARQWADAHPNITATAQTALAVAEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTV					
	310	320	330	340	350	360
m238.pep	DGEMAGGNKPIKSLPNSAAEKRKQNF EKFN SNWSSASFD SVHKLTLP NAPGILSPDKVKT					
g238	DGEMAGGNRPPKSI-TSEGKANAATYPKLVNQLNEQNLNNIAAQDPRLSLAIHEGKKNF					
	370	380	390	400	410	420
m238.pep	RYTSLDGKITIIKDNENNYFRIHDNSR KQYLD SNGNAVK TGNLQGKQAKDY LQQQTHIRN					
g238	IGTATYEEADRLGKIWVGE GARQTS GGGWLSRDGTRQYRPPT EKKSQFAT TGIQANFETY					
	430	440	450	460	470	480

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 891>:

```
a238.seq (partial)
  1 ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
 51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTGCGGGCAG TGTAAAAAAT CGGGTTTACG CCGTCCAAAC
201 ATTTGATGCA ACTGCGGTCG GCCCATACT GCCTATTACA CACGAACGGA
251 CAGGATTTGA AGGCATTATC GGTTATGAAA CCCATTTTTC AGGACATGGA
301 CATGAAGTAC ACAGTCCGTT CGATAATCAT GATTCAAAAA GCACTTCTGA
351 TTTTCAGCGGC GGCCTAGACG GTGGTTTAC CGTTTACCAA CTTTCATCGGA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCCGGAGG AGCAAGGGAT ATATACAGCT ACTATGTCAA
501 AGGAACCTCA ACAAAAACAA AGAGTAATAT TGTCCCCGA GCCCCATTTT
551 CAGACCGCTG GCTAAAAGAA AATGCCGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCTGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATATTCG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT CATTTAGGAA ATTTAAGTCC CGAAGCACAA CTTGCGGCTG
851 CAACCGCATT ACAAGACAGT GCTTTTGC GG TAAAAGACGG TATCAATTCC
901 GCCAGACAAT GGGCTGATGC CCATCCGAAT ATAAGTCAA CAGCCCAAAC
951 TGCCCTTGCC GTAGCAGAGG CCGCAACTAC GGTTTGGGGC GGTAAAAAAG
1001 TAGAACTTAA CCCGACCAA TGGGATTGGG TTAATAATAC CGGCTATAAA
1051 ACACCTGCTG TTCGCACCAT GCATACTTTG GATGGGGAAA TGGCCGGTGG
1101 GAATAGACCG CCTAAATCTA TAACGTCCAA CAGCAAAGCA GATGCTTCCA
1151 CACAA
```

This corresponds to the amino acid sequence <SEQ ID 892; ORF 238.a>:

```
a238.pep (partial)
  1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYEPPGGKYHL
 51 FGNARGSVKN RYVAVQTFDA TAVGPILPIT HERTGFEGII GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS
151 DYPPPGGARD IYSYYVKGTS TKTKSNIVPR APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDIRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQOTLQGIN HLGNSPEAQ LAAATALQDS AFAVKDGINS
301 ARQWADAHPN ITATAQTALA VAEAATTVWG GKKVELNPTK WDWVKNTGYK
351 TPAVRTMHTL DGEMAGGNRP PKSITSNSKA DASTQ
```

m238/a238 91.9% identity in 385 aa overlap

	10	20	30	40	50	60
m238.pep	MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAKHYEPPGGKYHL FGNARGSVK					
a238	MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAKHYEPPGGKYHL FGNARGSVKN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m238.pep	RVYAVQTFDATAVSPVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHSDSKSTSDFSG					
a238	RVYAVQTFDATAVGPILPITHERTGFEGIIGYETHFSGHGHEVHSPFDHSDSKSTSDFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m238.pep	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYYVKGTSTKTKTNIVPQ					
a238	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYYVKGTSTKTKSNIVPR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m238.pep	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMDVIRGIVQGAVNPFLMG					
a238	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMDIRGIVQGAVNPFLMG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m238.pep	FQGVGIGAIT DSAVSPVTD TAAQOTLQGIN DLGKLSPEAQ LAAASLLQDS AFAVKDGINS					

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|||||
a238      FQGVGIGAITDSAVSPVTDTAQQTLQGINHLGNLSPEAQLAAATALQDSFAVKDGIN
           250      260      270      280      290      300

           310      320      330      340      350      360
m238.pep  AKQWADAHPNITATAQTALSAEAAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTL
           ||:|||||
a238      ARQWADAHPNITATAQTALAVAEAAATTVWGGKKVELNPTKWDWVKNTGYKTPAVRTMHTL
           310      320      330      340      350      360

           370      380      390      400      410      419
m238.pep  DGEMAGGNKPIKSLP-NSAAEKRKQNFEEKFNSNWSSASFDSVHKTLPNAPGILSPDKVK
           |||||:| ||: ||: |
a238      DGEMAGGNRPPKSITSNSKADASTQ

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 893>:

```

g239.seq
1  atgttcacc ataaaggat tccccgaac cggcggatgg aggttttgtt
51  tttctgccc cgccctgat gttcgtgat tcgccaaacg cgcctgttgc
101 agcctcattt gcgcataatc ctgctccaag gcgatttcct gttttttcgc
151 cttgtccaaa gctgtgaagt tgagcctgta ctggttttgc tgcatacaca
201 cggaaaaagc ggaaacgcac accgcaagca gcagaaagaa attcgaattt
251 ttcattgccg ttcagacgtt tttctctgtt attattccgg tatcggaccg
301 gcagtcgct cgcacacacg caaaactgct ctctcgccc tcgggttggc
351 ggcaatttcc gcttcacccg gctttaatgc cctgcccacg attttcaggg
401 gcggatcggg caaatccgct tctctgaccg ccgcccagct cggcaggggc
451 tcgtgttgcg aatatttttt gacaaaactgc ttcacaatgc ggtcttccaa
501 cgaatggaaa gcaatgaccg ccaaacgccc gccctctttc agacggcaca
551 tgacctgcgg caataccgcc cctacttctt caagctcgcg gttataaag
601 atcgcgattg cctggaaggt gcgctgcgca ggatcctgcc cccgctcgcg
651 agtacggacg ttttgtgcca cgatctgcgc cagcttgccg gttgtatcga
701 ttggactttc cggcgttgc gcgacaatgg cgcgcacaat ctggcggcta
751 aaccgtctt caccataa

```

This corresponds to the amino acid sequence <SEQ ID 894; ORF 239.ng>:

```

g239.pep
1  MFHHKGIARN RRMEVLFFCR RPDRFVIRQT RLLQPHLR II LLQGDFFFR
51  LVQSCEVEPV LVLHHNGKS GNAHRKQKE IRFVHCRSDV FLCYSGIGP
101 AVRSATR KTA LLALGLAAIS ASPGFNALPT IFRGSGKSA SLTAAQLGRG
151 SCCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRMTCGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARTIWR L
251 NRSSP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 895>:

```

m239.seq
1  ATGCTCCACC ATAAAGGTmy kGCCCCGAAAC CGGCKGATGG AGGTTTTGTT
51  TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATT T GCGCATAATC CTGCTCCAAG GCGATTTCTT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAAT TGAGCCTGTA CTGGTTTTGC TGCATCACAA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTC AATTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCC GCCTCACCCG GCTTTAATGC CCTGCCCACG ATTTTCAGGG
401 GCAGTCCGGG CAAATCCGCT TCCCTGACCG CCGCCCAGCG CGGCAGGGGC
451 GCGTGTGCG AATATTTTTT GACAAACTGC TTCACAATGC GATCTTCCAA
501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CTA CTCTT CAAGCTCGCG GTTAATAAAG
601 ATCGGACCG CTTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
651 AGTACGGACG TTTGTGCCA CGATCTGCGC CAGCTTGCGG GTTGATCGA
701 TTGGACTTTC CGCCCGTTGC GCAACAATGG CGCGCGCAAT CCGGCGGCTa
751 AACCGCTCTT cACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 896; ORF 239>:

m239.pep
 1 MLHHKGXARN RXMEVLFFCR RPDRFVVRQT RLLQPHLR II LLQGDFLFFR
 51 LIQSCEIEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
 101 AVRSATRKTA LLALGLAAIS ASPGFNALPT IFRGSSGKSA SLTAAQRGRG
 151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
 201 MRTAWKVRVA GSCPRSRVRT FCATICASLR VVSIIGLSARC ATMARAIIRRL
 251 NRSSP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 239 shows 93.7% identity over a 255 aa overlap with a predicted ORF (ORF 239.ng) from *N. gonorrhoeae*:

m239/g239

	10	20	30	40	50	60
m239.pep	MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLR I ILLQGDFLFFRLIQSCEIEPV					
	:					
g239	MFHHKGIARNRMEVLFFCRRPDRFVIRQTRLLQPHLR I ILLQGDFLFFRLVQSCEVEPV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m239.pep	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTA LLALGLAAIS					
g239	LVLLHHNGKSGNAHRKQOKEIRFVHCRSDVFLCYYSIGIGPAVRSATRKTA LLALGLAAIS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m239.pep	ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
g239	ASPGFNALPTIFRGSSGKSASLTAAQLGRGSCCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m239.pep	RRHMTGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIIGLSARC					
g239	RRHMTGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIIGLSARC					
	190	200	210	220	230	240
	250					
m239.pep	ATMARAIIRRLNRSSPX					
g239	ATMARTIWRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 897>:

a239.seq
 1 ATGCTCCACC ATAAAGGTAT TGCCCGAAAC CGGCGGATGG AGGTTTTGTT
 51 TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
 101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCTT GTTTTTTCGC
 151 CTTATCCAAA GCTGTGAAGT TGAGCCTGTA CTGGTTTTGC TGCATCACAA
 201 CGGAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTG
 251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
 301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCTCGCCC TCGGATTGGC
 351 GGCAATTTCC GCCTCACCCG GCTTTAATGC CCTGCCCAGG ATTTTCAGGG
 401 GCGGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCAGCG CGGAGGGG
 451 GCGTGTGCG AATATTTTTT GACAACTGC TTCACAATGC GGTCTTCCAA
 501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGACACA
 551 TGACCTGCGG CAATACTGCC CTAATTCTT CAAGCTCGCG GTTAATAAAG
 601 ATGCGGATTG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
 651 AGTACGGACG TTTTGTGCCA CGATCTGCGC CAGCTTGCGG GTTGTATCGA
 701 TTGGACTTTC CGCCCGTTGC GCAACAATGG CGCGCGCAAT CTGGCGGCTA
 751 AACCGCTCTT CACCATAA

This corresponds to the amino acid sequence <SEQ ID 898; ORF 239.a>:

```
a239.pep
  1 MLHHKGIARN RRMEVLFFCR RPDRFVVRQT RLLQPHLRRI LLQGDFLFFR
 51 LIQSCEVEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKTA LLALGLAAIS ASPGFNALPA IFRGSGSKSA SLTAAQRGRG
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTCGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIWRL
251 NRSSP*
```

m239/a239 97.3% identity in 255 aa overlap

	10	20	30	40	50	60
m239.pep	MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLRRIILLQGDFLFFRLIQSCEIEPV					
a239	MLHHKGIARNRRMEVLFFCRRPDRFVVRQTRLLQPHLRRIILLQGDFLFFRLIQSCEVEPV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m239.pep	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTAALLALGLAAIS					
a239	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTAALLALGLAAIS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m239.pep	ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
a239	ASPGFNALPAIFRGSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m239.pep	RRHMTCGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
a239	RRHMTCGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
	190	200	210	220	230	240
	250					
m239.pep	ATMARAIIRRLNRSSPX					
a239	ATMARAIWRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 899>:

```
g240.seq
  1 atgatagaag tcatacattt cttcggcgcc gaaacgcgca gacagtttgc
 51 ttgtgccgac gttggacgat ttctgcataa tgccgcgcac atccaaagag
101 gggtaaacad ggggtatcatc gcgcacggga gacggtccga ttttataagg
151 ctgcgtattc agccgttcgt tcaaatacgt tttgcccgca tccaatgcct
201 tcgcaatcac gaacggtttg attgccgaac cagggttcgat catatcggtt
251 acggcacggt tgcgccgctg ttcgctgtct gcccggccgg gtctgttggg
301 atcgtaggcg ggcgtattgg ccaaggcgag gatttcccc gtgcgggcat
351 ccaaaaccac caccgttcg gcttttgctt gatggtattc gaccgccttg
401 ttcaactctt cataggccaa ggtctgaatc ctctgatcga gggaaaggat
451 gatgtctttg ccgttttgcg gtgctttatt gcgcggggag tccaagtctg
501 ccacaatatt gccctgcggt tcccgcaaaa caacttcgc gccgtcttcg
551 ccatacaggc tgtcttcaag cgaaagtcc aaaccttctt gacctttgcc
601 gtcaatatcg gtaaatacga tgacgtgtgc aaacagggtt cccatcggtt
651 aatggcggtt taa
```

This corresponds to the amino acid sequence <SEQ ID 900; ORF 240.ng>:

```
g240.pep
  1 MIEVIHFFGA ETRRQFACAD VGRFLHNAAH IQRGVNMGII AHGRRSDFIR
 51 LRIQPFVQIG FARIQCLRNH ERFDCRTRFD HIGYGTVAFL FAVCPAGSVG
101 IVGGRIGQGE DFPRAGIQNH HRSGFCLMVF DRLVQLFIGQ GLNPLIEGKD
151 DVFAVLRCFI ARGVQAVHNI ALPVPQNNFR AVFAIQAVFK RKFQTFLTFA
```


551

```

251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AAACCACCAC CGTTCGGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTATTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAGGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCCC ATCGGGTAAT
651 GGCGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 904; ORF 240.a>:

```

a240.pep
  1 MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
 51 RIQPFVQIGF ARIQCLRNHK RFDCRTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIGQGED FPRAGIQNH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFIA RGVQAVHNIA LPVPQNDFA VFAMQAVFKR KFQTLTFAV
201 NIGKSDDVCK QVAHRVMAF*

```

m240/a240 99.1% identity in 219 aa overlap

	10	20	30	40	50	60
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF					
a240	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m240.pep	ARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQXHH					
a240	ARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQNH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m240.pep	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVERGFXARGVQAVHNIALPVPQNDFA					
a240	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVERGFIARGVQAVHNIALPVPQNDFA					
	130	140	150	160	170	180
	190	200	210	220		
m240.pep	VFAMQAVFKRKFTFLTFAVNIGKSDDVCKQVAHRVMAFX					
a240	VFAMQAVFKRKFTFLTFAVNIGKSDDVCKQVAHRVMAFX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 905>:

```

g241.seq
  1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
 51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AACCACCAC CGTTCGGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTaktGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCCC ATCGGGTAAT
651 GGCGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 906; ORF 241.ng>:

```

g241.pep
  1 MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS

```

```

51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVMTVR
101 TVDMTVCDL IGCIAHAFNR SFKADFHACQ RMVAVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 907>:

m241.seq (partial)

```

1  ..CGGCAATCAG TGGTGGTGAT GACCGTGC GG CCGTGGACA TGACCGTGTG
51  CGATTTCCTC ATCGGATGCA TCGCGCACGC TTTCAACTGT AGCCTTAAAG
101 CGGATTTTCA TGCCTGCCAA AGGATGGTTG CCGTCCACCA CCGCCTTGCC
151 GTCGGCAACA TCGGTACAC GATAGACGAC AACATCGCCG GTTTCAGGAT
201 CGTCGGCTTC AAACATCATG CCGACTTCGA CTTCAACAGG GAACACGCCC
251 GCATCTTCGA TACGGACCAA CTCCGGATCC TGCTCGCCGA ACGCATCGTC
301 GGGCGACAGC GCCACATCGA CCGTATCGCC GGCATCCTTA CCGTGCAACG
351 CCTCTTCAC CAAAGGGAAA ATGCCGTCGT AACC GCCGTG CAGATACGCA
401 ATCGGTCTT CGGTTTGTG CAAAAGCTGA TTGTTGGCAT CATACTCTC
451 ATAATGCAGC GAAACCACGG AATTTTTCAC GATAGCCATA TTTGTCCTTT
501 CAGGAACAGC AGATTAATTA CAGGCGCATT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 908; ORF 241>:

m241.pep (partial)

```

1  ..RQSVVMTVR AVDMTVCDL IGCIAHAFNC SLKADFHACQ RMVAVHRLA
51  VGNIGYTIDD NIAGFRIVGF KHHADDFNR EHARIFDTDQ LRILLAERIV
101 GRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
151 IMQRNHGIFH DSHICPFRNS RLITGAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 241 shows 91.5% identity over a 177 aa overlap with a predicted ORF (ORF 241.ng) from *N. gonorrhoeae*:

m241/g241

m241.pep				10	20	30
				RQSVVMTVR	AVDMTVCDL	IGCIAHAFNC
g241						
	70	80	90	100	110	120
m241.pep	40	50	60	70	80	90
	SLKADFHACQ	RMVAVHRLA	VGNIGYTIDD	NIAGFRIVGF	KHHADDFNR	EHARIFDTDQ
g241						
	130	140	150	160	170	180
m241.pep	100	110	120	130	140	150
	LRILLAERIV	GRQRHIDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFFGFV	QKLIVGIIHL
g241						
	190	200	210	220	230	240
m241.pep	160	170				
	IMQRNHGIFH	DSHICPFRNS	RLITGAFX			
g241						
	250	260				
	IMQRNHGIFC	NSHICPFRNS	RLITGAFX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 909>:

a241.seq

```

1  ATGCCAACAC GTCCAAC TCG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCAGC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCCTT TTCAGACGGC

```

a241.pap

1	MPTRPTRAAK	HPTPPTWLQT	AYCPRPPYRP	PSVQTHTPHE	PASSTCAAKS
51	ANRRENFHNA	QPTYLLHPSN	KMPSEMEQTL	FRRHQIPPSC	RQSVVVMTVR
101	TVDMTVCDFL	IGCIAHTFNR	SLKADFHAQ	RMVAVHHRLT	VGNIGYTIDD
151	NIAGFRIVGF	KHHADFDFNR	EHARIFNTDQ	LRILLAERIV	GRKRHIDRIA
201	GILTVQRLFH	QRENAAVTAV	QIRNRFFGFV	QKLIVGIIHL	IMQRNHGILH
251	DSHICPERNS	RLITGAF*			

m241.pep				10	20	30
				RQSVVVM	TVRAVDM	TVCDFLIGCIAHAFNC
a241						
	QPTYLLHPSN	KMPSEMEQ	TLFRRHQI	PPSCRQSVV	VMTRVDM	TVCDFLIGCIAHTFNR
	70	80	90	100	110	120
m241.pep						
	40	50	60	70	80	90
	SLKADFHACQ	RMVAVHHRL	AVGNIGYT	IDDNIAGF	RIVGFKHHAD	FDFNREHARIFD
a241						
	SLKADFHACQ	RMVAVHHRL	TVGNIGYT	IDDNIAGF	RIVGFKHHAD	FDFNREHARIFNT
	130	140	150	160	170	180
m241.pep						
	100	110	120	130	140	150
	LRILLAERIV	GRQRHIDRI	AGILTVQRL	FHQRENAV	VTAQIRNRFF	GFGVQKLIVGIIHL
a241						
	LRILLAERIV	GRKRHIDRI	AGILTVQRL	FHQRENAV	VTAQIRNRFF	GFGVQKLIVGIIHL
	190	200	210	220	230	240
m241.pep						
	160	170				
	IMQRNHGIFH	DSHICPFNR	NSRLITGA	FX		
a241						
	IMQRNHGILH	DSHICPFNR	NSRLITGA	FX		
	250	260				

g241-1.seq

```
1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTTCTCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCGGATT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCAACAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT CGTGCTGCCC CGGCCGGGCC TGTGGGATCA
301 GTAGCGGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGGTG CGGGCATCCA
351 AACCACCAC CGTTCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGCA
451 GTCTTTGCCG TTTTTCGGGG CTTTaktGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCGGTTCC CGCAAAACGA CTTCGCGGCC GTCTTGCCCA
551 TGCAAGCTGT CTTCAGCGA AAGTCCAAA CCTTCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTCAAA CAGGTTGCC ATCGGTAAT
651 GGCCTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

g241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYR PSVQTHTPHE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVVMVTR
101 TVDMTVCDLF IGCIAHAFNR SFKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 913>:

m241-1.seq

```

1  ATGCCAACAC GTCCAACCTG CGCTGCAAAC CCTCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCGTAC ACCGCGTGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTC TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAACGGA ACAAAACCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 GCCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACGC
351 TTTCAACTGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTGCC GTCGGAACA TCGGTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCG GCATCTTCGA TACGGACCAA CTCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGACAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTCCAC CAAAGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTTGTC CAAAGCTGA
701 TTGTTGGCAT CATACATCTC ATAATGCAGC GAAACCACGG AATTTTTCAC
751 GATAGCCATA TTTGTCTTTT CAGGAACAGC AGATAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 914; ORF 241-1>:

m241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYR PSVQTRTPRE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVVMVTR
101 AVDMTVCDLF IGCIAHAFNC SLKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVGF KHADFDNFNR EHARIFDTDQ LRILLAERIV GRQRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGIFH
251 DSHICPFRNS RLITGAF*

```

m241-1/g241-1 93.3% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
g241	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENSHNA					
	10	20	30	40	50	60
m241-1.pep	QPTYLLHPSNKMPSSETEQTLFRRHQIPPSQSVVVMVTRAVDMTVCDFLIGCIAHAFNC					
g241	QPTYLLHPSNKMPSSETEQTLFRRHQIPPSQSVVVMVTRVDMTVCDFLIGCIAHAFNR					
	70	80	90	100	110	120
m241-1.pep	SLKADFHACQRMVAVVHRLAVGNIGYTIDNDNIAGFRIVGFKHHADFDFNREHARIFDTDQ					
g241	SFKADFHACQRMVAVVHRLAVGNIGYTIDNDNIAGFRIVRFKHHTDLDFNRERARIFNTDQ					
	130	140	150	160	170	180
m241-1.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
g241	LRIMLTERIVGRKRHFDRIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFIQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
g241	IMQRNHGIFCNSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 915>:

a241-1.seq

```

1  ATGCCAACAC GTCCAACCTG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC

```



```

101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCAGC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCCCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CCGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATCTTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

a241-1.pep

```

1  MPTRPTRAAK HPTPTWLQT AYCPRPPYRP PSVQTHPHE PASSTCAAKS
51  ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSQ RQSVVVMVTR
101 TVDMTVCDLF IGCIAHTFNR SLKADFACQ RMVAVHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDFNR EHARIFNTDQ LRILLAERIV GRKRHDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFEGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241-1/a241-1 95.1% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPPTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
a241	MPTRPTRAAKHPTPPTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENFHNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m241-1.pep	QPTYLLHPSNKMPSETEQLFRRHQIPPSQSVVVMVRAVDMTVCDFLIGCIAHAFNC					
a241	QPTYLLHPSNKMPSEMEQLFRRHQIPPSQSVVVMVTVDMTVCDFLIGCIAHTFNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m241-1.pep	SLKADFACQRMVAVHRLAVGNIGYTIDNDNIAGFRIVGFKHHADFDFNREHARIFDQ					
a241	SLKADFACQRMVAVHRLTVGNIGYTIDNDNIAGFRIVGFKHHADFDFNREHARIFNTDQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m241-1.pep	LRILLAERIVGRQRHDRIAGILTVQRLFHQRENAVVTAVQIRNRFEGFVQKLIVGIIHL					
a241	LRILLAERIVGRKRHDRIAGILTVQRLFHQRENAVVTAVQIRNRFEGFVQKLIVGIIHL					
	190	200	210	220	230	240
	250	260				
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
a241	IMQRNHGILHDSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242.seq

```

1  atgatcggcg aacttggtgt tttgttcgtg atcgagcact tcaagcaacg
51  cgctggcggg atcgccccga aagtcgctgc ccaattgtgc gatttcgtcg
101 agcaggaaca acgggtttct tacgcctgct tttgccatat tctgcaaaat
151 cttgccgggc atagagccga tataggtacg gcggtgcccg cggatttcgc
201 tttcgtcgcg cacgccgccc aaggccatac ggacataatt cgcgccggtt
251 gctttggcga tggattcgcc caaagaggtt ttgccacgc cggaggggcc
301 gaccaaacac agaatcggac ctttgagctt gtccatacgt ttttggacgg
351 cgaggtattc caaaatccgt tctttgactt tttccaggcc gtagtggtcg
401 gcatccagca ccagtcggc tttggcgatg tctttgctga cgcgggattt
451 tttcttccac ggcagtcgga gcagggtgtc gatgtagttg cgtacgacgg

```

g242.ppt

m242.seq

m242 . pep

m242/g24290.3% identity in 289 aa overlap

	10	20	30	40	50	60
m242.pep	MIGKLVVLF	GIEHFEQRAGGIASEVV	TQFVDVFVEQE	QGVSFHAGFCHILQNLTGHRADIGA		
	:	:	: :	:	: :	
g242	MIGELVVL	FVIEHFKRAGGIAPKVAAQ	FVDFVEQEQRVS	YACFCHILQNLAGHRADIGT		
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAFVAHAAQSHADI	FPPRCFGDGFAQRGF	AHARRADQAQNRAFEVHTFLDGEVF			
		: :	: :			
g242	AVPADFAFVAHAAQGHDI	FPPRCFGDGFAQRGF	AHARRADQTQNRTELVHTFLDGEVF			
	70	80	90	100	110	120

```
a242.seq
1 ATGATCGGCG AACTTGTTGT TTTGCTCGGG ATCAAGCACT TCGAGCAACG
51 CGCTGGCGGG ATCGCCCCGG AAGTCGCTAN CCAATTTGTC GATTTCGTCG
101 AGCAGGAACA ATGGGTTTTT TACGCCGGCT TTTGCCATAT TCTGCAAAAT
151 CTTACGGGCG ATGGAGCCGA TATAGGTGCG GCGGTGTCCC CGGATTTGCG
201 TTTCTGTCGCG CAGCGCCGCC AAAGCCATGC GGACATATTT CCGCCCCGTT
251 GCTTTGGCGA TGGATTCGCC CAAAGAGGTT TTGCCACGC CTGGAGGGCC
301 GACCAGGCAC AGAATCGGGC CTTTGAGTTT GTCCATACGT TTTTGGACGG
351 CGAGGTATTC CAAATCCGTT TCTTTGACTT TTTCCAGGCC GTAGTGGTCG
401 GTATCCAGCA CCAATCCGGC TTTGGCGATG TCTTTGCTGA CGCGGGATTT
451 TTTCTTCCAC GGCAGTTCGA GCAGGGTGTC GATGTAAGTT CGTACGACGG
501 TGGATTCCGC AGACATCGCG GGCATCATTT TGAGCTTTTT CAGTTCCGAC
551 AGGCATTTTT CTTCGCTTC TTTGGTCATA CCGCCTTTT TGATATCTGC
601 TTCCAAGGCA TCCAGTTCGC CGTTTTTCGT TTCTTCGCCC AGTTCTTTGT
651 GTATCGCTTT AATCTGTTTC TTCAGATAAT ATTCGCGCTG GGATTTTTTC
701 ATTTGGCGTT TGACGCGTCC GCGTATCGCT TTTTCGGCCT GCATAATGTC
751 GAGTTCGGAT TCCAGCTGTG CCAGCAGGAA TTCCATCCGT TTGCCGATTT
801 CGGGAATTTT CAAACTGTG TGGCGTTGCG CCAGTTTCAA CTGCAAATGC
851 GCTGCGACCG TATCGGTTAG
```

a242.pep

1	MIGELVLLG	IKHFEQRAGG	IAPEVAXQFV	DFVEQEQWVF	YAGFCHILQN
51	LTGHGADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCFGDGFA	QRGFAHAWRA
101	DQAQNRAFEF	VHTFLDGEVF	QNPFFDFFQA	VVVGIQHQSG	FGDVADAGF
151	FLPRQFEQGV	DVVAYDGGFG	RHRHHFELF	QFGQAFFFRF	FGHTRLFDIC
201	FGGIQFAVVF	FFAQFFGVYR	NLFVQIIFAL	GGFHAFDAS	AYAFFGLHNV
251	EGFGQLCQOE	FHPFADFGNF	QNLLALRQFO	LMQRCDRIG*	

	10	20	30	40	50	60
m242.pep	MIGKLVVLF	GIEHFEQR	AGGIASEV	VTQFVDF	VEQEQGV	FHAGFCHILQNL
a242	MIGELVVLL	GGIKHFEQ	RAGGIAP	EVAXQFV	DFVEQEQ	WVVFYAGFCHILQNL
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAF	VAHAAQ	SHADIF	PPRCFG	DGFAQ	RGF
a242	AVSPDFAF	VAHAAQ	SHADIF	PPRCFG	DGFAQ	RGF
	70	80	90	100	110	120
	130	140	150	160	170	180
m242.pep	QNPFFD	FFQAVV	VGIQH	QSGFG	DVFDAG	FFLPRQLEQ

g243.seq

1	ATGGTaatcg	tctGGTTGcC	cgAGTTaccg	CCGATGCCGG	CGACGATGGG
51	CATCAGCGCG	GCGAGTGC GA	CGATTTTTTC	gatactgcCT	TCAAACGCGC
101	CGATGACGCG	GCTGGCGAGG	AAGGCGGTGC	AGAGTTGAC	GGCGAGCCAC
151	ATCCAGCGGT	TTTTGACGGA	ATCCAAGACG	GGGGCGAACA	GGTCTTCCTC
201	TTCCCTGCAA	CATGCCATGT	TCAACATATC	CGCTTCGGAT	TC'TTCGCGGA
251	TCACGTCCAC	CTCTCGTCT	ATGGTAATCc	tgCCGATGAG	CTTTTTGTTT
301	TCATCAACGA	CGGGCGCGGT	AACCAGTCG	TAG	

g243.pep

1 MVIVWLPELP PMPATMGISA ASATIFSILP SNAPMTRLAR KAVQRLTASH
51 IQRFLTESKT GANRSSSSCK PAMFNISASD SSRTTSTISS MVILEMSFLF
101 SSTTGAVTKS *

m243.seq

1	ATGGTAATCG	TCTGGTTGCC	CGAGTTACCG	CCTATGCCGG	CGACGATGGG
51	CATCAGCGCG	GyGAGTGCGA	CGATTTTTTC	GATGCTGCCT	TCAAACGCGC
101	CGATAACACG	GyTGCGCAGG	AAGCGGTTGC	AGAGGTTGAC	GGCGAGCCAC
151	ATCCAGyGGT	TTTTCAACCGA	ATCCACACAG	GGGGCGAaY	GGTCTTCCTC
201	TTCCTCGAA	CCCGCCATAT	TCAGCATATC	CGCTTCCGAT	TCTTCGCGGA
251	TCACGTCAC	CATCTCGTCG	ATGGTAATCC	TGCCGATGAG	CTTTTTGTTT
301	TCATCGACGA	CGGGCGCGGT	AACCAAGTCG	TAG	

m243 . pep

```

1  MVIVWLPELP PMPATMGISA XSATIFSMLP SNAPITRLAR KAVQRLTASH
51 IQXFFTESHT GANRSSSSCK PAIFSISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 243 shows 92.7% identity over a 110 aa overlap with a predicted ORF (ORF 243.ng) from *N. gonorrhoeae*:

m243/g243

```

      10      20      30      40      50      60
m243.pep  MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g243      MVIVWLPELPPMPATMGISAASATIFSILPSNAPMTRLARKAVQRLTASHIQRFLTESKT
          10      20      30      40      50      60

      70      80      90     100     110
m243.pep  GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g243      GANRSSSSCKPAMFNISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX

```

70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1   ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCCTC
201 TTCTTGCAAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTTCTGTA ACGGTCACCC TGCCGATGAG CTTTTTGTTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1   MVIVWLPELP PMPATMGISA ASATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQRFLTESKT GANKSSSSCK PAIFNISASD SSRITSTISS TVTLPMSEFL
101 SSTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT					
a243	MVIVWLPELPPMPATMGISAASATIFSMLPSNAPITRLARKAVQRLTASHIQRFLTESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX					
	:					
a243	GANKSSSSCKPAIFNISASDSSRITSTISSTVTLPMSEFLFSSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1   atgccgcctg aagcccggcc ggcgggttca gacggcattg ccgctttact
51  tcgatcggtt tatacgaaa acgcgcttca ggaaataaat cagattatcc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccgggag
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcacgcctg atggatatcc
251 ggatcgagct tatcgcccgcc tttaggattg atttccttga tttgcgtggc
301 atcaaacgcc ttctgcaact cattcaaagt catctgcaca cccattttca
351 gcgcacgcaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acattttcac ggcaaaacttc tgtccggcga acttgtgcgt
451 atcggaattt tcctgctggt ggcggcgggc caggttttgc tcgtttgcca
501 aagcgcgcag ttgttcgtct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggctcggcg gcagcctggt cctgtacacc
601 gtccgcattt cctactgtct cgacggttcc caccgcctcc acattttcaa
651 ccgcttcttc actgttttgc tgcgtgtgtc gttcgctcat atcgatatcc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgcag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgccgac
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1   MPPEARPAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LPCHRNHSRA
51  QHTVQGQITL LHHTNHGIGF LLTGHRHLRL MDIRIELIAR FRIDFLDLRG
101 IKRLLQLIQS HLHTHFQRIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFQLRFQL GNPRLQILIS RLGGSLFLYT
201 VRISYCLDGF HLRHIFNRFF TVLLLCFLAH IVSLKTNWKS KSGYYPKIR
251 TFSRNFQQRQ EISHPPNTL PQKPYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

```
m244.seq
```

560

```

1  ATGCCGTCTG AAGCCCGACA GCGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGCGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCT CTTTCATACA CCCACCACGG
201 TATTCGGCTC CTGTTTCGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGGTTG ATTTCCCTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAACCTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TyCTGCTGGT GCGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCTG CTCGTCTTTC AACTGCGTTT CCAGCTCGGC AATCCGCGCC
551 TGCAAATCCT CATAAGCCGG CTCTGCGGCA GCCTGTTCTT GCACACCGTC
601 CGCATTTTCT ACTGTTTTCGA CGGTTTCCAC CGCCTCCACA TTTTCAACCG
651 CTTCTTCACT GTTTTGCTGC TGTGTCTGTT CGCTCATATC GTATCCCTTA
701 AAACAAATTG GAAATCAAAA TCCAGTTATT ACCCGCGCAA GATAAGGACA
751 TTTTCAAGAA ACTTCAAKCA AAACAGAGA ATTTCAAATT CATTTTCAAA
801 TCCCCTACCG AAAAAATAAT ATAGACGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 932; ORF 244>:

```

m244 . pep
1  MPSEARQAGS DGIAALLRSV YTONALQEIN QIIPQTPSGF LLRHRNHSRA
51  QHAVGQRITL LHHTHHGIRL LFACHRLHRL MDIRIELIAR FRVDFDLRLS
101 IKCFLQLVQS HLHAHFQRIE IAALIQRHF QIILDRQHFH GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAL LVFQLRFQLG NPRLQILISR LCGSLFLHTV
201 RISYCFDGFH RLHIFNRFFT VLLCLFAHI VSLKTNWWSK SSIYPKIRT
251 FSRNFXQQR ISNSFSNPLP KKXYRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 244 shows 86.3% identity over a 277 aa overlap with a predicted ORF (ORF 244.ng) from *N. gonorrhoeae*:

M244/G244

	10	20	30	40	50	60
m244 . pep	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244	MPPEARPAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLPCHRNHSRAQHTVQGQITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244 . pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRLSIKCFLQLVQSHLHAHFQRIE					
g244	LHHTNHGIGFLLTGHRLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m244 . pep	IAALIQRHFQIILDRQHFHKGKLLSGELVRIRNFLLVAAAQVLLVCQSAALLVFQLRFQL					
g244	ITALIQRHFQIILDRQHFHKGKLLSGELVRIGNFLLVAAAQVLLVCQSAQLFVQLRFQL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244 . pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFT VLLCLFAHIVSLKTNWWS					
g244	GNPRLQILISRLGGSFLYTVRISYCLDGFHRLHIFNRFFT VLLCLFAHIVSLKTNWWS					
	190	200	210	220	230	240
	250	260	270			
m244 . pep	KSSYYPRKIRTFSRNFXQQRISNSFSNPLPKXYRRX					
g244	KSGYYPSKIRTFSRNFKQRQEISHPPNTLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1   ATGCCGTCTG AAGCCCGACA GGCGGGTTC A GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCTT CTTTCATCAG CCCACCACGG
201 TATTGGGTTC CTGTTTCGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTCCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAACCTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATF TCCTGCTGGT GCGGCGGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAAACGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATTT CCTACTGTCT CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTCG TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTAAACAAA TTGGAATCA AAATCCAGTT ATTACCCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCTA CCGAAAAAT AATATAGACG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1   MPSEARQAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAQ LLVFQLRFL GNPRQLILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQRQ RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

m244.pep	10	20	30	40	50	60
	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244	10	20	30	40	50	60
	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
m244.pep	70	80	90	100	110	120
	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
a244	70	80	90	100	110	120
	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAHFQRIE					
m244.pep	130	140	150	160	170	179
	IAALIQKRHFQIILDRQHFH GKLLSGELVRIRNFLLVAAAQVLLVCQSA-LLVFQLRFL					
a244	130	140	150	160	170	180
	IAALIQKRHFQIILDRQHFH GKLLSGELVRIRNFLLVAAAQVLLVCQSAQLLVFQLRFL					
m244.pep	180	190	200	210	220	239
	GNPRQLILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFT VLLCLFAHIVSLKTNWKS					
a244	180	190	200	210	220	240
	GNPRQLILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFT VLLCLFAHIVSLKTNWKS					
m244.pep	240	250	260	270		
	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKXYRRX					
a244	240	250	260	270		
	KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKKXYRRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1   atgccgctg aagcccgcc gccgggttca gacggcattg ccgctttact
```

g244-1.pgp

m244-1.seq

m244-1.pgp

m244-1/G244-1 86.3% identity in 277 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTSPSGFLLRHRNHSRAQHAVGQRITL					
g244-1	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTSPSGFLPCHRNHSRAQHTVGQGITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	: :					
g244-1	LHHTNHGIGFLTGHRLHRLMDIRIELIARFRIDFLDLRGIKRLLQIQSHLHTHFQRIE					
	70	80	90	100	110	120

563

	130	140	150	160	170	180
m244-1.pep	IAALIQKRHFQIILDRQHFH GKLLSGELVRIRN FLLVAAAQVLLVCQSAALLVFQ LRFQL					
g244-1	ITALIQKRHFQIILDRQHFH GKLLSGELVRIRN FLLVAAAQVLLVCQSAQLFVFQ LRFQL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
g244-1	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	250	260	270			
m244-1.pep	KSSYYPRKIRTF SRNFXQXQRISNSFSNPLPKKX					
g244-1	KSGYYPSKIRTF SRNFKQRQEISHPPNTLPQPKYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 939>:

a244-1.seq

```

1  ATGCCGTCTG AAGCCCGACA GCGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCT CTTCATCAGC CCCACCACGG
201 TATTGGGTTT CTGTTGCTTC GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTCCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC  GGCAAACTTC TGTCGGCGCA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GCGGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCAGCTC  GGCAATCCGC
551 GCCTGCAAT  CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCAATT CCTACTGTCT CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTGC TGCTGTGTCT GTTCGTCAT  ATCGTATCCC
701 TTAAACAAA  TTGAAATCA  AAATCCAGTT ATTACCGCG CAAGATAAGG
751 ACATTTTCAA GAACTTCAA  GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCCTA CCGAAAAAT  AA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 244-1.a>:

a244-1.pep

```

1  MPSEARQAGS DGIAALLRSV YTONALQEIN QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRN FLLVAAA QVLLVCQSAQ LLVFQ LRFQL GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNREF TVLLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFKQRQ RISNSFSNPL PKK*

```

m244-1/a244-1 96.8% identity in 274 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244-1	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
a244-1	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244-1.pep	IAALIQKRHFQIILDRQHFH GKLLSGELVRIRN FLLVAAAQVLLVCQSA-LLVFQ LRFQL					
a244-1	IAALIQKRHFQIILDRQHFH GKLLSGELVRIRN FLLVAAAQVLLVCQSAQLLVFQ LRFQL					
	130	140	150	160	170	180
	180	190	200	210	220	239
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
a244-1	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFT VLLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240

565

	70	80	90	100	110	120
	130	140	150			
m246 . pep	HRFAFDHQLAVFGCDDVVDNLAFGRGFCP					
g246	HGFAFDHQLAVFGCDDVVDNLAFGRGFRPVYFHAQLSQVFFQLLQQRGX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246 . seq (partial)

```

1   ATGCACGGGC GGAACGGTGG TACTCAAGCG ACCGTTGCCT TCGTTTTCCT
51  CCAGACACAG CGTACCTGTT TCAGCAACGG CGAAGTTCAC GCCACTCAAA
101 CCGACATCGG CAGTGCTGTA AATATCGCGC AGTGCTTTAC GGGCGAAGCC
151 GGTCAAGTTGG TCTACGTCGT CCGTTAACGG TGTGCCGAGG TTTTGGTGGA
201 ACAGTTCGCT AACCTGTTCT TTGGTTTAT GGATTGCGGG CATCACGATA
251 TGGGTCGGTT TTTCACCTGC CATTGGACG ATGAACGCG CCAAGTCGCT
301 TTCCACCGCT TTAATGCCTT TTGCTTCAAG ATAATGGTTC AGCTCGATTT
351 CCTCGCTGAC CATCGATTG CTTTGACCA TCAGCTGCC GTTTTGGCT
401 GTGATGATGT CGTGGATGAT TTCGCAGGCT TCGGCCGGTG TTTCCGCCCA
451 GTGTACTTTT ACGCCCAACT TGGTCAGGTT TTCTTCCAGC TGCTCCAGCA
501 G

```

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246 . pep (partial)

```

1   MHGRNGGTQA TVAFVFHQ TQ RTCF SNGEVH ATQTDIGSAV NIAQCFTGEA
51  GQLVYVVR*R CAEVLVEQFA NLFFGFMDCG HHDMGRFFTC HLDDELAQVA
101 FHRENAFCFK IMVQLDFLAD HRFAFDHQLA VFGCDDVDD FAGFGRCFRP
151 VYFYAQLGQV FFQLLQQ

```

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246 . pep	MHGRYGGTQATVAFVFHQ TQ RTCF SNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
a246	MHGRNGGTQATVAFVFHQ TQ RTCF SNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m246 . pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDELAQVAFYRFNAFCFKIMXQLDFLAD					
	:					
a246	CAEVLVEQFANLFFGFMDCGHHDMGRFFACHLDELAQVAFHRENAFCFKIMVQLDFLAD					
	70	80	90	100	110	120
	130	140	150			
m246 . pep	HRFAFDHQLAVFGCDDVVDNLAFGRGFCP					
a246	HRFAFDHQLAVFGCDDVDDFAGFGRCFRPVYFYAQLGQVFFQLLQQ					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247 . seq

```

1   atgaaacgta aaatgctaaa cgtaccaaag ggcggttatg atggtatgaa
51  gggttttacc attgttgaat ttctggttgc gggcctgctc agtataattg
101 tcctgatagc ggtcgtatcg agttacttta catcccggaa attaaatgat
151 gtggcaaacg agcgtcttgc cattcaacag gatttgcgga atgcggcaac
201 attaatgtc cgcgatgcaa gaatggcggg gagcttcggt tgttttcaata
251 tgtccgagca tactaaagac gatattgttg attcaagtaa tcaaaactcaa
301 tctaaccctg caaaacccgg tgccaaacaa gaaaatcccc ttttttcctt
351 aaaaaggagc ggcattgata acaactgat tcccgttgct gaatccatag
401 atattaaata tccgggtttt atccagcgcc ttaacgcatt ggttttccaa
451 tacggtatcg atgatcttga tgcgagtgt gagactgttg tagtcagcag
501 ctgttccaaa atagcaaaac cgggtaagaa aatatctacc ttgcaagaag
551 caaagagtgc attacagatt actaatgatg ataaacaaaa tggaaatatc

```

566

```

601 acccgtcaga aacatgtggt caatgcctat gcggtcggca ggtttgccaa
651 taatgaggaa agtttggtcc gtttccaatt ggatgataag ggcaagtggg
701 gtaatcctca gttgctcgtg aaaaagggtta aacgtatgga tgtgcggtat
751 atttatgttt ccggttggtcc tgaagatgaa gatgccggca aagaggaaaa
801 attcagatat acgaataaat tcgacaaatc caaaaatgct gttacgcctg
851 ccgggggtgga ggttttattg gatagcggcc ttaatgccaa gattgccgct
901 tcttcagaca atagtattta tgcttaccgt atcaatgcga caatacgcg
951 gggaaatgta tgcgcaaaca gaacactttg a

```

This corresponds to the amino acid sequence <SEQ ID 948; ORF 247.ng>:

g247.pep

```

1 MKRKMLNVPK GGYDGMKGFT IVEFLVAGLL SIIVLIAVVS SYFTSRKLND
51 VANERLAIQQ DLRNAATLIV RDARMAGSFG CFNMSEHTKD DIVDSSNQQT
101 SNLAKPGAKQ ENPLFSLKRS GMDKQLIPVA ESIDIKYPGF IQRNLALVFQ
151 YGIDDLDAESA ETVVVSSCSK IAKPGKKIST LQEAQSALQI TNDDKQNGNI
201 TRQKHVVNAY AVGRFGNNEE SLFRFQLDDK GKWGNPQLLV KKVKRMDVRY
251 IYVSGCPEDE DAGKEEKFRY TNKFDKSKNA VTPAGVEVLL DSGLNAKIAA
301 SSDNSIYAYR INATIRGGNV CANRTL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 949>:

m247.seq (partial)

```

1 ATAGACGTA AAATGCTAAA CGTwsyArAA GGCAGTTATG ATGGTATGAA
51 AGGTTTTACC ATTATTGAAT TTTTGGTTGC GGGCCTGCTC AGTATGATTG
101 TCCTGATGGC GGTCGGATCG AGTTACTTCA CATCCCGGAA ATTAAATGAT
151 GCGGCAAACG AGCGTCTTGC CGCGCAACAG GATTTCGCGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CGGCTTCGGT TGTTTCAATA
251 TGTCCGAGCA TCCTGCAACT GATGTTATTC CCGATACGAC GCAACAAAAT
301 TCTCCTTTTT CCTTAAAAAG GAACGGTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAAATT TTTCCAGGTT GGTCAGCGAT
401 TGATTTTTTCA ATACGGAATC GATGATGTTA ATGCAAGCAC CGCGACTACC
451 GTCGTCAGCA GCTGTGCCGC AATATCGAAA CCGGGCAAGC AAATCCCCTAC
501 TTTAGAAGAT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AAGTTTGTTC CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAATCCTC AGTTGC...

```

This corresponds to the amino acid sequence <SEQ ID 950; ORF 247>:

m247.pep (partial)

```

1 XRRKMLNVXX GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51 AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPDTTQQN
101 SPFSLKRNGI DKLIPIAESS NINYQNFFQV GSALIFQYGI DDVNASTATT
151 VVSSCAAISK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEESLF RFQLDDKQKW GNPQL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 247 shows 69.3% identity over a 238 aa overlap with a predicted ORF (ORF 247.ng) from *N. gonorrhoeae*:

m247/g247

```

          10      20      30      40      50      60
m247.pep  XRRKMLNVXXGSYDGMKGFTIIEFLVAGLLSMIVLMAVGSSYFTSRKLND AANERLAAQQ
          :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
g247      MKRKMLNVPKGGYDGMKGFTIVEFLVAGLLSIIVLIAVVS SYFTSRKLNDVANERLAIQQ
          10      20      30      40      50      60

          70      80      90      100
m247.pep  DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQQNSPFSLKRN
          |||:|:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|
g247      DLRNAATLIVRDARMAGSFGCFNMSEHTKDDIVDSSNQTSNLAKPGAKQENPLFSLKRS
          70      80      90      100      110      120

          110      120      130      140      150      160
m247.pep  GIDK-LIPIAESSNINYQNFFQVGSALIFQYGIDVDNASTATTVVSSCAAISKPGKQIPT
          |:|:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:| :||:|

```

```
a247.seq
1  ATGAGACGTA  AAATGCTAAA  CGTACCAAAA  GGCAATTATG  ATGGTATGAA
51  GGGTTTTACC  ATTATTGAAT  TTTTGGTTGC  GGGCATGCTC  AGTATGATTG
101 TCCTGATGCG  GGTCGGATCG  AGTTACTTCA  CATCCCGGAA  ATTAAATGAT
151 GCGGCAAAAC  AGCGCTCTTT  CGCGCAACAG  GATTTCGGGA  ATGCGGCAAC
201 ATTGATTGTC  CGCGATGCAA  GAATGGCAGG  GGGCTTCGGT  TGTTTCAATA
251 TGTCCGAGCA  TACTAAAAAT  GATATTATTG  TTGATCCAAG  TAAGCAAAC
301 CAACATGTCC  CTGTAAAACC  CGGTGCCAAA  CAAGAAAATC  CCCTTTTTTC
351 TTTAGAGTGG  GCTAATACTA  ATAATACTAA  TAATAATACA  GCTAAATTGA
401 TTCCTATTGC  TGAATCCACA  GATATTAAAT  ATCCGGGTTT  TGCCAGGCT
451 CGTCCGGCAT  TGATTTTCCA  ATACGGCATC  GATGATCTTG  ATGCGAGTGC
501 TGAGACTGTT  GTAGTCAGCA  GCTGTTCCAA  AATAGCAAAA  CCGGGTAAGA
551 AAATACTCTAC  CTTGCAAGAA  GCAAAGAGTG  CATTACAGAT  TACTAATGAT
601 GATAAACAAA  ATGGAATAT  CACCCGTCAA  AGGCATGTGG  TCAATGCC
651 TGCGGTCGGC  AGGATTGCCG  GTGAGGAAGG  TTTGTTCCGC  TTCCAATTGG
701 ATGATAAGGG  CAAGTGGGGT  AATCCTCAGT  TGCTCGTGAA  AAAGATTAGA
751 CATATGAAAG  TGCGGTATAT  CTATGTTTCC  GACTGTCCTG  AAGATGACGA
801 TGCCGGCAAA  GAGGAAAAAT  TCAAATATAC  GGGTACATTC  GACAGCTCCA
851 CAAATGCTGT  TACGCCCGCC  GGGGTGGAGG  TTTTATTGAG  TANCGGTACT
901 GATACCAAGA  TTGCGCGTTC  TTCAGACAAT  CATATTATG  CTACCGTACT
951 CGATGCGACA  ATACGCGGGG  GAAATGTATG  CGCAAAACAGA  ACCTTTTGA
```

```
a247.pep
1  MRRKMLNVPK GNYDGMKGFT IIEFLVAGML SMIVLMAVGS SYFTSRKLN
51  AANERLSAQQ DLRNAATLIV RDARMAGGFG CFNMSEHTKN DIIIVDSPKQT
101 QHVPVKPGAK QENPLFSLEW ANTNTNTNNT AKLIPIAEST DIKYPGFAQA
151 RPALIFQYGI DDLDASAETV VVSSCSKIAK PGKKISTLQE AKSALQITND
201 DKQNGNITRQ RHVVNAYAVG RIAGEEGLFR FQLDDKGKGW NPQLLVKKIR
251 HMKVRIIYVS DCPEDDDAGK EEKFKYTGTF DSSTNAVPTA GVEVLLSXGT
301 DTKIAASSDN HIYAYRIDAT IRGGNVCANR TL*
```

	10	20	30	40	50	60
m247.pep	XRRKMLNVXXGSYDGMKGFTTIEFLVAGLLSMIVLMAVGSSYFTSRKLNDAAANERLAAQQ					
		:				
a247	MRRKMLNVPKGNVDGMKGFTTIEFLVAGLLSMIVLMAVGSSYFTSRKLNDAAANERLSAQQ					
	10	20	30	40	50	60
	70	80	90		100	
m247.pep	DLRNAATLIVRDARMAGFGFCFNMSEHPATDVI-----PDTTQQNSPFSLK-					
			:		:	
a247	DLRNAATLIVRDARMAGFGFCFNMSEHTKNDIIVDPSKQTQHVPVKPGAKQENPLFSLEW					
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	-----RNGIDKLIPIAESNNINYQNFFQVGSALIFQYGIDVDNASTATTVVSSCAAISK					
	:		:	:		:
a247	ANTNNTNNNTAKLIPIAESTDIKYPGFAQARPALIFQYGIDDLDAETAETVVVSSCSKIAK					
	130	140	150	160	170	180

568

	170	180	190	200	210	220
m247.pep	PGKQIPTLEDAKKELKIPDQDKEQNGNIARQRHVVNAYAVGRIADEESLFRFQLDDKGKW					
	: :: : : :: : :					
a247	PGKKISTLQEAKSALQITNDDK-QNGNITRQRHVVNAYAVGRIAGEEGLFRFQLDDKGKW					
	190	200	210	220	230	
m247.pep	GNPQL					
a247	GNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEFKYTGTFDSSTNAVTPAGVEVLLSXG					
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 953>:

g247-1.seq (partial) ..

1	CCCGGTGCCA	AACAAGAAAA	TCCCCTTTT	TCCTTAAAAA	GGAGCGGCAT
51	GGATAAACAA	CTGATTCCCG	TGCTGAATC	CATAGATATT	AAATATCCGG
101	GTTTTATCCA	GCGCCTTAAC	GCATTGGTTT	TCCAATACGG	TATCGATGAT
151	CTTGATGCGA	GTGCTGAGAC	TGTTGTAGTC	AGCAGCTGTT	CCAAAATAGC
201	AAAACCGGGT	AAGAAAATAT	CTACCTTGCA	AGAAGCAAAG	AGTGCATTAC
251	AGATTACTAA	TGATGATAAA	CAAAATGGAA	ATATCACCCG	TCAGAAACAT
301	GTGGTCAATG	CCTATGCGGT	CGGCAGTTT	GGCAATAATG	AGGAAAGTTT
351	GTTCCGCTTC	CAATTGGATG	ATAAGGGCAA	GTGGGGTAAT	CCTCAGTTGC
401	TCGTGAAAAA	GGTTAAACGT	ATGGATGTGC	GGTATATTTA	TGTTTCCGGT
451	TGTCCTGAAG	ATGAAGATGC	CGGCAAAGAG	GAAAAATTCA	GATATACGAA
501	TAAATTCGAC	AAATCCAAAA	ATGCTGTTAC	GCCTGCCGGG	GTGGAGGTTT
551	TATTGGATAG	CGGCCTTAAT	GCCAAGATTG	CCGCTTCTTC	AGACAATAGT
601	ATTTATGCTT	ACCGTATCAA	TGCGACAATA	CGCGGGGGAA	ATGTATGCCG
651	AAACAGAACA	CTTTGA			

This corresponds to the amino acid sequence <SEQ ID 954; ORF 247-1.ng>:

g247-1.pep (partial) ..

1	PGAKQENPLF	SLKRSMDKQ	LIPVAESIDI	KYPGFIQRLN	ALVFQYGIDD
51	LDASAEVTVV	SSCSKIAKPG	KKISTLQEAK	SALQITNDDK	QNGNITRQKH
101	VVNAYAVGRF	GNNEESLFRF	QLDDKGKWN	PQLLVKKVVR	MDVRYIYVSG
151	CPEDEDAGKE	EKFRTYTNKFD	KSKNAVTPAG	VEVLDSGLN	AKIAASSDNS
201	IYAYRINATI	RGGNVCANRT	L*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 955>:

m247-1.seq

1	ATGAGACGTA	AAATGCTAAA	CGTACCAAAA	GGCAGTTATG	ATGGTATGAA
51	AGGTTTTACC	ATTATTGAAT	TTTTGGTTGC	GGGCCTGCTC	AGTATGATTG
101	TCCTGATGGC	GGTCGGATCG	AGTTACTTCA	CATCCCGGAA	ATTAAATGAT
151	GCGGCAACAC	AGCGTCTTGC	CGCGCAACAG	GATTTCGGGA	ATGCGGCAAC
201	ATTGATTGTC	CGCGATGCGA	GAATGGCAGG	CGGCTTCGGT	TGTTTCAATA
251	TGTCCGAGCA	TCCTGCAACT	GATGTTATTC	CCGATACGAC	GCAACAAAAT
301	TCTCCTTTTT	CCTTAAAAAG	GAACGGTATA	GATAAACTTA	TTCCCATAGC
351	GGAATCTTCA	AATATCAATT	ATCAGAATTT	TTTCCAGGTT	GGTAGCGCAT
401	TGATTTTTCA	ATACGGAATC	GATGATGTTA	ATGCAAGCAC	CGCGACTACC
451	GTGTCGAGCA	GCTGTGCCGC	AATATCGAAA	CCGGGCAAGC	AAATCCCTAC
501	TTTAGAAGAT	GCAAAAAAAG	AATTGAAGAT	TCCGGATCAG	GATAAGGAGC
551	AAAATGGCAA	TATAGCGCGT	CAAAGGCATG	TGGTCAATGC	CTATGCGGTC
601	GGCAGGATTG	CCGATGAGGA	AGGTTTGTTT	CGCTTCCAAT	TGGATGATAA
651	GGGCAAGTGG	GGTAATCCTC	AGTTGCTCGT	GAAAAAGGTT	AGACATATGA
701	AAGTGCGGTA	TATCTATGTT	TCCGGCTGTC	CTGAAGATGA	CGATGCCGGC
751	AAAGAGGAAA	CATTCAAATA	TACGGATAAA	TTGACAGCG	CCCAAAATGC
801	TGTTACGCCC	GCCGGGGTGG	AGGTTTATT	GAGTAGCGGT	ACTGATACCA
851	AGATTGCCGC	TTCTTCAGAC	AATCATATTT	ATGCTTACCG	TATCGATGCG
901	ACAATACGCG	GGGGAAATGT	ATGCGCAAAC	AGAACACTTT	GA

This corresponds to the amino acid sequence <SEQ ID 956; ORF 247-1>:

m247-1.pep

1	MRRKMLNVPK	GSYDGMKGFT	IEFLVAGLL	SMIVLMAVGS	SYFTSRKLND
51	AANERLAAQQ	DLRNAATLIV	RDARMAGGFG	CFNMSEHPAT	DVIPDTTQQN
101	SPFSLKRNGI	DKLIPIAESS	NINYQNFFQV	GSALIFQYGI	DDVNAATATT
151	VVSSCAAIK	PGKQIPTLED	AKKELKIPDQ	DKEQNGNIAR	QRHVVNAYAV
201	GRIADEEGLF	RFQLDDKGKW	GNPQLLVKKV	RHMKVRYIYV	SGCPEDDDAG
251	KEETFKYTDK	FDSAQNAVTP	AGVEVLLSSG	TDTKIAASSD	NHIYAYRIDA
301	TIRGGNVCAN	RTL*			

m247-1 / g247-1 72.1% identity in 222 aa overlap

	70	80	90	100	110	120
m247-1.pep	NAATLIVRDARMAGGFGCFNMSEHPATDVIPD	TQQNSPFLSKRNGIDK-LIPIAESSNI				
g247-1				PGAKQENPLFSLKRS	GMDKQLIPVAESIDI	
				10	20	30
	130	140	150	160	170	180
m247-1.pep	NYQNFFQVGSALIFQY	GIDDDVNASTATTVVSSCAAISKPGKQIPTLED	AKKELKIPDQDK			
g247-1	KYPGFIQRLNALVFQY	GIDDLASAETVVVSSCSKIAKPGKKISTLQ	EAKSALQITNDDK			
	40	50	60	70	80	90
	190	200	210	220	230	240
m247-1.pep	EQNGNIARQHRHVVNAYAVGRIAD-EEGLFRFQ	LDDKGKGNPQLLVKKVRHMKVRYIYVS				
g247-1	-QNGNITRQKHVVNAYAVGRFGNNEESLFRFQ	LDDKGKGNPQLLVKKVRMDVRYIYVS				
	100	110	120	130	140	
	250	260	270	280	290	300
m247-1.pep	GCPEDDDAGKEETF	KYTDKFD	SAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDAT			
g247-1	GCPEDDAGKEEKFRY	TNKF	DKSKNAVTPAGVEVLLD	SGLNAKIAASSDNSIYAYRINAT		
	150	160	170	180	190	200
	310					
m247-1.pep	IRGGNVCANRTLX					
g247-1	IRGGNVCANRTLX					
	210	220				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 957>:

a247-1.seq (partial)

```

1  AATAATACAG CTAATTGAT TCCTATTGCT GAATCCACAG ATATTAAATA
51  TCCGGGTTTT GCCCAGGCTC GTCGCGCATT GATTTTCCAA TACGGCATCG
101 ATGATCTTGA TGCAGTGTCT GAGACTGTTG TAGTCAGCAG CTGTTCCAAA
151 ATAGCAAAAC CGGGTAAGAA AATATCTACC TTGCAAGAAG CAAAGAGTGC
201 ATTACAGATT ACTAATGATG ATAAACAAAA TGGAAATATC ACCCGTCAAA
251 GGCATGTGGT CAATGCCTAT GCGGTCGGCA GGATTGCCGG TGAGGAAGGT
301 TTGTTCGGCT TCCAATTGGA TGATAAGGGC AAGTGGGGTA ATCCTCAGTT
351 GCTCGTGAAA AAGATTAGAC ATATGAAAGT GCGGTATATC TATGTTCCG
401 ACTGTCCTGA AGATGACGAT GCCGGCAAA AGGAAAAATT CAAATATACG
451 GGTACATTCG ACAGCTCCAC AAATGCTGTT ACGCCCGCCG GGGTGGAGGT
501 TTTATTGAGT AGCGGTACTG ATACCAAGAT TGCCGCTTCT TCAGACAATC
551 ATATTTATGC TTACCGTATC GATGCGACAA TACGCGGGGG AAATGTATGC
601 GCAAACAGAA CACTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 958; ORF 247-1.a>:

a247-1.pep (partial)..

```

1  NNTAKLIPIA ESTDIKYPGF AQARPALIFQ YGIDDLASA ETVVVSSCSK
51  IAKPGKKIST LQEAKSALQI TNDDKQNGNI TRQRHVVNAY AVGRIAGEEG
101 LFRFQLDDKG KWGNPQLLVK KIRHMKVRYI YVSDCPEDDD AGKEEFKYT
151 GTFDSSTNAV TPAGVEVLLS SGTDTKIAAS SDNHIYAYRI DATIRGGNVC
201 ANRTL*

```

m247-1 / a247-1 80.6% identity in 206 aa overlap

				10	20	30
a247-1.pep				NNTAKLIPIA	ESTDIKYPGFAQARPALIFQ	
m247-1	GFGCFNMSEHPATDVIPD	TQQNSPFLSKRNGIDKLIPIAESSNIN	YQNFFQVGSALIFQ			
	80	90	100	110	120	130
	40	50	60	70	80	89
a247-1.pep	YGIDDLASAETVVVSSCSKIAKPGKKISTLQ	EAKSALQITNDDK-QNGNITRQRHVVN				
m247-1	YGIDDVNASTATTVVSSCAAISKPGKQIPTLED	AKKELKIPDQDKEQNGNIARQHRHVNA				
	140	150	160	170	180	190
	90	100	110	120	130	140
a247-1.pep	YAVGRIAGEEGLFRFQ	LDDKGKGNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEFKY				

570

```

m247-1      YAVGRIADEEGLFRFQLDDKGKGNPQLLVKKVRHMKVRYIYVSGCPEDDDAGKEETFKY
            200      210      220      230      240      250

a247-1.pep  150      160      170      180      190      200
            TGTFDSSSTNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            |   |||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m247-1      TDKFDSAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            260      270      280      290      300      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 959>:

```

g248.seq
1  atgcgcaaac agaacacttt gacaggaatc cgcacttctg acggacagag
51  ggggtccgca ctgtttatcg tgctgatggt gatgatagtc gtggcctttt
101 tggttgtaac tgccgccagc tcctacaata ccgaacagag gatcagtgcc
151 aacgaatcag acaggaaatt ggctttgtct ttagccgagg cgcctttgcg
201 ggagggcgaa tttcaggttt tggatttggg atatgctgcg gacagtaagg
251 ttacgtttag cgaaaactgt gaaaaaggct tgtgtaccgc agtgaatgtg
301 cggacaaata ataattgtag tgaagaggct tttggcaata tcgtggtgca
351 aggcaagccc gccgttgagg cggtgaaacg ttcttgccct gcaaagtctg
401 gcaaaaattc taccgacctg tgcattgaca ataaagggat ggaatataat
451 aaaggcgcgg caggcgtcag caaaatgccg cgctatatta tcgaatatatt
501 aggcgtgaag aacggacaaa atgtttatcg gggtactgcc aaggcttggg
551 gtaagaatgc caataccgtg gtcgtccttc aatcttatgt aggcaataat
601 gatgagcaat aa

```

This corresponds to the amino acid sequence <SEQ ID 960; ORF 248.ng>:

```

g248.pep
1  MRKQNTLTGI PTSDGQRGSA LFIVLMVMIV VAFLVVTAAG SYNTEQRISA
51  NESDRKLALS LAEALREGE FQVLDLEYAA DSKVTFSENC EKGLCTAVNV
101 RTNNNGSEEA FGNIVVQKPK AVEAVKRSCP AKSGKNSTDL CIDNKGMEYN
151 KGAAGVSKMP RYIEYLGVK NGQNVYRVTA KAWGKNANTV VVLQSYVGN
201 DEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 961>:

```

m248.seq (partial)
1  ..GGGTTTGCAC TGTTAATCGT GCTGATGGTG ATrATCGTCG TGGCT.TyWT
51  gGwTGTAAct GCCGCGCAGT CTTACAATAC cGAGCAGCGK ATCAGTkCCA
101 ACGAATCAGA CAGGAAATTG GCTwTGTCTT TGGCCGAGKc GkCTwTGCgG
151 GAAGGCGAAC TTCAGTTTTT GGATTTGGAA TATGATACGG ACAGTAAGGT
201 TACATTTAGC GAAAACTGTG GAAAAGGTCT GTsTGCCGCA GTGAATGTGC
251 GGACAAATAA TGATAATGAA GAGGCTTTTG ACAATATCGT GGTGCAAGGC
301 AAGCCCACCG TTGAGGCGGT GAAGCGTTCT TGCCCTGCAA ATTCTACCGA
351 CCTGTGCATT GACAAGAAAG GGwTGGAAAT TAAGAAAGGC ACGAGAAGCG
401 TCAC.AAAAT GCCACGTTAT ATTATCGAAT ATTTGGGCGT GwAGAACGGA
451 GAAAATGTTT ATCGGGTTAC TGCCAAGGCT TGGGGtAAG ATGCCAATAC
501 CGTGGTGCCT CTTCAATCTT ATGTAAGCAA TAATGATGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 962; ORF 248>:

```

m248.pep (partial)
1  ..GFALLIVLMV XIVVAFXXVT AAQSYNTEQR ISXNESDRKL AXSLAEXXXR
51  EGELQVLDLE YDTSKVTFS ENCGKGLXAA VNVRTNNDNE EAFDNIVVQG
101 KPTVEAVKRS CPANSTDLCI DKKGXEYKKG TRSVTKMPRY IIEYLGvXNG
151 ENVYRVTAKA WGKNANTVVV LQSYVSNND *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 248 shows 81.1% identity over a 185 aa overlap with a predicted ORF (ORF 248.ng) from *N. gonorrhoeae*:

m248/g248

```

m248.pep
            10      20      30      40
            GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
            | ||: |||| | |||| | ||||| ||||| ||||| |||||

```



```

g248      MRKQNTLTGTSDGQRGSAFIVLMVMIVVAFLLVTTAAQSYNTEQRISANESDRKLALS
           10          20          30          40          50          60

           50          60          70          80          90          100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGKGLXAAVNVRTNND-NEEAFDNI VVQGKP
           |||  |||:||||| :||||||| ||| :||||||| : ||| |||||
g248      LAEAAALREGEFQVLDLEYAADSKVTFSENCEKGLCTAVNVRTNNGSEEAFGNIVVQGKP
           70          80          90          100          110          120

           110          120          130          140          150
m248.pep  TVEAVKRSCPA---NSTDLCIDKKGXKEYKKGTRSVTKMPRYII EYLG VXNGENVYRVTA
           :||||||| |||||:| ||:|: :|:||||||| ||| :|||||
g248      AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRYII EYLG VKNGQNVYRVTA
           130          140          150          160          170          180

           160          170          180
m248.pep  KAWGKNANTVVVLQSYVSNNDEX
           ||||||||| |||||:|||
g248      KAWGKNANTVVVLQSYVGNNDQX
           190          200

```

a248.seq

1	ATGCGCAAAC	AGAACACTTT	GACGGGAATC	CCGACTTCTG	ACGGACAGAG
51	GGGGTTTGCA	CTGTTTATCG	TGCTGATGGT	GATGATCGTC	GTGGCTTTTT
101	TGGTTGTAAC	TGCCGCGCAG	TCTTACAATA	CCGAGCAGCG	GATCAGTGCC
151	AACGAATCAG	ACAGGAAATT	GGCTTTGTCT	TTGGCCGAGG	CGGCTTTGCG
201	GGGAAGCGAA	CTTCGGTTTT	TGGATTGGGA	ATATGATACG	GACAGTAAGG
251	TTACATTTAG	CGAAAACGTG	GGAAAAGGTC	TGTGTACCGC	AGTGAATGTG
301	CGGACAAATA	ATGATAATGA	AGAGGCTTTT	GACAATATCG	TGGTGCAAGG
351	CAAGCCCACC	GTTGAGGCGG	TGAAGCGTTC	TTGCACTGCA	AAATCTACAG
401	GCCTGTGTCAT	TGACAATAAA	GGGATGGAAT	ATAAGAAAGG	CACGCAAAGC
451	GTCAGCAAAA	TGCCACGTTA	TATTATCGAA	TATTTGGGCG	TGAAGAACGG
501	AGAAAATGTT	TATCGGGTTA	CTGCCAAGGC	TTGGGGTAAG	AATGCCAATA
551	CCGTGGTCGT	CCTTCAATCT	TATGTAAGCA	ATAATTGATGA	GTAA

a248.pep

1	MRKQNTLTGI	PTSDGQRGFA	<u>LFIVLMVMIV</u>	VAFLVVTAQ	SYNTEQRISA
51	NESDRKLALS	LAEEAALREGE	LQVLDLEYDT	DSKVTFSENC	GKGLCTAVNV
101	RTNNDNEEAF	DNIVVQ GKPT	VEAVKRSCTA	KSTGLCIDNK	GMEYKKGTS
151	VSKMPRYIIE	YLGVKNGENV	YRVTAKAQWK	NANTVVVLOS	YVSNND*E

		10	20	30	40		
m248.pep		GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS					
		:					
a248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS	10	20	30	40	50	60
		50	60	70	80	90	100
m248.pep	LAEXXXREGELQVLDLEYDTSKVTFSENCGKGLXAAVNVRTNNDNEEAFDNIVVQGKPT						
	:						
a248	LAEAAALREGELQVLDLEYDTSKVTFSENCGKGLCTAVNVRTNNDNEEAFDNIVVQGKPT	70	80	90	100	110	120
		110	120	130	140	150	160
m248.pep	VEAVKRSCPANSTDLCIDKKGXEYKKGTRSVTKMPRYIIIEYLGXNGENVYRVTAKEAWGK						
	: : : :						
a248	VEAVKRSTAKSTGLCIDNKGMEYKKGTSVSKMPRYIIIEYLGXNGENVYRVTAKEAWGK	130	140	150	160	170	180
		170	180				
m248.pep	NANTVVVLQSYVSNNDEX						

a248
 |||||
 NANTVVVLQSYVSNNDEX
 190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 965>:

m248-1.seq

```

1  ATGCGCAAAC AGAACAACCTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CCGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTAG CGAAAACGTG GGAAGAGTTC TGTGTGCCCG AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCCCTGCA AATTCTACCG
401 ACCTGTGCAT TGACAAGAAA GGGATGGAAT ATAAGAAAGG CACGAGAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCGG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 966; ORF 248-1>:

m248-1.pep

```

1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFLVVTAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCAAVNV
101 RTNNDNEEAF DNIVVQGKPT VEAVKRSCPA NSTDLCIDKK GMEYKKGTRS
151 VSKMPRYIE YLGVKNGENV YRVTAKAWGK NANTVVVLQS YVSNNDE*

```

m248-1/g248 89.1% identity in 202 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAQSYNTEQRISANESDRKLALS					
g248	MRKQNTLTGIPTSDGQRGSALFIVLMVMIVVAFLVVTAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	119
m248-1.pep	LAEALREGELQVLDLEYDTDSKVTFSENCGKGLCAAVNVRTNND-NEEAFDNIVVQGKP					
	: : : : :					
g248	LAEALREGELQVLDLEYAADSKEVTFSENCEKGLCTAVNVRTNNGSEEAFGNIVVQGKP					
	70	80	90	100	110	120
	120	130	140	150	160	170
m248-1.pep	TVEAVKRSCPA----NSTDLCIDKKGMEYKKGTRSVSKMPRYII EYLGVKNGENVYRVTA					
	: : : : : :					
g248	AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRYII EYLGVKNGQNVYRVTA					
	130	140	150	160	170	180
	180	190				
m248-1.pep	KAWGKNANTVVVLQSYVSNNDEX					
	:					
g248	KAWGKNANTVVVLQSYVGNNDQX					
	190	200				

m248-1/a248 97.0% identity in 197 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAQSYNTEQRISANESDRKLALS					
a248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m248-1.pep	LAEALREGELQVLDLEYDTDSKVTFSENCGKGLCAAVNVRTNNDNEEAFDNIVVQGKPT					
	: : : : :					
a248	LAEALREGELQVLDLEYDTDSKVTFSENCGKGLCTAVNVRTNNDNEEAFDNIVVQGKPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m248-1.pep	VEAVKRSCPANSTDLCIDKKGMEYKKGTRSVSKMPRYII EYLGVKNGENVYRVTA KAWGK					
	: : : : : :					
a248	VEAVKRSC TAKSTGLCIDNKGMEYKKGTSVSKMPRYII EYLGVKNGENVYRVTA KAWGK					
	130	140	150	160	170	180

```

                190
m248-1.pep  NANTVVVLQSYVSNNDEX
            |||||
a248       NANTVVVLQSYVSNNDEX
                190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 967>:

```

g249.seq
1  atgaagaata atgattgctt ggcctgaaa aatccccagt ccggtatggc
51  gttgatagaa gtcttggtcg ctatgctcgt tctgaccatc ggtatatttg
101 cattgctgtc cgtacagttg cggacagtcg cttccgtcag ggaggcggaa
151 acgcaaacca tcgtcagcca aatcacgcaa aacctgatgg aaggaatggt
201 gatgaatccg accattgatt tggacagcaa caagaaaaac tatagtcttt
251 acatgggaaa acagacacta tcagctgtgg atggtgagtt tatgcttgat
301 gccgagaaaa gtaaggcgca gttggcagag gaacaattga agagatttag
351 tcatgagctg aaaaatgcct tggcgatgc ggtagctatt cattacgccg
401 tctgcaagga ttcgtcgggt gacgcgcgga cattgtccga cagcgggtgt
451 ttttcttcaa attgcgacaa taaggcaaac ggggatactt tgattaaagt
501 attgtgggta aatgattcgg caggggattc ggatatttcc cgtacgaatc
551 ttgaagtgag cggcgacaat atcgtatata cctatcaggc aagggtcggg
601 ggtcgtgaat ga

```

This corresponds to the amino acid sequence <SEQ ID 968; ORF 249.ng>:

```

g249.pep
1  MKNNDCLRLK NPQSGMALIE VLVAMLVLT GILALLSVQL RTVASVREAE
51  TQTIVSQITQ NLMEGMLMNP TIDLDSNKKK YSLYMGKQTL SAVDGEFMLD
101 AEKSKAQLAE EQLKRFSHEL KNALPDVAI HYAVCKDSSG DAPTLSDSGA
151 FSSNCDNKAN GDTLIKVLWV NDSAGDSDIS RTNLEVSGDN IVYTYQARVG
201 GRE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 969>:

```

m249.seq
1  ATGAAGAATA ATGATTGCTT CCGCCTGAAA GATTCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTACAGTTG CGGACAGTCN NNNNNNNNNN NNNNNNNNNN
151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNTTGATGG AGGGAATGTT
201 GATGAATCCG ACCATTGATT CCGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATTT TGCGATTGAT
301 GCCATGAAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTAG
351 TTATGAGCTG AAAAAATGCCT TGCCGGATGC GGCAGCCATC CATTACGCCG
401 TCTGCAAGGA TTCGTCGGGT AACGCGCCGA CATTGTCCGG CAATGCTTTT
451 TCTTCAAATT GCGACAATAA GGCAAACGGG GATACTTTAA TTAAAGTATT
501 GTGGGTAAAT GATTCGGCAG GGGATTCCGA TATTTCCCGT ACGAATCTTG
551 AGGTGAGCGG CGACAATATC GTATATACTT ATCAGGCAAG GGTCCGAGGT
601 CCGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 970; ORF 249>:

```

m249.pep
1  MKNNDCFRLK DSQSGMALIE VLVAMLVLT GILALLSVQL RTVXXXXXXXX
51  XXXXXXXXXXX XLMEGMLMNP TIDSDSNKKK YNLYMGNHTL SAVDGDFAID
101 AMKTKQLAE AQLKRFSYEL KNALPDAAAI HYAVCKDSSG NAPTLSGNAF
151 SSNCDNKANG DTLIKVLWVN DSAGDSDISR TNLEVSGDNI VYTYQARVGG
201 RE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 249 shows 81.3% identity over a 203 aa overlap with a predicted ORF (ORF 249.ng) from *N. gonorrhoeae*:

m249/g249

```

                10      20      30      40      50      60
m249.pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXX
            |||||:|:|: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

574

```

g249      MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
           10      20      30      40      50      60

           70      80      90      100     110     120
m249.pep  XLMEGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTGQLAEQKRFSEYEL
           |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g249      NLMEGMLMNPTIDSDSNKKNYSLYMGKQTLTSAVDGEFMLDAEKSQAQLAEQKRFSEH
           70      80      90      100     110     120

           130     140     150     160     170     179
m249.pep  KNALPDAAAIHYAVCKDSSGNAPTLSGN-AFSSNCDNKANGDTLIKVLWVNDSDAGSDSDIS
           |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g249      KNALPDAAAIHYAVCKDSSGDAPTLSDSGAFSSNCDNKANGDTLIKVLWVNDSDAGSDSDIS
           130     140     150     160     170     180

           180     190     200
m249.pep  RTNLEVSGDNIVYTYQARVGGREX
           |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g249      RTNLEVSGDNIVYTYQARVGGREX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 971>:

```

a249.seq
1   ATGAAGAATA ATGATTGCTT CCGCCTGAAA AACCCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGGTCG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTTCAGTTG CGGACAGTCG CTTCCGTCAG GGAGGCAGAG
151 ACGCAAACCA TCGTCAGTCA AATCACGCAA AACCTGATGG AAGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATCATGCA CTATCAGTTG TGGATGGCGA TTTTCAGGTT
301 GATGCCATAA AACTAAGAC GCAGTTGGCA GAGGCACAAT TGAAGAGATT
351 TAGTTATGAG CTGAAAAATG CCTTGCCGGA TCGCGCAGCC ATCCATTACG
401 CCGTCTGCAA GGATTGCTCG GGTGTTGCGC CGACATTGTC CGCCGGCAGT
451 ACTTTTCTT CAAATTGCGA TGGTAGTGCA AATGGGGATA CTTTGATTAA
501 AGTATTGTGG GTAAATGATT CGGCAGGGGA TTCGGATATC GCCCGTACGA
551 ATCTTGAGAC GAACGGCAAC AATATCGTAT ATACCTATCA GGCAAGGGTC
601 GGAGGTCGGG AATGA

```

This corresponds to the amino acid sequence <SEQ ID 972; ORF 249.a>:

```

a249.pep
1   MKNNDCFRLK NPQSGMALIE VLVAMLVLTIGILALLSVQL RTVASVREAE
51  TQTIVSQITQ NLMEGMLMNP TIDSDSNKKN YNLYMGNHHA LSVVDGDFQV
101 DAIKTKTQLA EAQLKRFSYE LKNALPDAAA IHYAVCKDSS GVAPTLASGS
151 TFSSNCDGSA NGDTLIKVLW VNSAGDSDI ARTNLETNGN NIVYTYQARV
201 GGRE*

```

m249/a249 81.9% identity in 204 aa overlap

```

           10      20      30      40      50      60
m249.pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXX
           |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a249      MKNNDCFRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
           10      20      30      40      50      60

           70      80      90      100     110     119
m249.pep  XLMEGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTGQLAEQKRFSEYEL
           |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a249      NLMEGMLMNPTIDSDSNKKNYNLYMGNH-HALSVVDGDFQVDAIKTKTQLAEQKRFSEYEL
           70      80      90      100     110     120

           120     130     140     150     160     170
m249.pep  LKNALPDAAAIHYAVCKDSSGNAPTLS-GNAFSSNCDNKANGDTLIKVLWVNDSDAGSDSI
           |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a249      LKNALPDAAAIHYAVCKDSSGVAPTLASGSTFSSNCDGSANGDTLIKVLWVNDSDAGSDSI
           130     140     150     160     170     180

```

```
m249.pep      180       190       200
               SRTNLEVSGDNIIVYTYQARVGGREX
               :|:||||::|:|||||
a249          ARTNLETNGNNIIVYTYQARVGGRX
               190       200
```

1	ATGAAGAAT	ATGATTGCTT	CCGCCTGAAA	GATTCCCAGT	CCGGTATGGC
51	GCTGATAGAA	GTCTTGGGTG	CTATGCTCGT	TCTGACCATT	GGTATTTTGG
101	CACATAATTG	TGTACAGTTG	CGGACAGTCG	CTTCCGTCAG	GGAGGCGGAG
151	ACACAAACCA	TCGTCAGCCA	AATCACGCAA	AACCTGATGG	AGGGAATGTT
201	GATGAATCCG	ACCATTGATT	CGGACAGCAA	CAAGAAAAAC	TATAATCTTT
251	ACATGGGAAA	CCATACACTA	TCAGCTGTGG	ATGGCGGATT	TGGCGATTAT
301	GGCATGAAAA	CTAAGGGGCA	ATTGGCAGAT	GCACAAATTG	AGAGATTTAG
351	TTATGAGCTG	AAAAATGCGT	TGCCCGATGC	GGCAGCCATC	CATTACGCCG
401	TCTGCAAGGA	TTCGTCGGGT	AACGCGCCGA	CATTGTCCGG	CAATGCTTTT
451	TCTTCAAATT	GCGACATAAA	GGCAAACGGG	GATACTTTAA	TTAAAGTATT
501	GTGGGTAAAT	GATTCCGGCAG	GGGATTCCGA	TATTTCCCGT	ACGAATCTTG
551	AGGTGACGGG	CGACAATATC	GTATATACTT	ATCAGGCAAG	GGTCGGAGGT
601	CGGGAATGA				

1	MKNNDCFRLK	DSQSGMALIE	<u>VLVAMLVLTl</u>	<u>GILALLSVQL</u>	RTVASVREAE
51	TQTIVSQITQ	NLMEGMLMNP	TIDSDSNKKN	YNLYMGNH7L	SAVDGDFAlD
101	AMKTKGQLAE	AQLKRFSYEL	KNALPDAAAI	HYAVCKDSSG	NAP7LSGNAF
151	SSNCDNKANG	DTLIKVLWVN	DSAGDSDISR	TNLEVSGDNI	V7TYQARVGG
201	RE*				

		10	20	30	40	50	60			
m249-1.pep		MKNND	CFRLKDSQSGMALIEVLV	AMLVLTIGILALLSVQLRT	VASVRE	AETQTIV	SQITQ			
		:	:	:	:	:	:			
g249		MKNND	CLRLKNPQSGMALIEVLV	AMLVLTIGILALLSVQLRT	VASVRE	AETQTIV	SQITQ			
		10	20	30	40	50	60			
		70	80	90	100	110	120			
m249-1.pep		NLMEG	MLMNPTIDSDSNKKNY	LYMGNHTLSAVDGD	FAIDAMKT	KGQLAE	AQLKRFSYEL			
		:	:	:	:	:	:			
g249		NLMEG	MLMNPTIDLDSNKKNY	SLYMGKQTL	SAVDGEF	MLDAEKS	KAQLAEELKRFSHEL			
		70	80	90	100	110	120			
		130	140	150	160	170	179			
m249-1.pep		KNALP	DAAAIH	YAVCKDSSGNAPT	LSGN-AFSS	NCNDKANG	DTLIKVLWV	ND	SAGD	SDIS
		:	:	:	:	:	:	:	:	:
g249		KNALP	DAVAIH	YAVCKDSSGDAPT	LSDSGAFSS	NCNDKANG	DTLIKVLWV	ND	SAGD	SDIS
		130	140	150	160	170	180			
	180	190	200							
m249-1.pep		RTNLEV	SGDNIV	YTYQ	ARVGG	REX				
		:	:	:	:	:				
g249		RTNLEV	SGDNIV	YTYQ	ARVGG	REX				
		190	200							

Query: 73 DSDSNKKNYNLYMGNHHALSVVDGDFQVDAIKTKTQLAEA---QLKRFSYELKNALPDAA 129

576

D + M G A + T L + A + L ++ ++KN LP A
 Sbjct: 72 LYDVKDQ-----MATQSDFFKAKGSAPFTAPSSCTPLPDAIKDRLGCAEQVKNELPGAG 126
 Query: 130 AI---HYAVCKDSSGVAPTLASGSTFSSNCDGSANGDTL-IKVLWVNDASAGDSDIARTNL 185
 + Y +C+ S +CDG G L I++ W + A ++
 Sbjct: 127 DLLKSDYYICRSSK-----PGDCDG--KGSMLIIRLAWRGKQACVNAADSSA 172
 Query: 186 ETN 188
 +T+
 Sbjct: 173 DTS 175

m249-1/a249 90.7% identity in 204 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLK	DSQSG	MALIE	VLVAM	LVLTIG
a249	MKNND	CFRLK	NPQSG	MALIE	VLVAM	LVLTIG
	10	20	30	40	50	60
	70	80	90	100	110	119
m249-1.pep	NLM	EGMLM	NPTID	SDSNK	KNYNL	YMGNH-
a249	NLM	EGMLM	NPTID	SDSNK	KNYNL	YMGNH-
	70	80	90	100	110	120
	120	130	140	150	160	170
m249-1.pep	LKN	ALPDAAA	IHYAV	CKDSS	GNAPT	LS-GNA
a249	LKN	ALPDAAA	IHYAV	CKDSS	GNAPT	LS-GNA
	130	140	150	160	170	180
	180	190	200			
m249-1.pep	SRT	NLEVSG	DNIVY	TYQAR	VGGREX	
a249	ART	NLETNG	NNIVY	TYQAR	VGGREX	
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 975>:

g250.seq

```

1  atgacgcaca cagcctctcc acgtgatgaa ttcatacgcg gcataaaaga
51  aagttcgccc atgctgattg ggcttttgcc ttgggcattg atactcggta
101 tgcagggcgg gcaaaaaggt atgggccggc tggaaatgct gctgatgacg
151 gggatgaact ttgccggcgg ctccgaattt gccacggtca acctgtgggc
201 ggaacctctg ccgatactgc ttatcgccac cataaccttt atgattaatt
251 cgcggcatat cctgatgggg ggcggcgctt gccacgcaca tgaaagaaat
301 accgctgaaa aaagccgcgc ccgcgctgtt ttttatgtgt ga
  
```

This corresponds to the amino acid sequence <SEQ ID 976; ORF 250.ng>:

g250.pep

```

1  MHTASPRDE FIRGIKESSP MLIGLLPWAL ILGMQGGQKG MGRLEMLLMT
51  GMNFAGGSEF ATVNLWAEPL PILLIATITF MINSRHILMG GGACHAHERN
101 TAEKSRRARV FYV*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 977>:

m250.seq

```

1  ATGCACACCT TCCCCGCATA ACGAATTTAT ACGCGGCATC AAAGAAAGTT
51  CGCCTATGCT GATTGGGCTG CTGCCTTGGG CATTAATACT CGGTATGCAG
101 GCGGACAAA AAGGCATGAG CTGGCTGGAA ATGTTGTTGA TGACCAGTAT
151 GAACTTCGCC GCGGCTCCG AGTTTGCCAC GGTCAACCTG TGGGCSGAAC
201 CTCTGCCGAT ACTGCTTATC GCCACCGTAA CCTTTATGAT TAATTCTCGG
251 CATATCCTGA T.GGGGGCGG CGCTTGCCCC GCACCTGAAA GGAaTACCGC
301 TGAAAAAAGC CGTGCCCGCA CTGTTTTTTA TGTGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 978; ORF 250>:

m250.pep

```

1  MHTPSPHNEF IRGIKESSPM LIGLLPWALI LGMQGGQKGM SWLEMLLMTS
51  MNFAGGSEFA TVNLWAEPLP ILLIATVTFM INSRHILMGG GACPAPERNT
101 AEKSRRARTVF YV*
  
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 250 shows 91.0% identity over a 111 aa overlap with a predicted ORF (ORF 250.ng) from *N. gonorrhoeae*:

m250/g250

```

              10      20      30      40      50      59
m250.pep    MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMWLEMLLMTSMNFAGGSEF
              || ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g250         MHTASPRDEFIRGIKESSPMLIGLLPWALILGMQGGQKGMGRLEMLLMTGMNFAGGSEF
              10      20      30      40      50      60

              60      70      80      90      100     110
m250.pep    ATVNLWAEPLPILLIATVTFMINSRHILMGGGACPAPERNTAEKSRARTVIFYVX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g250         ATVNLWAEPLPILLIATITFMINSRHILMGGGACHAHERNTAEKSRARAVFYV
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 979>:

a250.seq

```

1  ATGACACACA TAAGCTCGCC CCGTAACGAA TTTATACGCG GCATCAAAGA
51 AAGTTCGCCC ATGCTGATCG GGCTTTTGCC TTGGGCATTA ATACTCGGTA
101 TGCAGGGTGG AAAAAAGGC ATGAGCTGGC TGGAAATGTT GTTGATGACC
151 GGTATGAACT TCGCCGGCGG CTCCGAGTTT GCCACGGTCA ACCTGTGGGC
201 GGAACCTCTG CCGATACTGC TTATCGCCAC CGTAACCTTT ATGATTAATT
251 CTCGGCATAT CCTGATGGGG G.CGGCACTT GCCCCGCACC TGAAAGAAAT
301 ACCGCTGAAA AAAGCCGTGC CCGCACTGTT TTTTATGTGT GA

```

This corresponds to the amino acid sequence <SEQ ID 980; ORF 250.a>:

a250.pep

```

1  MTHISSPRNE FIRGIKESSP MLIGLLPWAL ILGMQGGQKG MSWLEMLLMT
51  GMNFAGGSEF ATVNLWAEPL PILLIATVTF MINSRHILMG XGTCPAPERNTAEKSRARTV
101 TAEKSRARTV FYV*

```

m250/a250 94.6% identity in 111 aa overlap

```

              10      20      30      40      50
59
m250.pep    MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMWLEMLLMTSMNFAGGSEF
              |
              ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a250         MTHISSPRNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMWLEMLLMTGMNFAGGSEF
              10      20      30      40      50
60

              60      70      80      90      100     110
m250.pep    ATVNLWAEPLPILLIATVTFMINSRHILMGGGACPAPERNTAEKSRARTVIFYVX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a250         ATVNLWAEPLPILLIATVTFMINSRHILMGXGTCPAPERNTAEKSRARTVIFYVX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 981>:

g251.seq

```

1  atgcctgacc caatagggat tcttttcgct gccgtcgggg ttgatttttt
51  tgccgtttgtt ttgagggggc gttttcaacg aataggcgcg gttggcatgt
101 tgataataat aatcctgatg gcggagggtcg gaaccaaacc ggtcgttaacc

```

g251.pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 983>:

m251.seq

This corresponds to the amino acid sequence <SEQ ID 984; ORF 251>:

m251.pcp

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 251 shows 85.2% identity over a 243 aa overlap with a predicted ORF (ORF 251.ng) from *N. gonorrhoeae*:

m251/g251

m251.pep TVDAARRAVRISIVAQAADLPRNDISPAYGDP
IGAGFTAVGADFFAVVLRGRVRRIGAVG
g251 MPDPIGILFAAVGVDFFAVVLRGRFQRI
GAVG

40 50 60 70 80 90

10 20 30

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	100	110	120	130	140	150
m251.pep	MLIIIIILMAEIRAKAVKPEIHAQVVADFGGIEGFFECRLQEPVAFPNHAIGFVIGKRLV					
	: :	:			: :	
g251	MLIIIIILMAEVGKTIVTEVDAQVVADFGGIEGFFECRLQEPVAFPNHAVGVVGRRLV					
	40	50	60	70	80	90
	160	170	180	190	200	210
m251.pep	GTRAAIFVRTVGRVRLKMIQTALPVVREAGIIRPSVFIGIGIDIFQTVAAFGVRLV					
		:				
g251	GTRAAIFVRTVGGTVRLKMIQTALPVVREAGIIRPSVFIGIGIDIFQTVAAFGVRLV					
	100	110	120	130	140	150
	220	230	240	250	260	270
m251.pep	VKHARTVFRAHQRTVFAVGKQSAVFVARVFAVTGQRTLFFICIKNRLGQECRNRIAR					
		:	:			
g251	VKHARTVFRAHLRTVFTVGNQPAVFAARVFAVASYRS-VFFIFIKNRLGQECRNRIAR					
	160	170	180	190	200	210
	280	290	300			
m251.pep	VESLLRVFEYAADVPLILKTKTRAEQPRPAFVX					
	:	:				
g251	VESLLRAFEYAADVFPVFKTKTRAEQPRPAFVX					
	220	230	240			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 985>:

```
a251.seq
1  ATGCGTGCTG CGGTAGTCGT AGCGCAACCC CGCGCCGACA TCCGCCACCC
51  TGCCCAAACG GACATTGTCC CGAACTGCCG CGTAATAGCT TTTGCCGTTG
101 ATGCTGCGCG GCGTGCAGTC CGTATAAGTA TTGTTGCCCA AGCGGCAGAT
151 TTGCCCCGTA ACCACATTTT CCCTGCCTAT GCTGACCCAA TAGGGTTGGT
201 CCTTGCCGCC GTTGGGGTTG GCGGTTTTAG GGGGCGTTTT CGACGAATAG
251 GCGCGGTTGG CATGTTGATA ATAATAATCC TGATGGCGGA GATTAGAGTC
301 AAAGCGGTCA AAACCGAGAT TCACGCTCAG GTTGTGGCGG ATTTTGGCGG
351 TATCGAAGGA TTTTTTGAAT GCCGCCTGCA AGAGCCTGTG GCTTCCCGCG
401 TAAATCACGC GGTCGGATTT GTAGTAGGAA AACGGCTTGT CGGCACTCGG
451 GCGGCAATAT TTGTCCGAAC CGTCGGCAGA ACAGTGCCTC TGCTGAAAAT
501 GATTGTCCAA ACCGATGCCC TGCCGGTCGT AAGAGAGGCG GGCATAATCC
551 ACCCAAGTGT CTTTATCGGC ATTGGTATAG ACATATTCCA AACCCTAGCG
601 GCTTTTGGTG TGCGTCTCGT CGTAAAACAC GCCCGTACCG TATTCGCGCG
651 CCACCAGCGC ACCGTTTTCG CCGTTGGTAA ACAGACCGCC GTATTTGTGG
701 TCGCCCGCGT ATTTGCGGTT GCCTCTTATC GGTCCTGATT TTCTATTTTC
751 ATCAAAAACC GCCTTGGTCA GGAATGCCGG AACCCTCATA TCGCGCGTGT
801 CGAAAGTTTG TTGCGTGTGT TCGAGTATGC CGCCGATGTA GTGCCGTTTG
851 TTTTCAAAC GAAAACCCGG GCGGAACAGC CACGATCGGC TTTCGTATGA
```

This corresponds to the amino acid sequence <SEQ ID 986; ORF 251.a>:

```
a251.pep
1  MRAAVVVAQP RADIRPPAQT DIVPNCRVIA FAVDAARRAV RISIVAQAAD
51  LPRNHISPAY ADPIGLVLAA VGVGGFRGRF RRIGAVGMLI IILMAEIRV
101 KAVKTEIHAQ VVADFGGIEG FFECLRLQEPV AFPVNHAVGF VVGKRLVGTR
151 AAIFVRTVGR TVRLLKMIVQ TDALPVVREA GIIHPSVFIG IGIDIFQTVA
201 AFGVRLVVKH ARTVFRAHQR TVFAVGKQTA VFVVARVFAV ASYRSVFSIF
251 IKNRLGQECR NRHIARVESL LRVFEYAADV VPVFEKTKTR AEQPRSAFV*
```

m251/a251 88.5% identity in 304 aa overlap

	10	20	30	40	50	60
m251.pep	MRAAVVVAQARADIRPPAQTDIVPNCRVIAFTVDAARRAVRISIVAQAADLPRNDISPAY					
a251	MRAAVVVAQPRADIRPPAQTDIVPNCRVIAFAVDAARRAVRISIVAQAADLPRNHISPAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m251.pep	GDPIGAGFTAVGADFFAVVLRGRVRRIGAVGMLIIILMAEIRAKAVKPEIHAQVVADFG					
	:	: :				

```

a251      ADPIGLVLAAGVGVGFF----RGRFRRIGAVGMLIIILMAEIRVKAVKTEIHAQVVDFFG
              70              80              90              100             110

m251.pep      130              140              150              160              170              180
GIEGFFECLRLQEPVAFPVNHAIGFVIGKRLVGTRAAIFVRTVGRTVRLLKMI IQTDALPV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a251      GIEGFFECLRLQEPVAFPVNHAVGVVVGKRLVGTRAAIFVRTVGRTVRLLKMIVQTDALPV
              120              130              140              150              160              170

m251.pep      190              200              210              220              230              240
VREAGIIRPSVFIFIGIDIFQTVAAFGVRLVVKHARTVFRAHQRTVFAVGKQSAVFVVAR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a251      VREAGIIHPSVFIFIGIDIFQTVAAFGVRLVVKHARTVFRAHQRTVFAVGKQTAVFVVAR
              180              190              200              210              220              230

m251.pep      250              260              270              280              290              300
VFAVTGQRTLFFICIKNRLGQECNRNRIARVESLLRVFEYAADVVPILIKTKTRAEQPR
||||:|:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a251      VFAVASYSR-VFSIFIKNRLGQECNRNRIARVESLLRVFEYAADVVPFVKTKTRAEQPR
              240              250              260              270              280              290

m251.pep      PAFVX
              ||||
a251      SAFVX
              300

```

g253.seq

This corresponds to the amino acid sequence <SEQ ID 988; ORF 253.ng>:

g253 . pep

1	MIDRDRMLRD	TLERVVAGSF	WLWVVVASMM	FTAGFSGTYL	LMDNQGLNFF
51	<u>LVLAGVLGMN</u>	<u>TLMLAVLAT</u>	LFLRVKGRF	FSSPATWFRG	KGPVNQAVLR
101	<u>LYADQWRQPS</u>	<u>VRWKIGATAH</u>	<u>SLWLCTLLGM</u>	<u>LVSVLLLLLV</u>	ROYTFNWEST
151	LLSNAASVRA	VELLAWLPKS	LGFPVPDARA	VIEGRLNGNI	ADARAWSGLL
201	<u>VGSIVCYGIL</u>	<u>PRLLAWVCK</u>	ILLKTSENGL	DLEKTYQYQAV	IRRWQNKITD
251	<u>ADTRRETVSA</u>	<u>VSPKIVLNDL</u>	<u>PKWALMLETE</u>	<u>WDQGWQFEGR</u>	<u>LAQEWLDKGV</u>

301 AANREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRQIV RLSEAAQGGGA
 351 VVQLLAEQGL SDDLSEKLEH WRNALTECGA AWLEPDRVAQ EGRLKDQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 989>:

m253.seq
 1 ATGATTGACA GGAACCGTAT GCTGCGGGAG ACGTTGGAAC GTGTGCGTGC
 51 GGGGTCGTTC TGGTTGTGGG TGGTGGCGGC GACGTTTGCA TTTTTCACCG
 101 GTTTTTCAGT CACTTATCTT CTAATGGACA ATCAGGGTCT GAATTTCTTT
 151 TTGGTTTTGG CGGGCGTGTT GGGCATGAAT ACGCTGATGC TGGCAGTATG
 201 GTTGGCAATG TTGTTCCTGC GTGTGAAAGT GGGGCGTTTT TTCAGCAGTC
 251 CGGCGACGTG GTTTCGGGGC AAAGACCCTG TAAATCAGGC GGTGTTGCGG
 301 CTGTATGCGG ACGAGTGGCG GCAACCTTCG GTACGTTGGA AAATAGGCGC
 351 AACGTCGCAC AGCCTGTGGC TCTGCACGCT GCTCGGAATG CTGGTGTCCG
 401 TATTGTTGCT GCTTTTGGTG CGGCAATATA CGTTCAACTG GGAAAGCACG
 451 CTGTTGAGCA ATGCCGCTTC GGTACGCGCG GTGGAAATGT TGGCATGGCT
 501 GCCGTCGAAA CTCGGTTTCC CTGTCCCCGA TGCGCGGGCG GTCATCGAAG
 551 GCCGTCTGAA CGGCAATATT GCCGATGCGC GGGCTTGGTC GGGGCTGCTG
 601 GTCGGCAGTA TCGCCTGCTA CGGCATCCTG CCGCGCCTGC TGGCTTGGGT
 651 AGTGTGTAAG ATCCTTTTGA AAACAAGCGA AAACGGATTG GATTTCGAAA
 701 AGCCCTATTA TCAGGCGGTC ATCCGCGCGT GGCAGAACAA AATCACCAGT
 751 GCGGATACGC GTCGGGAAAC CGTGTCCGCC GTTTCACCGA AAATCATCTT
 801 GAACGATGCG CCGAAATGGG CGGTATGCTT GGAGACCGAG TGGCAGGACC
 851 GCGAATGGTT CGAGGGCAGG CTGGCGCAGG AATGGCTGGA TAAGGGCGTT
 901 GCCACCAATC GGAACAGGTG TGCCGCGCTG GAGACAGAGC TGAAGCAGAA
 951 ACCGGCGCAA CTGCTTATCG GCGTGCAGCG CCAAACCTGT CCGGACCGCG
 1001 GCGTGTTCGC GCAGATTGTC CGACTCTCGG AAGCGGCGCA GGGCGGCGCG
 1051 GTGGTGCAGC TTTTGGCGGA ACAGGGGCTT TCAGACGACC TTTCGGAAAA
 1101 GCTGGAACAT TGGCGTAACG CGCTGGCCGA ATGCGGCGCG GCGTGGCTTG
 1151 AGCCTGACAG GCGGCGCAG GAAGGGCGTT TGAAAGACCA ATAA

This corresponds to the amino acid sequence <SEQ ID 990; ORF 253>:

m253.pep
 1 MIDRNRMLRE TLERVRAGSF WLWVVAATFA FFTGFSVTYL LMDNQGLNFF
 51 LVLAVGLGMN TLMLAVWLAM LFLRVKVGFR FSSPATWFRG KDPVNQAVLR
 101 LYADEWRQPS VRWKIGATSH SLWLCTLLGM LVSLLLLLLV RQYTFNWEST
 151 LLSNAASVRA VEWLAWLPSK LGFPVPDARA VIEGRLNGNI ADARAWSGLL
 201 VGSIAACYGIL PRLLAUVVCK ILLKTSENGL DLEKPYQAV IRRWQNKITD
 251 ADTRRETQSA VSPKILNDA PKWAVMLETE WQDGEWFEGR LAQEWLDKGV
 301 ATNREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRQIV RLSEAAQGGGA
 351 VVQLLAEQGL SDDLSEKLEH WRNALAECCA AWLEPDRAAQ EGRLKDQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 253 shows 94.7% identity over a 397 aa overlap with a predicted ORF (ORF 253.ng) from *N. gonorrhoeae*:

m253/g253

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLEVRAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAVGLGMN					
	: : : : :					
g253	MIDRDRMLRDTLEVRAGSFWLWVVASMMFTAGFSGTYLLMDNQGLNFFLVLAVGLGMN					
	10	20	30	40	50	60
m253.pep	TLMLAVWLAMFLRVKVGRRFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
g253	TLMLAVWLATLFLRVKVGRRFSSPATWFRGKGPVNQAVLRRLYADQWRQPSVRWKIGATAH					
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMFLRVKVGRRFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
g253	TLMLAVWLATLFLRVKVGRRFSSPATWFRGKGPVNQAVLRRLYADQWRQPSVRWKIGATAH					
	70	80	90	100	110	120
m253.pep	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
g253	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
g253	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m253 . pep	VIEGRLNGNIADARAWSGLLVGSIA CYGILPRLLAWVVKILLKTS ENGLDLEKPYQAV					
	: : : : :					
g253	VIEGRLNGNIADARAWSGLLVGSIVCYGILPRLLAWVVKILLKTS ENGLDLEKTYQAV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m253 . pep	IRRWQNKITDADTRRET VSAVSPKII LNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	: : : : :					
g253	IRRWQNKITDADTRRET VSAVSPKIVLNDAPKWALMLETEWQDQGWFEGR LAQEWLDKGV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m253 . pep	ATNREQVA ALET ELKQKPAQL LIGVRAQTV PDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	: : : : : :					
g253	AANREQVA ALET ELKQKPAQL LIGVRAQTV PDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
	370	380	390			
m253 . pep	SDDLSEKLEHWRNALAE CGAAWLEPDRAAQEGRLKDQX					
	: : :					
g253	SDDLSEKLEHWRNALTE CGAAWLEPDRAVAQEGRLKDQX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 991>:

```

a253 . seq
1   ATGATCGACA GGAACCGTAT GCTGCGGGAG ACGTTGGAAC GTGTGCGTGC
51  GGGGTCGTTC TGGTTGTGGG TGGCGGCGGC GACGTTTGCG TTTTTCACCG
101 GTTTTTCAGT TACTTATCTT CTAATGGACA ATCAGGGTCT GAATTTCTTT
151 TTGGTTTGG CGGGCGTGTT GGGCATGAAT ACGCTGATGC TGGCAGTATG
201 GTTGGCAATG TTGTTCCCTG CCGTGAAAGT GGGGCGTTTT TTCAGCAGTC
251 CGGCGACGTG GTTTCGGGGC AAAGACCCTG TCAATCAGGC GGTGTTGCGG
301 CTGTATGCGG ACGAGTGGCG GCAACCTTCG GTACGTTGGA AAATAGGCGC
351 AACGTGCGAC AGCCTGTGGC TCTGCACGCT GCTCGGAATG CTGGTGTCGG
401 TATTGTTGCT GCTTTTGGTG CGGCAATATA CGTTCAACTG GGAAAGCAGC
451 CTGTTGGGCG ATTCGTTCTC GGTACGGCTG GTGGAAATGT TGGCATGGCT
501 GCCTGCGAAA CTGGGTTTTC CCGTGCTGA TGC GCGGGCGG GTCATCGAAG
551 GTCGTCTGAA CGGCAATATT GCCGATGCGC GGGCTTGGTC GGGGCTGCTG
601 GTCGCGCAGTA TCGCCTGCTA CGGCATCCTG CCGCGCCTCT TGGCTTGGGC
651 GGTATGCAAA ATCCTTTTGA AAACAAGCGA AAACGGCTTG GATTTGAAAA
701 AGCCCTATTA TCAGGCGGTC ATCCGCCGCT GGCAGAACAA AATCACCAGT
751 GCGGATACGC GTCGGGAAAC CGTGTCCGCC GTTTCGCCGA AAATCGTCTT
801 GAACGATGCG CCGAAATGGG CGGTCATGCT GGAGACCGAA TGGCAGGACG
851 GCGAATGGTT CGAGGGCAGG CTGGCGCAGG AATGGCTGGA TAAGGGCGTT
901 GCCGCCAATC GGGAACAGGT TGCCGCGCTG GAGACAGAGC TGAAGCAGAA
951 ACCGGCGCAA CTGCTTATCG GCGTGCGCGC CCAAAGTGTG CCCGACCGCG
1001 GCGTGTTGCG GCAGATCGTC CGACTTTCGG AAGCGGCGCA GGGCGGCGCG
1051 GTGGTGCAGC TTTTGGCGGA ACAGGGGCTT TCAGACGACC TTTCGGAAAA
1101 GCTGGAACAT TGGCGTAACG CGCTGACCGA ATGCGGCGCG GCGTGCTGG
1151 AACCCGACAG AGCGGCGCAG GAAGGCCGTC TGAAAACCAA CGACCGCACT
1201 TGA

```

This corresponds to the amino acid sequence <SEQ ID 992; ORF 253.a>:

```

a253 . pep
1   MIDNRMLRE TLERVRAGSF WLWVAATFA FFTGFSVTYL LMDNQGLNFF
51  LVLAVLGMN TLMLAVWLAM LFLRVKVGRF FSSPATWFRG KDPVNQAVLR
101 LYADEWRQPS VRWKIGATSH SLWLCTLLGM LVSLLLLLV ROYTFNWEST
151 LLGDSSSVRL VEMLAWLPK LGFPVPDARA VIEGRLNGNI ADARAWSGLL
201 VGSIA CYGIL PRLLAWAVCK ILLKTS ENGL DLEKPYQAV IRRWQNKITD
251 ADTRRET VSA VSPKIVL NDA PKWAVMLETE WQDGEWFEGR LAQEWLDKGV
301 AANREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRQIV RLSEAAQGGA
351 VVQLLAEQGL SDDLSEKLEH WRNALTECGA AWLEPDRAAQ EGRLKTNDR
401 *

```

m253/a253 97.2% identity in 395 aa overlap

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLERVAGSFVLWVVAATFAFFTGFSTVYLLMDNQGLNFFLVLAGVGLGMN					
	:					
a253	MIDRNRMLRETLERVAGSFVLWVVAATFAFFTGFSTVYLLMDNQGLNFFLVLAGVGLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMFLRVKVGRRFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
a253	TLMLAVWLAMFLRVKVGRRFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLSNAASVRAVELAWLPSKLGFPVPDARA					
	:					
a253	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLGDSSSVRLVEMLAWLPAKLGFPVPDARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m253.pep	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLLAWVCKILLKTSENGLDLEKPPYQAV					
	:					
a253	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLLAWAVCKILLKTSENGLDLEKPPYQAV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m253.pep	IRRWQNKITDADTRRETSAVSPKIIILNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	:					
a253	IRRWQNKITDADTRRETSAVSPKIVLNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m253.pep	ATNREQVAALETTELKQKPAQLLIGVRAQTVPDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	:					
a253	AANREQVAALETTELKQKPAQLLIGVRAQTVPDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
	370	380	390			
m253.pep	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGRLKDQX					
	:					
a253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGRLKTNDRTX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcggtttgat
51  tctggcggcg gcaggtttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgatcggg tttacggcat cagccttctt
151 ctgctctatt tgagttcctc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccgttt gactgggttt ctttgagaaa cgggcccggc
301 tggacggtat tttcactgtc ctggctgctg gcggctgcag gaatcgaca
351 agaactcacc atcggacgga aaagcgaaaa acgtctgctg tctattgcga
401 tttatatcgt aatgggctgg atggtcttgg cggtaatgaa atccctgaca
451 gcctcactcc cgccggcagg actggcttgg ctggcggcag gcggtatgct
501 gtacagcgtc ggcatttact ggtttgtaaa cgatgaaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtattgg gcggcagcat aacccaattt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence <SEQ ID 994; ORF 254.ng>:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLMLLKT IGHGDGYRIF SVSVYGISLL

```

```

51  LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG
101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLL SIAIYIVMGW MVLAVMKSLT
151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
201 VSVYGYVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 995>:

```

m254.seq (partial)
1  .GTATCGGTTT ACGGCATCAG CCTTCTTCTG CTCTATTTGA GTTCCTGGCT
51  GTACCACGGA ATTGCAGCCG GAAAACTGAA AAGCATTTTG AAAAAACCG
101 ACCACTGCAT GATTTATGTG CTGATTGCCG GAAGCTACAC ACGGTTTGCA
151 CTGGTTTCTT TGAGAAACGG GCCGGGCTGG ACGGTATTTT CACTGTCCTG
201 GCTGCTGGCG GCTGCAGGAA TCGACAAGA ACTCACCATC GGACGGAAAA
251 GCGAAAAACG TCTGCTGTCT ATTGTGATT ATGTCGTCAT GGGTTGGATG
301 GTCTTGGCGG TAATGAAATC CCTGACAGCC TCACTCCCGT CGGCAGGACT
351 GGCTTGGCTG GCGGCAGGCG GTATGCTGTA CAGTGTCCGC ATTTACTGGT
401 TTGTAAACGA TGAAAAATC CGACACGGGC ACGGAATCTG GCATCTGTTC
451 GTATTGGGCG GCAGCATCAC CCAATTGTG AGCGTGACG GTTACGTAAT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 996; ORF 254>:

```

m254.pep (partial)
1  .VSVYGISLLL LYLSSWLYHG IAAGKLKSI KKTDHCMYI VLIAGSYTPFA
51  LVSLRNGPGW TVFSLSWLLA AAGIAQELTI GRKSEKRLLS IYIYVVMGWM
101 VLAVMKSLTA SLPSAGLAWL AAGGMLYSVG IYWFVNDEKI RHGHGIWHLF
151 VLGGSITQFV SVYGYVI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 254 shows 97.6% identity over a 167 aa overlap with a predicted ORF (ORF 254.ng) from *N. gonorrhoeae*:

m254/g254

m254 . pep				10	20	30
				VSVYGISLLL	LYLSSWLYHG	IAAGKLKSI
g254	HLSGLILAAAGL	MMLLKTIGH	GDGYRIFSV	VSVYGISLLL	LYLSSSLYHG	IAAGKLKSI
	20	30	40	50	60	70
m254 . pep		40	50	60	70	80
		KKTDHCMYI	VLIAGSYTP	FALVSLRNG	PGWTVFSL	SWLLAAAG
g254		KKTDHCMYI	VLIAGSYTP	FALVSLRNG	PGWTVFSL	SWLLAAAG
	80	90	100	110	120	130
m254 . pep		100	110	120	130	140
		IVIYVVMG	WMLAVMK	SLTASLPS	AGLAWLA	AAGGMLY
g254		IAIYIVMG	WMLAVMK	SLTASLPP	AGLAWLA	AAGGMLY
	140	150	160	170	180	190
m254 . pep		160				
		VLGGSITQ	FVSVYGY	VIX		
g254		VLGGSITQ	FVSVYGY	VIX		
		200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 997>:

```

a254 . seq
1  ATGTATACAG GCGAACGCTT CAATACTTAC AGCCATTTGA GCGGTTTGAT
51  TCTGGCGGCG GCAGGTTTGG CGCTGATGCT GCTGAAAACC ATAGGACACG
101 GGGACGGCTA CCGTATCTTC AGCGTATCGG TTTACGGCAT CAGCCTTCTT
151 CTGCTCTATT TGAGTTCCTC GCTGTACCAC GGAATTGCAG CCGGAAAAC
201 GAAAAGCATT TTGAAAAAAA CCGACCACTG CATGATTTAT GTGCTGATTG
251 CCGGAAGCTA CACACCGTTT GCACTGGTTT CTTTGAGAAA CGGCCCGGGC

```

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```

301 TGGACGGTAT TTTCACGTGCT CTGGCTGCTG GCGGCTGCAG GAATCGCACA
351 AGAACTCACC ATTGGACGGA AAAGCGAAAA ACGACTGCTG TCTATTGCGA
401 TTTATATCGT AATGGGCTGG ATGGTCTTGG CGGTAATGAA ATCCCTGACA
451 GCCTCACTCC CGCCGGCAGG ACTGGCTTGG CTGGCGGCAG GCGGTATGCT
501 GTACAGCGTC GGCATTTACT GGTTTGTAAG CGATGAAAAA ATCCGACACG
551 GGCACGGAAT CTGGCATCTG TTCGTATTGG GCGGCAGCAT CACCCAATTT
601 GTCAGCGTGT ACGGTTACGT AATCTGA

```

This corresponds to the amino acid sequence <SEQ ID 998; ORF 254.a>:

a254.pep

```

1  MYTGERFNTY SHLSGLILAA AGLALMLLKT IGHGDGYRIF SVSVYGISLL
51  LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG
101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLL SIAIYIVMGW MVLAVMKSLT
151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
201 VSVYGYVI*

```

m254/a254 97.6% identity in 167 aa overlap

30					10					20
m254.pep										
VSVYGISLLLLLYLSSWLYHGIAAGKLKSIL										
a254										
HLSGLILAAAGLALMLLKTIGHGDGYRIFSVSVYGISLLLLLYLSSSLYHGIAAGKLKSIL										
	20	30	40	50						60
70										
	40	50	60	70						80
90										
m254.pep										
KKTDHCMYIVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS										
a254										
KKTDHCMYIVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS										
	80	90	100	110						120
130										
	100	110	120	130						140
150										
m254.pep										
IVIIYVVMGWMVLAVMKSLTASLPSAGLAWLAAGGMLYSVGIYWFVNDEKIRHGHGIWHLF										
a254										
IAIYIVMGWMVLAVMKSLTASLPPAGLAWLAAGGMLYSVGIYWFVNDEKIRHGHGIWHLF										
	140	150	160	170						180
190										
		160								
m254.pep		VLGGSITQFVSVYGYVIX								
a254		VLGGSITQFVSVYGYVIX								
		200								

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 999>:

This corresponds to the amino acid sequence <SEQ ID 1000; ORF 255.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1001>:

This corresponds to the amino acid sequence <SEQ ID 1002; ORF 255>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 255 shows 88.8% identity over a 188 aa overlap with a predicted ORF (ORF 255.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHA	FDFGVD	DAHHRV	GDFG	IEAVKN	RFAQAD
	:					
g255	MVGQEALRGQFVAVFAAALRYAVKTCADFHA	FDFGVD	DAHHRV	GDFG	IEAVEN	GFAQTD
	:					
	10	20	30	40	50	60
	70	80	90	100	110	120
m255.pep	GCFDMQLRADGIQGFAH	AVHIVF	QLGNL	AMVGGK	KRILGN	VFAAFK
	:					
g255	GGFDMQFRADGIQGFAHT	VHIVFQ	FGDL	ALVGGK	KRILGN	VFAAFK
	:					
	70	80	90	100	110	120
	130	140	150	160	170	180
m255.pep	FRAEFFFQ	PPFNGS	GSNAGG	GFTGG	APAAAA	AVVARA
	:					
g255	FRAEFFFQ	PPFNGS	GGNAGC	GFAGGT	PAAPV	VARTV
	:					

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	130	140	150	160	170	180
	189					
m255.pep	AALVGIADX					
	:					
g255	AALVGVADX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1003>:

```
a255.seq
1  GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCCG TGTTGCTGCG
51  CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCAC GCCTTTGACG
101 GCGTTGATGC CCATCATGGC GTAGGCGATT TCGGCATCGA GGCGGTCGAA
151 TACGGGTTTCG CCCAAGCCGA CGGGACGTT GGCGGCTTCA ATATGCAGCT
201 TCGCGCCGAC GGAATCCAAG GATTGCGCA CGCTGTCCAT ATAGTTTTC
251 AGCTCGGCAA TTTGGCTATG GTTGGCGGCA AAAAAAGGAT TTTGGGAAAT
301 GTGTTGCGAG CCTTCAAACC GGATTTCTTT TCGCCGACT TGGGTAACGT
351 AGGCGGTGAT TTCCGTGCCG AATTTTCTT TCAACCATT TTTGGCAACG
401 GCTCCGGCGG CAACGCGGGC GCGGTTTCG CGGGCGGAAC TCCTGCCGCC
451 GCCCCGGTAG TCGCGCGTGC CGTATTTGTG CCAATAGGTA TAGTCGGCGT
501 GGCCGGGGCG GAAGCTGGTG GCGATGTTGC CGTAGTCTTT GCTGCGCTGG
551 TCGGTATTGC GGATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1004; ORF 255.a>:

```
a255.pep
1  VVGQEALRGE FVAVFAAALR YAVKTCADFH AFDGVDAAHG VGDFGIEAVE
51  YGFAQADGDV GGFNMQLRAD GIQGFHAVH IVFQLGNLAM VGGKKRILGN
101 VFAAFKPDEF FADLGNVGGD FRAEFFFQPF FGNGSGGNAG GGFAGGTPAA
151 APVVARAVFV PIGIVGVAGA EAGGDVAVVF AALVGIAD*
```

m255/a255 93.1% identity in 188 aa overlap

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDFGIEAVKNRFAQADRD					
	:					
a255	VVGQEALRGEFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDFGIEAVEYGFAQADGDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m255.pep	GCFDMLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDEFADLGNVGGD					
	: : : : : : : : : : :					
a255	GGFNMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDEFADLGNVGGD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m255.pep	FRAEFFFQPFNGSGSNAGGGFTGGAPAAA VVARAVFVPIGIVGVAGAEAGGDVAVVF					
	: : : : : : : : : :					
a255	FRAEFFFQPFNGSGSNAGGGFAGGTPAAAPVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	130	140	150	160	170	180
	189					
m255.pep	AALVGIADX					
a255	AALVGIADX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1005>:

```
g256.seq
1  atgctcgcgg tacgcaatcg gggttggcac ggcgcagtcg tccatttcg
51  cagctcgcgc ggcgtagcga acaccgccc ggtgttctac cacttgggtg
101 ataccgccga aatcgccttt gctttggaca cgctcaccgc gcgttaccgt
151 gaaatatacg ccgtcggcgt atcgctgggc ggcaacgcgc cggcaaaata
201 tttgggcgaa cagggcaaaa aggcattgcc gcacgcctcg gccgcggtat
251 ccgccccgtg tgatgcagag gcggcaggca gccgcttcga cagcggcatc
301 acgcggctgc tctacacgcg ctacttcctc cgcacactga taccctaaagc
```

```

351 acgttcgctc caaggttttc agacggcatt tgccgcaggg tgcaaaacac
401 tgggcgagtt tgacgaccgt ttcaccgcac cgctgcacgg ctttgccgac
451 cggcacgact actaccgcca aacttcctgc aaaccgctgc tcaaacacgt
501 tgccaaaccg ctgctcctgc tcaatgccgc caacgacccc ttctgcegc
551 ccgaagccct gccccgtgca gacgaagcgt ccgaagccgt taccctgttc
601 caacctgcac acggcgggca cgcgggcttt gtcagcagca ccggcggcag
651 gctgcacctg caatggctgc cgcagaccgt cctgtcctat tttgacagct
701 tccgcacaaa caggcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1006; ORF 256.ng>:

g256.pep

```

1 MLAVNRGWH GAVVHFRSCG GVANTAPVIFY HLGDIAEIAF ALDTLTARYR
51 EIYAVGVSLG GNAPAKYLGE QGKKALPHAS AAVSAPVDAE AAGSRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLLNAANDP FLPPEALPRA DEASEAVTLF
201 QPAHGGHAGF VSSTGGRHLH QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1007>:

m256.seq

```

1 ATGCTTGCGG TACGCGATCG GGGTTGGCAC GCGTAGTCG TCCATTTCGG
51 CAGCTGCGGC GGCATTGCCA ACACCGCTCC GGTGTTCTAC CA.CTtGGCG
101 ATACCGCCGA AATCGCCTTT ACTTTGGACA CGTTCGCCGC GCGTTACCGT
151 GAAAtATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGGCAAAA AGGCATTGCC GCAAGCCGCT GCCGTCATCT
251 CCGCCCCCGT CGATGCAGAG GCGGCAGGCA GACGCTTCGA CAGCGGCATC
301 ACGCGGCTGC TCTACACGCG CTAATTCCTC CGCACCCTGA TACCCAAAGC
351 AAAATCGCTC CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGC TTCACCGCAC CGCTGCACGG CTTTGCCGAC
451 CGGCACGACT ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCCCT GCCCGCGCA GACGAAGTAT CCGAAGCCGT TACCCTGTTT
601 CAGCCGGCAT ATGGTGGTCA TGTCGGCTTT GTCAGCAGCA CCGGCGGCAG
651 GCTGCACCTG CAATGGCTGC CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1008; ORF 256>:

m256.pep

```

1 MLAVRDRGWH GVVVHFRSCG GIANAPVIFY XLGDIAEIAF TLDTFAARYR
51 EIYAVGVSLG GNALAKYLGE QGKKALPQAA AVISAPVDAE AAGRFRDSGI
101 TRLLYTRYFL RTLIPKAKSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPAYGGHGVF VSSTGGRHLH QWLPQTVLSY FDSFRTNRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 256 shows 92.9% identity over a 239 aa overlap with a predicted ORF (ORF 256.ng) from *N. gonorrhoeae*:

m256/g256

	10	20	30	40	50	60
m256.pep	MLAVRDRGWHGVVHFRSCGGIANAPVIFYHLGDIAEIAFTLDTFAARYREIYAVGVSLG					
	: : : : : : : : :					
g256	MLAVNRGWHGAVVHFRSCGGVANTAPVIFYHLGDIAEIAFALDTLTARYREIYAVGVSLG					
	10	20	30	40	50	60
m256.pep	GNALAKYLGEQGKKALPQAAVISAPVDAEAAAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
	: : : : : : : :					
g256	GNAPAKYLGEQGKKALPHASAAVSAPVDAEAAAGSRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHYYRQTSCPKLLKHVAKPLLLLNAVNDP					
	: : : : : : : : :					
g256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHYYRQTSCPKLLKHVAKPLLLLNAANDP					
	130	140	150	160	170	180

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	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
g256	FLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

```
a256.seq
1  ATGCTCGCGG TACGCGATCG GGGTTGGAAC GCGTAGTCG TCCATTTCCG
51  CAGCTGCGGC GGCCTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGCG
101 ATACCGCCGA AATTGCCTTT ACTTTGGACA CGCTCGCCGC GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGGCGAAA ACGCGTGCC GCAAGCCGCC GCCGTCATCT
251 CCGCACCCGT CGATGCAGAG GCGGCAGGCA ACCGCTTCGA CAGCGGCATC
301 ACACGGCTGC TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC
351 ACGGTCGCTC CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAT
451 CGGCACGACT ACTACGCCA AACTTCCTGC AAACCGCTGC TCAACACCGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCGCT GCCCGCGCA GACGAAGTGT CCGAAGCCGT TACCCTGTTC
601 CAGCCGACAC ACGGTGGTCA TGTCGGCTTT GTCGGCAGCA CCGCGGCAG
651 GCTGCACCTG CAATGGTTGC CGCAGACCGT CCTGTCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

```
a256.pep
1  MLAVRDRGWN GVVVHFRSCG GVANTAPVFY HLGDTAEIAF TLDTLAARYR
51  EIYAVGVSLG GNALAKYLGE QGENALPQAA AVISAPVDAE AAGNRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPTHGGHVGF VGSTGGRLHL QWLPQTVLSY FDSFRTNRR*
```

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256.pep	MLAVRDRGWHGVVVHFRSCGGIANTAPVFYXLDGTAEIAFTLDTFAARYREIYAVGVSLG					
	: : : : :					
a256	MLAVRDRGWNQVVVHFRSCGGVANTAPVFYHLGDTAEIAFTLDTLAARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQGGKALPQAAVISAPVDAEAAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
	: : : : :					
a256	GNALAKYLGEQGENALPQAAVISAPVDAEAAGNRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSCKPLLKHVAKPLLLLNAVNDP					
	: : : : :					
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSCKPLLKHVAKPLLLLNAVNDP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVGFVGSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

```
g256-1.seq
1  ATGATTTTGA CACCGCCGGA CAGCCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAT TCCTGCAACA CCGCGACCC GCATACCGCC
```

```

101 GCGAGATGCT TCCCGACAGC ACGGGTAAAA CAAAACCGC CTACGACTTT
151 TCAGCAGGCG GCATTTCGCC CGATGCGCCG CTGGTCGTGC TGTTTCACGG
201 TTTGGAAGGA AGCAGCCGCA GCCATTACGC GGTGGAAGTG ATGCTCGCGG
251 TACGCAATCG GGGTTGGCAC GCGCAGTCG TCCATTTCGG CAGCTGCGGC
301 GCGGTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGTG ATACCGCCGA
351 AATCGCCTTT GCTTTGGACA CGCTCACC GC GTTACCGT GAAATATACG
401 CCGTCGGCGT ATCGCTGGGC GGCAACGCGC CGGCAAAATA TTTGGGCGAA
451 CAGGCAAAAA AGGCATTGCC GCACGCCTCG GCCGCCGTAT CCGCCCCCGT
501 TGATGCAGAG GCGGCAGGCA GCCGCTTCGA CAGCGGCATC ACGCGGCTGC
551 TCTACACGCG CTA CTTCCTC CGCACACTGA TACCCAAAGC ACGTTCGCTC
601 CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC TGGGCGAGTT
651 TGACGACCGT TTCACGCGAC CGCTGCACGG CTTTGCCGAC CGGCACGACT
701 ACTACGCGCA AACTTCCTGC AAACCGCTGC TCAAACACGT TGCCAAACCG
751 CTGCTCCTGC TCAATGCCGC CAACGACCCC TTCTTGCCGC CCGAAGCCCT
801 GKKKALPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLI PKARSL
851 ACGGCGGGCA CGCCGGCTTT GTGAGCAGCA CCGGCGGCAG GCTGCACCTG
901 CAATGGCTGC CGCAGACCGT CCTGTCCTAT TTTGACAGCT TCCGCACAAA
951 CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1012; ORF 256-1.ng>:

g256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQHPAP AYRREMLPDS TGKTKTAYDF
51 SAGGISPDAP LVVLFHGLEG SSRSHYAVEL MLAVNRGWH GAVVHFRSCG
101 GVANTAPVYF HLGDTAEIAF ALDTLTARYR EIYAVGVSLG GNAPAKYLGE
151 QGKKALPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLI PKARSL
201 QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD RHDYYRQTSC KPLLKHVAKP
251 LLLLNAAANDP FLPEALPRA DEASEAVTLF QPAHGHHAGF VSSTGGRLLHL
301 QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1013>:

m256-1.seq

```

1 ATGATTTTAA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51 CGACACGATT GCCGCCAAAT TCCTGCAACG CCCCGCGCCC GCATACCGCC
101 GAGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAAGTCGC CTACGACTTT
151 TCAGACGGCA TTTCGCCCGA TCGCGCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAAGGAAGC AGCCGCAGCC ATTACGCGGT CGAAGTATGAT CTTGCGGTAC
251 GCGATCGGGG TTGGCACGGC GTAGTCGTCC ATTTCCGCAG CTGCGGCGGC
301 ATGCGCAACA CCGCTCCGGT GTTCTACCAC TTGGGCGATA CCGCCGAAAT
351 CGCCTTTACT TTGGACACGT TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAATATTTT GGGCGAACAG
451 GGCAAAAAGG CATTGCCGCA AGCCGCTGCC GTCATCTCCG CCCCCTCGCA
501 TGCAGAGGCG GCAGGCAGAC GCTTCGACAG CGGCATCAGC CGGCTGCTCT
551 ACACGCGCTA CTTCCTCCGC ACCCTGATAC CCAAAGCAAA ATCGCTCCAA
601 GGTTTTTCAGA CGGCATTTCG CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGCTTC ACCGCACCGC TGCACGGCTT TGCCGACCGG CACGACTACT
701 ATGCGCAAAC TTCTTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCCGCCCG AAGCCCTGCC
801 CCGCGCAGAC GAAGTATCCG AAGCCGTAC CCTGTCCAG CCGGCATATG
851 GTGGTCATGT CGGCTTTGTC AGCAGACCGC GCGGCAAGCT GCACCTGCAA
901 TGGCTGCCGC AGACCGTCCT GTCCTATTTT GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1014; ORF 256-1>:

m256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQRPAP AYRRELLPDS TGKTKVAYDF
51 SDGISPDAPL VVLFHGLEGS SRSHYAVELM LAVRDRGWHG VVVHFRSCG
101 IANTAPVYFH LGDTAEIAFT LDTFAARYRE IYAVGVSLGG NALAKYLGEQ
151 GKKALPQAAA VISAPVDAEA AGRRFDSGIT RLLYTRYFLR TLIPKAKSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFADR HDYYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PAYGGHVG FV SSTGGRLLHLQ
301 WLPQTVLSYF DSFRTNRR*

```

m256-1/g256-1 93.1% identity in 319 aa overlap

```

          10      20      30      40      50      59
m256-1.pep MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFS-DGISPDAP
          |||:|||||:|||||:|||||:|||||:|||||
g256-1      MILTPPDTPFFLRNGNADTIAAKFLQHPAPAYRREMLPDSTGKTKTAYDFSAGGISPDAP
          10      20      30      40      50      60

          60      70      80      90     100     110     119
m256-1.pep LVVLFHGLEGSSSRSHYAVELMLAVRDRGWHGVVHFRSCGGIANTAPVYFHLGDTAEIAF

```

591

```

|||||
g256-1  LVVLFHGLEGSSRSHYAVELMLAVRNRGWHGAVVHFRSCGGVANTAPVIFYHLGDTAEIAF
          70      80      90      100     110     120

120      130      140      150      160      170      179
m256-1.pep  TLDTFAARYREIYAVGVSLGGNALAKYLGEQKKALPQAAAVISAPVDAEAGRRFDSGI
          :|||:|||||
g256-1  ALDTLTARYREIYAVGVSLGGNAPAKYLGEQKKALPHASAAVSAPVDAEAGSRFDSGI
          130      140      150      160      170      180

180      190      200      210      220      230      239
m256-1.pep  TRLLYTRYFLRTLIPKAKSLQGFQTAFAGCKTLGEFDDRFAPLHGFADRHDYRQTSC
          |||||
g256-1  TRLLYTRYFLRTLIPKARSLQGFQTAFAGCKTLGEFDDRFAPLHGFADRHDYRQTSC
          190      200      210      220      230      240

240      250      260      270      280      290      299
m256-1.pep  KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHVGVFVSSTGGRLHL
          |||||
g256-1  KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAHGGHAGFVSSTGGRLHL
          250      260      270      280      290      300

300      310      319
m256-1.pep  QWLPQTVLSYFDSFRTNRRX
          |||||
g256-1  QWLPQTVLSYFDSFRTNRRX
          310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1015>:

a256-1.seq

```

1  ATGATTTTGA  CACCGCCGGA  CACACCCTTT  TTCCTCCGCA  ACGGCAATGC
51  CGACACGATT  GCCGCCAAAT  TCCTGCAACG  CTCCGCACCT  GCATACCGCC
101  GCGAGCTGCT  TCCCGACAGC  ACGGGTAAAA  CCAAACCGC  CTACGACTTT
151  TCAGACGGCA  TTTCGCCCGA  TCGCGCGCTG  GTCGTGCTGT  TTCACGGTTT
201  GGAGGGCGGC  AGTGGCAGCC  ATTACGCGGT  CGAACTGATG  CTCGCGGTAC
251  GCGATCGGGG  TTGGAACGGC  GTAGTCGTCC  ATTTCCGCAG  CTGCGCGCGC
301  GTAGCGAACA  CCGCCCCGGT  GTTCTACCAC  TTGGGCGATA  CCGCCGAAAT
351  TGCCTTTACT  TTGGACACGC  TCGCCGCGCG  TTACCGTGAA  ATATACGCCG
401  TCGGCGTATC  GCTGGGCGGC  AACGCGCTGG  CAAAATATTT  GGGCGAACAG
451  GCGGAAAACG  CGCTGCCGCA  AGCCGCGGCC  GTCATCTCCG  CACCCGTCGA
501  TGCAGAGGCG  GCAGGCAACC  GCTTCGACAG  CGGCATCACA  CGGCTGCTCT
551  ACACGCGCTA  CTTCTCCGCG  ACACGATAC  CCAAAGCACG  GTCGCTCCAA
601  GGTTTTCAGA  CGGCATTTGC  CGCAGGGTGC  AAAACACTGG  GCGAGTTTGA
651  CGACCGTTTC  ACCGCACCGC  TGCACGGCTT  TGCCGATCGG  CACGACTACT
701  ACCGCCAAAC  TTCCTGCAAA  CCGCTGCTCA  AACACGTTGC  CAAACCGCTG
751  CTCCTGCTCA  ATGCCGTCAA  CGACCCTTTC  CTGCCGCCCG  AAGCGCTGCC
801  CCGCGCAGAC  GAAGTGTCGG  AAGCCGTTAC  CCTGTTCCAG  CCGACACACG
851  GTGGTCATGT  CGGCTTTGTC  GGCAGCACCG  GCGGCAGGCT  GCACCTGCAA
901  TGGTTGCCGC  AGACCGTCCT  GTCCTATTTC  GACAGCTTCC  GCACAAACAG
951  GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1016; ORF 256-1.a>:

a256-1.pep

```

1  MILTPPDTPF  FLRNGNADTI  AAKFLQRSAP  AYRRELLPDS  TGKTKTAYDF
51  SDGISPDAPL  VVLFHGLEGG  SGSHYAVELM  LAVDRGWNG  VVHFRSCGG
101  VANTAPVFIH  LGDTAEIAFT  LDTLAARYRE  IYAVGVSLGG  NALAKYLGEQ
151  GENALPQAAA  VISAPVDAEA  AGNRFDSGIT  RLLYTRYFLR  TLIPKARSLQ
201  GFQTAFAGC  KTLGEFDDRF  TAPLHGFADR  HDYRQTSCCK  PLLKHVAKPL
251  LLLNAVNDPF  LPPEALPRAD  EVSEAVTLFQ  PTHGGHVGFV  GSTGGRLLHQ
301  WLPQTVLSYF  DSFRTNRR*

```

a256-1/m256-1 95.6% identity in 318 aa overlap

```

          10      20      30      40      50      60
a256-1.pep  MILTPPDTPFFLRNGNADTIAAKFLQRSAPAYRRELLPDSTGKTKTAYDFSDGISPDAPL
          |||||
m256-1  MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFSDGISPDAPL
          10      20      30      40      50      60

          70      80      90      100     110     120
a256-1.pep  VVLFHGLEGGSGSHYAVELMLAVDRGWNGVVHFRSCGGVANTAPVIFYHLGDTAEIAFT
          |||||
m256-1  VVLFHGLEGSSRSHYAVELMLAVDRGWNGVVHFRSCGGIANAPVIFYHLGDTAEIAFT

```

592

	70	80	90	100	110	120
a256-1.pep	130	140	150	160	170	180
	LDTLAARYREIYAVGVSLGGNALAKYLGEQGENALPQAAAVISAPVDAEAAGNRFDSGIT					
m256-1	130	140	150	160	170	180
	LDTFAARYREIYAVGVSLGGNALAKYLGEQKKALPQAAAVISAPVDAEAAGRRFDSGIT					
a256-1.pep	190	200	210	220	230	240
	RLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHYYRQTSCK					
m256-1	190	200	210	220	230	240
	RLLYTRYFLRTLIPKAKSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHYYRQTSCK					
a256-1.pep	250	260	270	280	290	300
	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPTHGGHVGFGVSTGGRLHLQ					
m256-1	250	260	270	280	290	300
	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHVGFGVSTGGRLHLQ					
a256-1.pep	310	319				
	WLPQTVLSYFDSFRTNRRX					
m256-1	310					
	WLPQTVLSYFDSFRTNRRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1017>:

g257.seq

```

1  atgggcaggc atttcgggcg cagacgtttt ctgacggctg ccgccgttgc
51  tgtggccggt gcggcggttt cttttttgcc gaatcctttt gccgccggcg
101 gcgaaaaacg caacatggat aaaaaacgcg atgaaaatgt gtttttctgg
151 aaagggtgtcg cgctgggttc cggcgcgagg ctgcgccctgt tcggcggtgga
201 cgacagacag gcggcggtatt tggccaataa ggttttggcg gaagtggcgc
251 gtttggaaaa aatgttcagc ctttaccgtg aagacagcct gatcagccgt
301 ctgaaccgcg acggttatct gacttcgcct ccggcggtatt ttttggaaat
351 gttgagcctg gccgcgatat tcacgcgctg a

```

This corresponds to the amino acid sequence <SEQ ID 1018; ORF 257.ng>:

g257.pep

```

1  MGRHFGRRRF LTAAAVAVAG AAVSFLPNPF AAGGEKRNMD KKRDENVFFW
51  KGVALGSGAE LRLFGVDDRQ AADLVNKLVA EVARLEKMFS LYREDSLISR
101 LNRDGYLTSP PADFLELLSL AAIIFTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1019>:

m257.seq

```

1  ATGGGCAGGC ATTTCGGGCG .CAGCGTTT CTGACGGTTG CCGCCGTTGC
51  GGCGGGGAC. GCGGCGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAACGGGGAT GAAAAACGCA ATGAAAATGT GTTTTCTTGG
151 AAAGGTGTCT CACTGGGTTC CGGTGCGGAC CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTTGGCG GAAGTGGCGC
251 GTTTGGAAAA ATTGTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGC
301 CTGAACAGGG ACGGTTATCT GACTTCGCCG TCGGCGGATT TTTTGGAACT
351 GKTGAGCCTG GCCGCGATAT TCACGCKCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1020; ORF 257>:

m257.pep

```

1  MGRHFGXQRF LTVAAVAAGX AAVSFLPNPF AADDEKRNKD EKRNEVFFW
51  KGVALGSGAX LRLFGVDDRR AADLVNKLVA EVARLEKLFS LYREDSLISR
101 LNRDGYLTSP SADFLELXSL AAIIFTX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 257 shows 88.0% identity over a 125 aa overlap with a predicted ORF (ORF 257.ng) from *N. gonorrhoeae*:

m257/g257

10

20

30

40

50

60

593

```

m257.pep      MGRHFGRQRF LTVAAVAAGTA AVSFLPNPFAADDEKRN GDEKRNEN VFFWKGV ALGSGAD
               |||||:||||:||||:| ||||| ||||| |:|:||||| |||||:|
g257          MGRHFGRRRR FLTAAAVAVAGA AVSFLPNPFAAGGEKRN MDKKRDEN VFFWKGV ALGSGAE
               10      20      30      40      50      60

               70      80      90      100     110     120
m257.pep      LRLFGVDDRR AADLVN KVLAEVAR LEKLFSLY REDSLIS RLNRDGYL TSPSAD FLELXSL
               |||||:||||:||||:| ||||| ||||| |:|:||||| |||||:|
g257          LRLFGVDDR QAADLVN KVLAEVAR LEKMFS LYREDS LISRLNR DGYLTSP PADFLE LLSL
               70      80      90      100     110     120

m257.pep      AAIFTXX
               |||||
g257          AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

```

a257.seq
  1  ATGGGCAGGC ATTTCTGGGCG CAGGCGTTTT TTGACAGTTG CCGCCGTTGC
 51  GGCGGCGGGC GCGGCGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101  ATGAAAAACG CAATAAAGAT GAAAAACGCA ATGAAAATGT GTTTTTCTGG
151  AAAGGTGTCT CACTGGGTTC CGGTGCGGAG CTCCGTCTGT TCGGTGTGGA
201  CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTTGGCG GAAGTGGCGC
251  GTTTGGAAAA AATGTTT CAGC CTTTACCGTG AAGACAGCCT GATCAGCCGT
301  CTGAACCGTG ACGGTTATTT GACTTCGCCG CCGGCGGATT TTTTGGAACT
351  GTTGAGCCTG GCCGTGATAT TCACGCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

```

a257.pep
  1  MGRHFGRRRF LTVAAVAAG AAVSFLPNPF AADDEKRNKD EKRNEN VFFW
 51  KGV ALGSGAE LRLFGVDDRR AADLVN KVLAEVAR LEKMFS LYREDS LISR
101  LNRDGYLTSP PADFLE LLSL AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

               10      20      30      40      50
60
m257.pep      MGRHFGXQRF LTVAAVAAGXAAVSFLPNPFAADDEKRN GDEKRNEN VFFWKGV ALGSGAX
               ||||| :|||||: |||||
|||||
a257          MGRHFGRRRR FLTAAVAAAGAAVSFLPNPFAADDEKRN KDEKRNEN VFFWKGV ALGSGAE
               10      20      30      40      50
60
               70      80      90      100     110
120
m257.pep      LRLFGVDDRR AADLVN KVLAEVAR LEKLFSLY REDSLIS RLNRDGYL TSPSAD FLELXSL
               |||||:||||:||||:| ||||| ||||| |:|:||||| |||||:|
||
a257          LRLFGVDDRR AADLVN KVLAEVAR LEKMFS LYREDS LISRLNR DGYLTSP PADFLE LLSL
               70      80      90      100     110
120

m257.pep      AAIFTXX
               |:|
a257          AVIFTRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1023>:

g258.seq

```

1   atgcgcgcgt tcctaccgat cgcagccata tgcgcgcgtcg tcctgctgta
51  cggattgacg gcggcgaccg gcagcaccag ttcgctggcg gattatttct
101 ggtggatagt ctcgttcagc gcaatgctgc tgctggtggt gtccgcgcgtt
151 ttggcacggt atgtcatatt gctgttgaaa gacaggcgca acggcgtggt
201 cggttcgcag attgccaaac gcctttccgg gatgttcacg ctggtcgccg
251 tactgcccgg cttgttctcg ttcggcattt ccgcgcagtt tatcaacggc
301 acgattaatt cgtggttcgg caacgacacc cacgaagccc tcgaacgcag
351 ccttaatttg agcaagtccg cactggattt ggccgcagac aatgccgtca
401 gcaacgccgt tcccgtagag atagacctca tcggcaccgc ctccctgtcg
451 ggcaatatgg gcagtgtgct ggaacactac gccggcagcg gttttgccc
501 gcttgccctg tacaatgccg caagcgggaa aatcgaaaaa agcatcaatc
551 cgcaccaatt cgaccagccg cttcccgaca aagaacattg ggaacagatt
601 cagcagaccg gttcggttcg gagtttgaa agcataggcg gcgtattgta
651 cgcgcaggga tggttgtcgg caggtagcga caacgggcgc gattacgcgc
701 tgttcttccg ccagccgatt ccgaaaaatg tggcacagga tgccgttctg
751 attgaaaagg cgcgggcgaa atatgccgaa ttgagttaca gcaaaaaagg
801 tttgcagacc ttttttctgg taaccctgct gattgcctcg ctgctgtcga
851 tttttcttgc gctggtaatg gcaactgtatt ttgcccgcgc tttcgtcgaa
901 cccattctgt cgcttgccga gggcgcaaag gcggtggcgc aggggtgattt
951 cagccagacg cgccccgtat tgcgcaacga cgagttcgga cgtttgacca
1001 agctgttcaa ccatatgacc gagcagcttt ccatcgccaa agaagcagac
1051 gaacgcaacc gccggcgcgga ggaagccgcc cgtcactacc tcgagtgcgt
1101 gttggatggg ttgactaccg gtgtggtggt ctentacccc ctctcttgtt
1151 gccgtaccgc ggtgttttcc acttgtcatt cctcccctct ttcttatttc
1201 taa

```

This corresponds to the amino acid sequence <SEQ ID 1024; ORF 258.ng>:

g258.pep

```

1   MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVSFS AMLLLVLSAV
51  LARYVILLK DRRNGVFGSQ IAKRLSGMFT LVAVLPGLFL FGISAQFNG
101 TINSWFGNDT HEALERSLNL SKSALDLAAD NAVSNAVVPQ IDLIGTASLS
151 GNMGSVLEHY AGSGFAQLAL YNAASGKIEK SINPHQFDQP LPDKEHWEQI
201 QQTGSVRSLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPI PENVAQDAVL
251 IEKARAKYAE LSYSKKGLQT FFLVTLIAS LLSIFLALVM ALYFARFEVE
301 PILSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVDLG LTTGVVVSYP LSCCRTAVFS TCHSSPLSYF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1025>:

m258.seq

```

1   ,ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTCG TCCTGTTGTA
51  CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTCTT
101 GGTGGATTGT TCGGTTTCAGC GCAATGCTGC TGCTGGTGTT GTCCGCCGTT
151 TTGGCACGTT ATGTCATATT GCTGTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTTCGAG ATTGCCAAAC GCCTTTCTGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCGG CGTGTTCCTG TTCGGCGTTT CCGCACAGTT CATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTTG AGCAAGTCCG CATTGAATTT GGCGGCAGAC AACGCCCTCG
401 GCAACGCCGT CCCCCTGCAG ATAGACCTCA TCGGCGCGGC TTCCCTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGCGACG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAAGCT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GAAAAAATC
601 CAACGGGCGG GTTCGGTCAG GGATTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGGC TGGCTGTCGG CGGGTACGCA CAACGGGCGC GATTACGCCT
701 TGTTTTTCCG TCAGCCGGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAAAAAGG
801 TTTGCAGACC TTTTCTCTGG CAACCCTGCT GATTGCCTCG CTGCTGTGCA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCGCGC TTTCTGCGAA
901 CCCGTCTTAT CGCTTGCCGA GGGGCGGAAG GCGGTGGCGC AAGGCGATTT
951 CAGCCAGACG CGCCCCGTGT TCGGCAACGA CGAGTTCGGA CGCTTGACCA

```


1001	AGTTGTTCAA	CCACATGACC	GAGCAGCTTT	CCATCGCCAA	AGAAGCAGAC
1051	GAGCGCAACC	GCCGCGCGCA	GGAAGCCGCC	AGGCATTATC	TTGAATGCGT
1101	GTTGGAGGGG	CTGACCACGG	GCGTGGTGGT	GTTTGACGAA	CAAGGCTGTC
1151	TGAAAACsTT	CAACAAAGCG	GCGGAACAGA	TTyTGggGAT	GCCGCTTACC
1201	CCCCtGTGGG	GCAGCAGCCG	GCACGGTtGG	CACGGCGTtT	CGGCGCAGCA
1251	GTCCCTGCTT	GCCGAAGTGT	TTGCCCCAT	CGGCGCGGCG	GCAGGTACGG
1301	ACAAACCGGT	CCATGTGAAA	TATGCCGCGC	CGGACGATGC	CAAAATCCTG
1351	CTGGGCAAGG	CAACCGTCTC	GCCCCAAGAC	AACGGCAACg	CGGTGGTAAT
1401	GGTGATTGAC	GACATCACCG	TTTTGATACA	CGCGCAAAAA	GAAGCCGCGT
1451	GGGGCGAAgT	GGCGaAgCGG	CTGGCACACG	AAATCCGCAA	TCCGCTCACG
1501	CCCATCCAGC	TTTCCGCCGA	ACgGsTGGCG	TkGAAATTGG	GCGGGAAGCT
1551	GGATGAGCAG	GATGCGCAAA	TCTTGACGCG	TTCGACCGAC	ACCATCGTCA
1601	AACAGGTGGC	GGCATTGAAG	GAAATGGTCG	AAGCATTCCG	CAATTATGCG
1651	CGTTCCCTT	GCATTCAAAT	GGAAAATCAG	GATTTGAACG	CCTTAATCGG
1701	CGATGTGTTG	GCATTGTATG	AAGCCGGTCC	GTGCCGGTtT	GCGGCGGACT
1751	TGCCGGCGAA	CCGCTGA			

This corresponds to the amino acid sequence <SEQ ID 1026; ORF 258>:

m258.pcp

1	<u>MRRFLPIAAI</u>	<u>CAVVLLYGLT</u>	<u>AATGSTSSLA</u>	<u>DYFWWIVAFS</u>	<u>AMLLLVL SAV</u>
51	<u>LARYVILLLK</u>	<u>DRRDGVFGSQ</u>	<u>IAKRLSGMFT</u>	<u>LVAVLPGVFL</u>	<u>FGVSAQFING</u>
101	<u>TINSWFGNDT</u>	<u>HEALERSLNL</u>	<u>SKSALNLAAD</u>	<u>NALGNAPVQ</u>	<u>IDLTGAASLP</u>
151	<u>QDMGRVLEHY</u>	<u>AGSGFAQLAL</u>	<u>YNAASGKIEK</u>	<u>SINPHKLDQP</u>	<u>FPGKARWEKI</u>
201	<u>GRAGSVRDLE</u>	<u>SIGGVLYAQG</u>	<u>WLSAGTHNGR</u>	<u>DYALFFRQDV</u>	<u>PKGVAEDAVL</u>
251	<u>IEKARAKYAE</u>	<u>LSYSKKG LQT</u>	<u>FFLATLLIAS</u>	<u>LLSTFLALVM</u>	<u>ALYFARRFVE</u>
301	<u>PVLSLAEGAK</u>	<u>AVAQGD FSQT</u>	<u>RPVLRNDEFG</u>	<u>RLTKLFNHMT</u>	<u>EQLSIAKEAD</u>
351	<u>ERNRRREEEA</u>	<u>RHYLEC VLEG</u>	<u>LTTGVVVFDE</u>	<u>QGCLKTFNKA</u>	<u>AEQILGMP LT</u>
401	<u>PLWGSSRRHG</u>	<u>HGVSAQQSLL</u>	<u>AEVFAAIGAA</u>	<u>AGTDKPVHVK</u>	<u>YAAPDDAKIL</u>
451	<u>LGKATVLPED</u>	<u>NGNGVMVLD</u>	<u>DITVLIHAQD</u>	<u>EAANGEVAAK</u>	<u>LAHEIRNPLT</u>
501	<u>PIQLSA PERX</u>	<u>XKLGGLKDEQ</u>	<u>DAQILTRSTD</u>	<u>TIVKQVAAKL</u>	<u>EMVEAFRNYA</u>
551	<u>RSPSLKLENQ</u>	<u>DLNALIGDVL</u>	<u>ALYEAGPCR F</u>	<u>AADLPANR*</u>	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 258 shows 90.9% identity over a 386 aa overlap with a predicted ORF (ORF 258.ng) from *N. gonorrhoeae*:

m258/g258

	10	20	30	40	50	60
m258.pep	MRRFLPIAAICAVVLLYGLTAATGSTSSLADYFWWIVAFSAMPLLVLSAVLARYVILLK					
	:					
g258	MRRFLPIAAICAVVLLYGLTAATGSTSSLADYFWWIVSFSAAMPLLVLSAVLARYVILLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m258.pep	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSNL					
	:					
g258	DRRNGVFGSQIAKRLSGMFTLVAVLPGLFLFGISAQFINGTINSWFGNDTHEALERSNL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m258.pep	SKSALNLAADNALGNVPVQIDLIGAASLPGDMGRVLEHYAGSGFAQLALYNAASGKIE					
	: : :					
g258	SKSALDLAADVNAVVPVQIDLIGTASLSGNMGSVLEHYAGSGFAQLALYNAASGKIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m258.pep	SINPHKLDQPPFGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQP					
	: : : : : : :					
g258	SINPHQFDQPLPDKEHWEIQQTGVSRSLESIGGVLYAQGWLSAGTHNGRDYALFFRQPI					
	190	200	210	220	230	240

	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAELSYSKKG	LQTF	FLATLLIASLLSIF	FLALVMALYFARRFVE		
	::					
g258	PENVAQDAVLIEKARAKYAELSYSKKG	LQTF	FLVTL	LLIASLLSIF	FLALVMALYFARRFVE	
	250	260	270	280	290	300
	310	320	330	340	350	360
m258.pep	PVLSLAEGAKAVAQGD	FSQTRP	VLNRN	DEFGRLTKLF	NHMQLSIAKEADERNRRREEAA	
	:					
g258	PILSLAEGAKAVAQGD	FSQTRP	VLNRN	DEFGRLTKLF	NHMQLSIAKEADERNRRREEAA	
	310	320	330	340	350	360
	370	380	390	400	410	420
m258.pep	RHYLEC	VLEGLTTGVVVFDE	QGCLKTFNKA	AEQILG	MP	LTP
g258	RHYLEC	VDGLTTGVVVS	YPLSC	RTAV	FSTCH	SSPLSYFX
	370	380	390	400		

a258.seq

1	ATGCGCCGTT	TTCTACCGAT	CGCAGCCATA	TGCGCCGTCG	TCCTGTTGTA
51	CGGACTGACG	GCGGCAACCG	GCAGCACCAG	TTCGCTGGCG	GATTATTTCT
101	GGTGGATTGT	TGCGTTCAGC	GCAATGCTGC	TGCTGGTGTT	GTCCGCCGTT
151	TTGGCACGTT	ATGTCATATT	GCCTTTGAAA	GACAGGCGCG	ACGGCGTATT
201	CGGTTCCGAC	ATTGCCAAAC	GCCTTTCCGG	GATGTTTACG	CTGGTTGCCG
251	TACTGCCCGG	CGTGTTTCTG	TTCCGCGTTT	CCGCACAGTT	TATCAACCGC
301	ACGTGTAATT	CGTGTTTCGG	CAACGATACC	CACAGGCGCG	TTGAACGCGC
351	CCTCAATTTG	AGCAAGTCCG	CATTGAATCT	GGCGGCAGAC	AACGCCCTTG
401	GCAACGCCAT	CCCCGTGCAG	ATAGACCTCA	TCGGCGCGGC	TTCCCTGCCC
451	GGGATATG	GCAGGGTGCT	GGAACATTAC	GCCGGCAGCG	GTTTTGCCCA
501	GCTTGCCCTG	TACAATGCCG	CAAGCGGCAA	AATCGAAAAA	AGCATCAACC
551	CGCACAAGCT	CGATCAGCCG	TTTCAGGTA	AGGCGCGTTG	GGAAAAAATC
601	CAACAGGCGG	GTCGCTCAG	GGATTGGAA	AGCATAGGCG	GCGTATTGTA
651	CGCGCAGGGC	TGGCTGTCCG	CAGGTACGCA	CAACGGGCGC	GATTACGCCCT
701	TGTTTTTCCG	TCAGCCGGTT	CCCAAAGGCG	TGGCAGAGGA	TGCCGCTCTTA
751	ATCGAAAAGG	CAAGGGCGAA	ATATGCTGAG	TTGAGTTACA	GCAAAAAAGG
801	TTTGCAAGCC	TTTTTCCTGG	CAACCCTGCT	GATTGCCTCG	CTGCTGTCGA
851	TTTTTCTTGC	ACTGGTCATG	GCACTGTATT	TCGCCCCGCC	TTTCGTCGAA
901	CCCGTCCTAT	CGCTTGCCGA	GGGGGCGAAG	GCGGTGGCGC	AAGGCGATTT
951	CAGCCAGACG	GCCCCGTGT	TGCGCAACGA	CGAGTTCCGA	CGCTTGACCA
1001	AGTTGTTCAA	CCCATGACG	GAGCAGCTTT	CCATCGCCAA	AGAAGCAGAC
1051	GAGCGCAACC	GCCGGCGCGA	GGAAGCCGCC	AGACATTATC	TCGAATGCGT
1101	GTTGGAGGGG	CTGACCACGG	GCGTGGTGGT	GTTTGACGAA	CAAGGCTGTC
1151	TGAAAACCTT	CAACAAAGCG	GCGGAACAGA	TTTTGGGGAT	GCCGCTTACC
1201	CCCCTGTGGG	GCAGCAGCCG	GCACGGTTGG	CACGGCGTTT	CGGCGCAGCA
1251	GTCCCTGCTT	GCCGAAGTGT	TTGCCGCCAT	CGGCGCGGCG	GCAGGTACGG
1301	ACAAACCGGT	CCATGTGAAA	TATGCCGCGC	CGGACGATGC	CAAAATCCTG
1351	CTGGGCAAGG	CAACGTCCT	GCCCGAAGAC	AACGGCAACG	GCGTGGTAAT
1401	GGTGATTGAC	GACATCACCG	TTTTGATACA	CGCGCAAAAA	GAAGCCGCGT
1451	GGGGCGAAGT	GGCAAAACGG	CTGGCACACG	AAATCCGCAA	TCCGCTCACG
1501	CCCATCCAGC	TTTCTGCCGA	ACGGCTGGCG	TGGAAATTGG	GCGGGAAGCT
1551	GGACGAGCAG	GACGCGCAAA	TCCTGACACG	TTCGACCGAC	ACCATCATCA
1601	AACAAGTGCG	GGCATTAATA	GAAATGGTCG	AGGCATTCCG	CAATTACGCG
1651	CGTTCCCCTT	CGCTCAAATT	GGAAAATCAG	GATTTGAACG	CCTTAATCGG
1701	CGATGTGTTG	GACTTGTACG	AAGCTGGTCC	GTGCCGGTTT	GCGGCGGAAC
1751	TTGCCGGCGA	ACCGCTGATG	ATGGCGGCGG	ATACGACCGC	CATGCGCGAG
1801	GTGCTGCACA	ATATTTTCAA	AAATGCCGCC	GAAGCGGCGG	AAGAAGCCGA
1851	TGTGCCCGAA	GTCAAGGTAA	AATCGGAAGC	GGGGCAGGAC	GGACGGATTG
1901	TCCTGACAGT	TTGCGACAAC	GGCAAGGGGT	TCGGCAGGGA	AATGCTGCAC
1951	AATGCCTTCG	AGCCGTATGT	AACGGACAAA	CCGGCTGGAA	CGGGATTGGG
2001	ACTGCCCGTG	GTGAAAAAAA	TCATTGAAGA	ACACGGCGGC	CGCATCAGCC
2051	TGAGCAATCA	GATGCGGGCG	GCGCGGTGTG	TCAGAATCAT	CTTGCCAAAA
2101	ACGGTAGAAA	CTTATGCGTA	G		

This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```
a258.pep
  1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
 51  LARYVILLK  DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101  TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151  GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201  QQAGSVRDLE SIGGVLYAQQ WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251  IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301  PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351  ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401  PLWGSSRHGW HGVSAQQSLL AEVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451  LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501  PIQLSAERLA WKLGGKLDEQ DAQILTRSTD TIIKQVAALK EMVEAFRNYA
551  RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AAELAGEPLM MAADTTAMRQ
601  VLNIFKNAA  EAAEEADVPE VRVKSEAGQD GRIVLTVCDN GKGFGREMLH
651  NAFEPYVTDK PAGTGLGLPV VKKIIEEHGG RISLSNQDAG GACVRIILPK
701  TVETYA*
```

m258/a258 99.0% identity in 584 aa overlap

	10	20	30	40	50	60
m258.pep	MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVAFSAML					
a258	MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVAFSAML					
	10	20	30	40	50	60
m258.pep	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL					
a258	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL					
	70	80	90	100	110	120
m258.pep	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL					
a258	DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL					
	130	140	150	160	170	180
m258.pep	SKSALNLAADNALGNAVVPQIDLIGAASLP					
a258	SKSALNLAADNALGNAVVPQIDLIGAASLP					
	190	200	210	220	230	240
m258.pep	SINPHKLDQFPFGKARWEKIQAGSVRDLESIGGVLYAQQWLSAGTHNGRDYALFFRQPV					
a258	SINPHKLDQFPFGKARWEKIQAGSVRDLESIGGVLYAQQWLSAGTHNGRDYALFFRQPV					
	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAE					
a258	PKGVAEDAVLIEKARAKYAE					
	310	320	330	340	350	360
m258.pep	PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT					
a258	PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT					
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTTGVVVFDEQGCLKTFNKA					
a258	RHYLECVLEGLTTGVVVFDEQGCLKTFNKA					
	430	440	450	460	470	480
m258.pep	AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPED					
a258	AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPED					

598

	430	440	450	460	470	480
	490	500	510	520	530	540
m258.pep	EAAWGEVAKRLAHEIRNPLTPIQLSAERXAXKLGGKLDEQDAQILTRSTDTIVKQVAALK					
a258	EAAWGEVAKRLAHEIRNPLTPIQLSAERLAWKLGGKLDEQDAQILTRSTDTIIKQVAALK					
	490	500	510	520	530	540
	550	560	570	580	589	
m258.pep	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNI FKNAAEAAEEADVPEVRVKSEAGQDGRIVLTVCDNGKGFGREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

g259.seq

```

1  atgatgatgc acgcttctgt ccaaagtcgt ttcgcaccga tactttatgt
51  tttgattttc tttgccggtt ttttgaccgc gcaaactctgg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgtccgcatt gtccgccgtc
151 gcgctggtgt ggctggcgtg ggcgttcgtg tcggtgcgtt caaaggctaa
201 ggcagaaaag ttctaccgcg aaaaaatgat acagaacgaa agcatacacc
251 ccgtcctgca cgcttctttg caacacttgg aacacaagcc gcaaatgctc
301 gccctgctgg tcaaaaacca cggcaaaagg atggcgggaa aggtcaggtt
351 caaggcggaa gtgctgcccg acgacgaaga cgcgcgacg attgccgccg
401 agttggcaaa aatggatatg ttcgcattgg ggacggacgc ggtcgcctcg
451 ggcgaaaact atgggcgctg gttcgccgat attttcgagt tgtcggcgcc
501 tttggaaagg cgcgcggtca aagggatact gaaactgacg gcggaatata
551 aaaaacatct tcggcgatgc ctgccgttcg gaaacggcgt tggatttggg
601 cgcgctcaat caggcggtga gggaaatctc gaaaacgccg gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

g259.pep

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALER RAFKGILKLT AEYKKHLRRC LPFGNGVGF
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

m259.seq (partial)

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGTT TTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTTCGT TCGGCGCGTT CAAAGGCCAA
201 GCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTGCA CGCCTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCAGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGACGC GGTCGCCTCG
451 GCGGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGmGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AA.AACATCT TCGGmGATGC CTGCCGTTTC GAAACGGCGT TGAGATTGGG
601 CGCACTCAAT CAGGCGTTGC AGGAGATTTT AAAACATCC GG..

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

m259.pep (partial)

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS

```

598

	430	440	450	460	470	480
	490	500	510	520	530	540
m258.pep	EAAWGEVAKRLAHEIRNPLTPIQLSAERXAXKLGGKLDEQDAQILTRSTDITIVKQVAALK					
a258	EAAWGEVAKRLAHEIRNPLTPIQLSAERLAWKLGGKLDEQDAQILTRSTDITIKQVAALK					
	490	500	510	520	530	540
	550	560	570	580	589	
m258.pep	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNI FKNAAEAAEEADVPEVRVKSEAGQDGRIVLTVCDNGKGFGREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

```

g259.seq
1  atgatgatgc acgcttctgt ccaaagtcgt ttcgcaccga tactttatgt
51  tttgattttc tttgccggtt ttttgaccgc gcaaatctgg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgtccgcatt gtccgcgctc
151 gcgctggtgt ggctggcgtg ggcgttcgtg tcggtgcgtt caaaggctaa
201 ggcagaaaag ttctaccgcg aaaaaatgat acagAACGAA agcatacacc
251 ccgtcctgca cgcttctttg caacacttgg aacacaagcc gcaaatgctc
301 gccctgctgg tcaaaaacca cggcaaaggc atggcgggaa aggtcaggtt
351 caaggcggaa gtgctgcccg acgacgaaga cgcgcgacag attgccgccc
401 agttggcaaa aatggatatg ttcgcattgg ggacggacgc ggtcgcctcg
451 ggcgaaacct atggcgcggt gttcgccgat attttcgagt tgcggcgggc
501 tttgaaagg cgcgcggtca aagggatact gaaactgacg cgggaatata
551 aaaaacatct tcggcgatgc ctgccgttcg gaaacggcgt tggatttggg
601 cgcgctcaat caggcggtga gggaaatctc gaaaacgccc gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

```

g259.pep
1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALER RAFKGILKLT AEYKKHLRRC LPFGNGVVGFG
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

```

m259.seq (partial)
1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GGCCTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCsTGCA CGCCTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACKGACGC GGTTCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTTCGmGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AA.AACATCT TCGGmGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCACTCAAT CAGGCGTTGC AGGAGATTTC AAAACATCC GG..

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

```

m259.pep (partial)
1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS

```

599

151 GETYGRVFAD IFELSXALEG RAFKGLMLKT AEYKXHLRRC LPFGNGVGVG
201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSALVWLAFAFV					
g259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSALVWLAFAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE					
	:					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTDASGETYGRVFADIFELSXALEGRAFKGMLKLT					
g259	VLPDDEDARTIAAELAKMDMFALGTDASGETYGRVFADIFELSAALERRAFKILKLT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKKHLRRLPFGNGVGVGRTQSGVAGDFKNIR					
	: : : :					
g259	AEYKKHLRRLPFGNGVGFRAQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

1	ATGATGATGC	ACGCTTCTGT	CCAAAGCCGT	TTCGCACCGA	TACTTTATGT
51	TTTGATTTTC	TTTGCCGGTT	TTTTGACCGC	GCAAATCTGG	TTCAATCAGA
101	AAGCCTATAC	TGAAGAGCTG	CCTCCGCTTC	TGTCGCGATT	GTCCGCCGTC
151	GCGCTGGTGT	GGCTGGCGTG	GGCGTTCGTG	TCGGCGCGTT	CAAAGGCTAA
201	GGCGGAAAAG	TTCTACCGCG	AAAAAATGAT	ACAGAACGAA	AGCATACACC
251	CCGCTCTGCA	CGCTTCTTTG	CAACACTTGG	AACACAAGCC	GCAAATGCTC
301	GCCCTGCTGG	TCAAAAACCA	CGGCAAAGGG	ATGGCGGAAC	AGGTCAGGTT
351	CAAGGCGGAA	GTGCTGCCCG	ACGACGAAGA	CGCGCGCAGC	ATTGCCGCCG
401	AGTTGGCAAA	AATGGATATG	TTTGCATTGG	GGACGGACGC	GGTCGCCTCG
451	GGCGAAACCT	ATGGACGCGT	GTTCCGCCGAT	ATTTTCGAGT	TGTCGGCGGC
501	TTTGGAAGGG	CGCGCGTTCA	AAGGAATGTT	GAAACTGACG	CGGGAATATA
551	AAAA.CATCT	TCGGCGATGC	CTGCCGTTGC	GAAACGCGCT	TGGAGTTGGG
601	CGCGCTCAAT	CAGGCGTTGC	AGGAGATTTC	AAAAACATCG	GAAAAGTCCA
651	A				

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

1	MMMHASVQSR	FAPILYVLIF	FAGFLTAQIW	FNQKAYTEEL	PPLLSALSAV
51	ALVWLAWAFV	SARSKAKAEK	FYREKMIQNE	SIHPVLHASL	QHLEHKPQML
101	ALLVKNHGKG	MAEQVRFKAE	VLPDDEDART	IAAELAKMDM	FALGTDASAS
151	GETYGRVFAD	IFELSAALEG	RAFKGMLKLT	AEYKXHLRRC	LPFGNGVGVG
201	RAQSGVAGDF	KNIGKVQ			

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSALVWLAFAFV					
a259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSALVWLAFAFV					

600

	10	20	30	40	50	60
m259.pep	70	80	90	100	110	120
a259	70	80	90	100	110	120
m259.pep	130	140	150	160	170	180
a259	130	140	150	160	170	180
m259.pep	190	200	210			
a259	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1035>:

g259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGTCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGTGCGTT CAAAGGCTAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATAACAC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCC ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGGCGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGA

```

This corresponds to the amino acid sequence <SEQ ID 1036; ORF 259-1.ng>:

g259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALE

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1037>:

m259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATAACAC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCC ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCATGCC TGCCGTTCCG AACGCGCGTT GGAGTTGGGC
601 GCACTCAATC AGCGGTTGCA GGAGATTTCA AAAACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1038; ORF 259-1>:

m259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALEG RAFKGLMLKT AEYKNIFGDA CRSETALELG
201 ALNQLQEIS KTSEKSRIF Y*

```

g259-1/m259-1 98.8% identity in 169 aa overlap

601

	10	20	30	40	50	60
g259-1.pep	MMMHASVQSRFAPILYVLIF	FAGFLTAQIW	FNQKAYTEEL	PPLLSALS	SAVALVWL	AWAFV
m259-1	MMMHASVQSRFAPILYVLIF	FAGFLTAQIW	FNQKAYTEEL	PPLLSALS	SAVALVWL	AWAFV
	10	20	30	40	50	60
	70	80	90	100	110	120
g259-1.pep	SVRSKAKAEK	FYREKMIQNE	SIHPVLHASL	QHLEHKPQML	LALLVKNHGK	MAEQVRFKAE
m259-1	SARSKAKAEK	FYREKMIQNE	SIHPVLHASL	QHLEHKPQIL	LALLVKNHGK	MAEQVRFKAE
	70	80	90	100	110	120
	130	140	150	160	169	
g259-1.pep	VLPDDEDARTIAAELAKMDM	FALGTD	AVASGETYGRV	FADIFEL	SAALE	
m259-1	VLPDDEDARTIAAELAKMDM	FALGTD	AVASGETYGRV	FADIFEL	SAALE	GRAFKGMLKLT
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

a259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGTTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGCGCGTT CAAAGGCTAA
201 GGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTGTGA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTTCG AAACGGCGTT GGAGTTGGGC
601 GCGCTCAATC AGGCGTTGCA GGAGATTTC AAAACATCG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

a259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQALQEIS KTSEKSKRIF_Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

	10	20	30	40	50	60
a259-1.pep	MMMHASVQSRFAPILYVLIF	FAGFLTAQIW	FNQKAYTEEL	PPLLSALS	SAVALVWL	AWAFV
m259-1	MMMHASVQSRFAPILYVLIF	FAGFLTAQIW	FNQKAYTEEL	PPLLSALS	SAVALVWL	AWAFV
	10	20	30	40	50	60
	70	80	90	100	110	120
a259-1.pep	SARSKAKAEK	FYREKMIQNE	SIHPVLHASL	QHLEHKPQML	LALLVKNHGK	MAEQVRFKAE
m259-1	SARSKAKAEK	FYREKMIQNE	SIHPVLHASL	QHLEHKPQIL	LALLVKNHGK	MAEQVRFKAE
	70	80	90	100	110	120
	130	140	150	160	170	180
a259-1.pep	VLPDDEDARTIAAELAKMDM	FALGTD	AVASGETYGRV	FADIFEL	SAALE	GRAFKGMLKLT
m259-1	VLPDDEDARTIAAELAKMDM	FALGTD	AVASGETYGRV	FADIFEL	SAALE	GRAFKGMLKLT
	130	140	150	160	170	180
	190	200	210	220		
a259-1.pep	AEYKNIFGDACRSETALEL	GALNQALQEIS	KTSEKSKRIF	YX		
m259-1	AEYKNIFGDACRSETALEL	GALNQALQEIS	KTSEKSKRIF	YX		
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

q260.pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1043>:

m260.seq

1	ATGGGTGCGG	GTATGGTATT	CGTGTCTTT	CGGCCGTTCT	CCAGCCTGTT
51	TCGAGCGTTG	TTCGAGGACA	GAGTCGGTAT	AGTCGAGGGA	GCGCACGATG
101	CCGCTGAATG	CGACTTCCTG	CCCAGGAAT	TTACCCGTAT	CCGGATCGGT
151	GATGTTTTTA	TTGATTGGT	AGGTCAGGTA	GCGGCCCGGC	TCTTTCAGGC
201	CTTTGGTGTA	AACCTCGGTG	CTTTGGTGT	ACAGCAGCCT	GCCTTCCGGG
251	CCCGAGw _r CA	sGCGCGyGC	GGCAGCGGTT	TCTTTGCGGG	AAACGATTTG
301	CGGATGCCGC	ATAAAGATGC	GGTAGAAGTT	GACATCGATG	GCGGGAATAC
351	CGTATCCGGA	CACTTCCTTA	TCCGGACTCA	TTTTGACGAC	GGGGATGCCG
401	TCTGTCTGTT	CCAAGCCGAG	GCGCGGTTTC	CCGTCAACGT	GGCGCAACAC
451	CAATACCTGG	TCCGGATAAA	TCAGGTCGGG	ATTGTGGATT	TGATCCCGGT
501	TCGCGT _v CCA	CAG			

m260.pep

1 MGAGMVFVVF RPFSSLFRAL FEDRVGIVEG AHDAAECDFL PEEFTRIRIG
51 DVFIDSVGQV AARLFQAFGV NPGAFGVQQP AFRARXXARX GSGFFAGNDL
101 RMPHKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVRINOVG IVDLIPVRVP Q

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 260 shows 89.5% identity over a 171 aa overlap with a predicted ORF (ORF 260.ng) from *N. gonorrhoeae*:

m260/g260

[illegible]

603

g260 GICPKYPTGCRPV
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

a260.seq
1 ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51 TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CCACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CCTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGAGCA GCGCGGCGC GGCAGCGGTT TCTTTGCGGG AAACGATTTG
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTCC CCGTCAACGT GGCGCAACAC
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTCCCA CAGGCGGCC CCATTGCCAC GGGCTGTACA GGTATTTGCC
551 CGAAATGCCC CACAGGGTGT CGCCCTGTTT GA

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

a260.pep
1 MGAGMVFFVF RPFSSLFRAL FEDRVGIVEG AHDAECDFL PEEFTRIRIG
51 DVFIDSVGV AARLFQAFGV NPGAQVQPP AFRAREQARR GSGFFAGNDL
101 RVPHKDAVEV DIDGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLQINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPY*

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVFFVFRPFSSLFRALFEDRVGIVEGAHDAECDFLPEEFTRIRIGDVFIDSVGVQV					
a260	MGAGMVFFVFRPFSSLFRALFEDRVGIVEGAHDAECDFLPEEFTRIRIGDVFIDSVGVQV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGAQVQPPAFRRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGNTVSG					
a260	AARLFQAFGVNPGAQVQPPAFRRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGNTVSG					
	70	80	90	100	110	120
	130	140	150	160	170	
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVRINQVGIVDLIPVRVPQ					
a260	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLQINQVGIVDLIPVRVPQAAXIATGCT					
	130	140	150	160	170	180
a260	GICPKCPTGCRPVX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

g261.seq
1 atggagcttg ggcataatcgt attccttggtg ctttgccgcgc gttcagacgg
51 cctttttact ttccagacat tccgccagcc cgcgttcgcg caagatacag
101 ctccggcatt cgcggcagcc gccgacgata cccttgtagc aggtgtgggt
151 ctgttcgcgc atgtagtcca acacgcccatt ttcgtccgcc aacgcccacg
201 tttgcccctt ggtaggtac atcagcgcgc tgtggatttg aaaatcgtag
251 tccatcgcca gattaagggt aacgttcatg gatttgacga acacgcgcgc
301 gcagtcggga tagcccgaaa aatcggtttc gcacacgccc gcgatgatgt
351 gccggatacc ctgccctttg gcaaaaatgg cggcgtaaaag caggaaaagc
401 gcgttacgcc cgtccacaaa ggtattggga acgcccgttg cggcggtttc
451 gatggcggcg gtttcgatgg cggcggtttc gtccatcagg gcgttggtgcg
501 taatctgccg catcaggctc aaatcgagta cggtttgact gacacccaaa
551 tcctgcgcga tccactctgc gcgttccagc tcgacggcat ggcgttgccc
601 gtatcggaag gtgatggcctt ggacgttttc gcgcccgtag gtttggtattg

651 cctgaatcag gcaggtggtc gaatcctgac cgccccgagaa gatgaccaag
701 gcttttttgggt ttga

This corresponds to the amino acid sequence <SEQ ID 1048; ORF 261.ng>:

g261.pep
1 MELGHIVFLV LCARSDGLFT FQTFRQPAFA QDTARAFAAA ADDTLVAGVG
51 LFADVQHAH FVRQRPRLRL GQVHQRRVDL KIVVHRQIKG NVHGFDEHAA
101 AVGIARKIGF AHARDDVPDT LPFGKNGGVK QEKRVTPVHK GIGNAVVGGF
151 DGGGFDGGGF VHQGVVRNLP HQAQIEYGLT DTQILRDPLC AFQLDGMALP
201 VSEGDGLDVF APVGLDCLNQ AGGRILTARE DDQGFLV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1049>:

m261.seq
1 ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGCGCGT GTTCAGACGG
51 CCTTTTACT TTCCAGATAT TCCGCCAGCC cGcGTTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGgCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCACGCCCAT TCGTCCGCC AACGCCACG
201 TTTGCGCCTT GGTGAGATAC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA AATTAAGGGT AACGTTTCATC GATTTGACAA ACACGTCGCG
301 GCAGTCGGGA TAGCCGGAGA AGTCGGTTTC GCACACGCCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 gCGTTGCGGC CGTCTACAAA GGTATTTCGGA ACGCCGTTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GgCTcAAGTC GAGTACGGTT TGTTTGACGC CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTG TTGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 1050; ORF 261>:

m261.pep
1 MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51 LLADIVQHAH FVRQRPRLRL GQIHQRRVDL KIIVHRQIKG NVHRFDKHVA
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGS
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAPVGL DCLNQAGGRI LTARKDDQGL LV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 261 shows 79.7% identity over a 237 aa overlap with a predicted ORF (ORF 261.ng) from *N. gonorrhoeae*:

m261/g261

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
	::					
g261	MELGHIVFLVLCARSDGLFTFQTFRQPAFAQDTARAFAAAADDTLVAGVGLFADVQHAH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m261.pep	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVAAVGIAGEVGFHAHARDDVPYP					
	::					
g261	FVRQRPRLRLGQVHQRRVDLKIVVHRQIKGNVHGFDEHAAAVGIARKIGFAHARDDVPDT					
	70	80	90	100	110	120
	130	140	150	160	170	
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGV-----VHQGIVRNLPHQAVQVEYGLF					
	:: : :					
g261	LPFGKNGGVKQEKRVTPVHKIGNAVVGGFDGGGFDGGGFVHQGVVRNLPHQAEYGLT					
	130	140	150	160	170	180
	180	190	200	210	220	230
m261.pep	DAQILRNPAFTQLDGMALPVLESNGLDVFAPVGLDCLNQAGGRILTARKDDQGLLVX					
	: : : :					
g261	DTQILRDPLCAFQLDGMALPVSEGDGLDVFAPVGLDCLNQAGGRILTAREDDQGFLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1  ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTCGCGCT GTTCAGACGG
51  CCTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCCAAG
201 TTTGCGCCTT GGTACAGATC ATCAGCGGCG TGTGGATTTG AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGAGGA AGTCGGTTTC GCACACGCCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GGCTCAAGTC GAGTACGGTT TGTTCGACGC CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1  MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPSLRL GQIHQRRVDL KIIVHRQIKG NVHGFDKHVT
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAQV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAPVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
a261	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQRAH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m261.pep	FVRQRPRRLRGQIHQRRVDLKIIVHRQIKGNVHRFDKHVAAVGIAGEVGFHAHARDDVPYP					
a261	FVRQRPSLRLRGQIHQRRVDLKIIVHRQIKGNVHGFDKHVTAVGIAGEVGFHAHARDDVPYP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAVEYGLFDAQIL					
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAVEYGLFDAQIL					
	130	140	150	160	170	180
	190	200	210	220	230	
m261.pep	RNPAGTFQLDGMALPVLESNGLDVFAPVGLDCLNQAGGRILTARKDDQGLLVX					
a261	RNPAGTFQLDGMALPVLESNGLDVFAPVGLDCLNQAGGRILTARKDDQGLLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1  atggcacgtt taaccgtaca caccctcgaa accgcccccg aagccgccaa
51  accgcgcgta gaggcgtac ccaaaaacaa cggtttatc cccaacctca
101 tcggcgattt ggcaaacgcc cccgaagctt tggcgtttta ccaagaagtc
151 ggcaagctca acgcccgcga cagcctgacc gccggcgaag tcgaagtgat
201 ccggatcatc gccgtccgca ccaaccaatg cagcttctgc gtggcagggc
251 acacaaaact cgcaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgcccccg ctttggcggc aggtaaatct gacgatgcc aactcggcgc
351 gcttgccgcc ttcacccaag ccgtaatggc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctcgaagcgg gctacaaccg gcagcaggca
```

451 gtcgaagtcg taatgggcgt agccttggca actttgtgca actacgccaa
501 caacctcgcc caaaccgaaa tcaaccccaa attqcaqqca tacgcctaa

This corresponds to the amino acid sequence <SEQ ID 1054; ORF 263.ng>:

g263.pep

```

1 MARLTVHTLE TAPEAAKPRV EAVPKNGFI PNLIGVLANA PEALAFYQEV
51 GKLNAANSLT AGEVEVIRII AVRTNQCSFC VAGHTKLATL KLLSEQSLN
101 AARALAAGKS DDAKLGALAA FTQAVMAKKG AVSDDELNAF LEAGYNRQQA
151 VEVVMGVALA TLCNYANL A QTEINPKLOA YA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1055>:

m263.seq (partial)

```

1      .GCAGCAGGCG AATTTGACGA TGCCAAACTC GGCGCGCTCG CCGCCTTCAC
51     CCAGCCGTA ATGGCGAAAA AAGCGCGGT ATCCGACGAG GAACTCAAAG
101    CATTTTTCGA TGCGGGCTAC AACCAGCAGC AGGCAGTCGA AGTCGTGATG
151    GCGGT .AsyC TgGCAACCTT GTGCAACTAC GTCAACAAC TC GGACAAAC
201    CGAAATCAAC CCGCAATTGC AGCCTTACGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1056; ORF 263>:

m263.pep (partial)

1	..GCAGCAGGCG	AATTTGACGA	TGCCAAACTC	GGCGCGCTCG	CCGCTTTCAC
51	CCAAGCCGTA	ATGGCGAAAA	AAGGCGCGGT	ATCCGACGAG	GAACTCAAAG
101	CATTTTTTCGA	TGCGGGCTAC	AACCAGCACT	AGGCAAGTCGA	AGTCGTGATG
151	GGCGT.AsyC	TgGCAACCTC	GTGCAACTAC	GTCAACAACC	TCGGACAAAC
201	CGAAATCAAC	CCCCGAATTGC	AGGCTTACGC	TCGA	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 263 shows 85.7% identity over a 77 aa overlap with a predicted ORF (ORF 263.ng) from *N. gonorrhoeae*:

m263/q263

m263.pep
AAGEFDDAKLGALAAFTQAVMAKKGAVSDE

g263 QCSFCVAGHTKLATLKKLLSEQSLNAARALAAGKSDDAKLGALAAFTQAVMAKKGAVSD

80 90 100 110 120 130

m263.pep ELKAFFDAGYNQQQAVEVMGVXLATLCNYVNNLGQTTEINPELQAYAX

g263 ELNAFLEAGYNRQQAVEVMGVXVALATLCNYANNLAQTTEINPKLQAYAX

140 150 160 170 180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1057>:

a263.seq

1	ATGGCACGTT	TAACCGTACA	CACCCTCGAA	ACCGCCCCCG	AAGCCGCCAA
51	AGCGCGCGTC	GAGGCGGTAC	TTCAAAACAA	CGGCTTTATC	CCCAACCTTA
101	TCGGCGTATT	ATCAAACGCC	CCCGAAGCCT	TGGCGTTTTA	CCAAGAAGTC
151	GGCAAGCTCA	ACGCCGCCAA	CAGCTGACC	GCCGGCGAAG	TCGAAGTAAT
201	CCAGATTATT	GCCGCCGCA	CCAACCAATG	CGGCTTCTGC	GTGGCAGGGC
251	ACACCAAATC	CGCAACCCTG	AAAAAACTCC	TTTCCGAACA	ATCCGTCAAA
301	GCCGCGCGCG	CTTTGGCGGC	AGGCGAATTT	GACGATGCTA	AACTCGGCGC
351	GCTCGCGCGC	TTTACCCAAG	CCGTAATGCG	AAAAAAAGGC	GCGGTATCCG
401	ACGAGGAAC	CAAGAGCAT	TTTGATGCGG	GCTACAACCA	CGACGAGGCA
451	GTCGAAGTCG	TGATGGGCGT	AGCCTTGGCA	ACTTTGTGCA	ACTACGTCAA
501	CAACCTCGGA	CAAACCGAAA	TCAACCCCGA	ATTGCGAGGCT	TACGCCTGA

This corresponds to the amino acid sequence <SEQ ID 1058; ORF 263.a>:

a263.pep

```

1 MARLTVHTLE TAPEAAKARV EAVLQNNGFI PNLIGVLSNA PEALAFYQEV
51 GKLNAANSLT AGEVEVIQII AARTNQCQFC VAGHTKLATL KKLLSEQSVK
101 AARALAAGEF DDAKLGALAA FTQAVMAKKG AVSDEELKAF FDAGYNQQQA
151 VEVVMGVALA TLCNYVNNLG OTEINPELOA YA*

```

m263/a263 97.4% identity in 77 aa overlap

```

                                     10      20      30
m263.pep                          AAGEFDDAKLGALAAFTQAVMAKKGAVSDE
                                   |||
a263      QCGFCVAGHTKLATLKKLLSEQSVKAARALAAAGEFDDAKLGALAAFTQAVMAKKGAVSDE
           80      90      100      110      120      130

           40      50      60      70
m263.pep  ELKAFFDAGYNQQQAVEVVMGXSLATLCNYVNNLGQTEINPELQAYAX
           |||
a263      ELKAFFDAGYNQQQAVEVVMGVALATLCNYVNNLGQTEINPELQAYAX
           140      150      160      170      180

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

```
g264.seq
1  ttgactttaa cccgaaaaac ccttttcctc ctcaccgcgc cgttcggcac
51  acactccctt cagacggcat ccgcgcgacg agtgggtcaag ccggaaaaaa
101 tgcacgcctc cgccaaccgc agctacaaag tcgccgaatt cacgcaaaac
151 ggcaacgcct cgtggtacgc cggcaggttt cagcgggcga aaactctcgg
201 cggagaccgc tacgatatga acgcctttac cgcgcgccac aaaaacctgc
251 ccatccccag ccatgtgcgc gtaaccaaca ccaaaaacgcg aaaaagcgtc
301 atcgtccgcg tcaacgaccg cggccccttc cacggcaacc gcatcatcga
351 cgtatccaaa gccgcgcgcg aaaaattggg ctttgtcagc caagggacgcg
401 cacacgtcaa aatcgaacaa atcgtcccgg gccaatccgc accggttgcc
451 gaaaacaaag acatctttat cgacttgaaa tctttcggta cgaacacga
501 agcacaagcc tatctgaacc aagccgcccc aaatttcgcg gcttcgtcat
551 caagcccgaa cctctcggtt gaaaaacgcg gttacgaata cgttgtcaaa
601 atgggcccgt ttgcctcgca ggaacgcgcg ccgaagccg aagcgcaggc
651 acgcggtatg gttcgggcgg tactgaacct cgggttga
```

This corresponds to the amino acid sequence <SEQ ID 1060; ORF 264.ng>:

g264.pep

1	<u>LTLTRKTLFL</u>	<u>LTAAFGTHSL</u>	<u>QTASADAVVK</u>	PEKLHASANR	SYKVAEFTQT
51	GNASWYGGRF	HGRKTSGGDR	YDMNAFTA AH	KTLPIPSHVR	VTNTKNGKSV
101	IVRVNDRGPF	HGNRIIDVS	AAAQKLGFVS	QGTAHVKIEQ	IVPGQSAPVA
151	ENKDIFIDLK	SFGTEHAQA	YLNQAAQNFA	ASSSSPNLSR	EKKRYEYVVK
201	MGPFASQERA	AEAEAQAQRM	VRVRLTSG*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

m264 . seq					
1	TTGACTTTAA	CCCGAAAAAC	CCTTTTTCCTT	CTCACCGCCG	CATTCGGCAC
51	ACACTCCCCTT	CAGACGGCAT	CCGCCACGC	AGTGGTCAAG	GCAGAAAAAC
101	TGCACGCCTC	CGCCAACCGC	AGCTACAAAG	TCGCCGGAAA	ACGTACACG
151	CCGAAAAACC	AAGTCGCCGA	ATTACAGCAA	ACCGGCAACG	CCTCGTGGTA
201	CGGCGGCAGT	TTTCACGGGC	GCAAACTTC	CGGCGGAGAA	CGATACGATA
251	TGAACGCCTT	TACCGCCGCC	CACAAAACCC	TGCCCATCCC	CAGCTATGTG
301	CGCGTAACCA	ATACCAAAAA	CGGCAAAAGC	GTCACTCGTCC	GCGTCAACGA
351	CCGCGGCCCC	TTCCACGGCA	ACCGCATCAT	CGACGTATCC	AAAGCCGCCG
401	CGCAAAAATT	GGGCTTTGTC	AACCAAGGGA	CGGCACACGT	CAAAATCGAA
451	CAAATCGTCC	CGGGCCAATC	CGCACCGETT	GCCGAAAACA	AAGACATCTT
501	TATCGACTTG	AAATCTTTTCG	GTACGGAACA	CGAAGCACAA	GCCTATCTGA
551	ACCAAGCCGC	CCAAACTTC	GCCGTTTCGT	CATCGGGTAC	GAACCTCTCG
601	GTTGAAAAAC	GCCGTTACGA	ATACGTCGTC	AAAAATGGGAC	CGTTTACCTC
651	GCAGGAACGC	CGCGCCGAAG	CCGAAGCTCA	GGCGCGCGGT	ATGGTTCGGG
701	CGGTATTGAC	CGCCGGCTGA			

This corresponds to the amino acid sequence <SEQ ID 1062; ORF 264>:

m264.pep

1	<u>LT</u> LTRKTLFL	<u>L</u> TAAFGTHSL	<u>Q</u> TASADAVVK	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGGR	FHGRKTSGE	RYDMNAFTAA	HKTLPIPSYV
101	RVNTNKGKGS	VIVRVNDRGP	FHGNRIIDVS	KAAAQKLGFV	NQGTAHVKIE
151	QIVPGQSAPV	AENKIDIFDL	KSFGEHEAQ	AYLNAAQNF	AVSSSGTNLS
201	VEKRRYEYVV	KMGPFTSOER	AAEAEOAARG	MVRVRLTAG*	

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 264 shows 91.6% identity over a 239 aa overlap with a predicted ORF (ORF 264.ng) from *N. gonorrhoeae*:

m264/g264

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
g264	LTLTRKTLFLLTAAFGTHSLQTASADAVVKPEKLHASANRSYKVA-----EFTQ					
	10	20	30	40		
	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
g264	TGNASWYGGRFHGRKTSGGDRYDMNAFTA AHKTLPIPSHVRVTNTKNGKSVIVRVNDRGP					
	50	60	70	80	90	100
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAA AQLG FVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFSGTEHEAQ					
g264	FHGNRIIDVSKAA AQLG FVSQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFSGTEHEAQ					
	110	120	130	140	150	160
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAE AQARGMVR AVLTAGX					
g264	AYLNQAAQNFAASSSPNLSVEKRRYEYVVKMGPFASQERAAEAE AQARGMVR AVLTSGX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1063>:

a264 . seq

1	TTGACTTTAA	CCCGAAAAAC	CCTTTTCCTC	CTCACCGCCG	CATTCCGGCAT
51	ACATTCCTTT	CAGACGGCAT	CCGCCGACGC	AGTGGTCAGG	GCAGAAAAAC
101	TGCACGCCTC	CGCCAACCGC	AGCTACAAAG	TCGCCGGAAA	ACGCTACACG
151	CCGAAAAACC	AAGTCGCCGA	ATTACGCAA	ACCGGCAACG	CCTCGTG GTA
201	CGGCGGCAGG	TTTCACGGGC	GCAAAACTTC	CGGCGGAGAA	CGATACGATA
251	TGAACGCCTT	TACCGCCGCC	CACAAAACCC	TGCCCATCCC	CAGCTATGTG
301	CGCGTAACCA	ATACCAAAAA	CGGC AAAAGC	GTCATCGTCC	GCGTCAACGA
351	CCGCGGCCCC	TTCCACGGCA	ACCGCATCAT	CGACGTATCC	AAAGCCGCCG
401	CGCAAAAATT	GGGCTTTGTC	AACCAAGGGA	CGGCGCACGT	CAAAATCGAA
451	CAAATCGTCC	CGGGCCAATC	CGCACCGGTT	GCCGAAAACA	AAGACATCTT
501	CATCGACTTG	AAATCTTTCG	GTACGGAACA	CGAAGCACAA	GCCTATCTGA
551	ACCAAGCCGC	CCAAAACCTG	GCTTCATCGG	CATCAAACCC	GAACCTCTCG
601	GTTGAAAAAC	GCCGTTACGA	ATACGTCGTC	AAATGGGAC	CGTTTGCCCTC
651	GCAGGAACGC	GCCGCCGAGG	CCGAAGCTCA	GGCGCGCGGT	ATGGTTCGGG
701	CGGTATTAAAC	CGCCGGTTGA			

This corresponds to the amino acid sequence <SEQ ID 1064; ORF 264.a>:

a264 . pep

1	LTLTRKTLFL	LTA AFGIHSF	QTASADAVVR	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGGR	FHGRKTS GGE	RYDMNAFTA A	HKTLPIPSYV
101	RVTNTKNGKS	VIVRVNDRGP	FHGNRIIDVS	KAAAQKLGFV	NQGT AHVKIE
151	QIVPGQSAPV	AENKDIFIDL	KSFSGTEHEAQ	AYLNQAAQNL	ASSASNPNLS
201	VEKRRYEYVV	KMGPFASQER	AAEAE AQARG	MVRAVLTAG*	

m264/a264 96.2% identity in 239 aa overlap

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
a264	LTLTRKTLFLLTAAFGIHSFQTASADAVVRAEKLHASANRSYKVAGKRYTPKNQVAEFTQ					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m264.pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264						
	70	80	90	100	110	120
	130	140	150	160	170	180
m264.pep	FHGNRIIDVSKAAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFSGTEHEAQ					
a264						
	130	140	150	160	170	180
	190	200	210	220	230	240
m264.pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPFQSERAAEAEQAQARGMVRVLTAGX					
a264						
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```

m265.seq
  1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
 51  GGC GCGGCTG ATGATTTTGT CTTGTTTGTG GTGTTGGTGT GCGGCGTGTC
101  CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGGCGGAA
151  ATGCTCAGCA GTGCGGTTGC GCGGAGGTC AAGAGAAGGT GTTTGATGTT
201  CATAT.TTTT GCCTTTGTAA ATCGTGGGTT GGAAAATGTG GATATTAATA
251  AGGTATCAAA TAACCGTCAG CCGGCGGTCA ATACCGCCCC AACCATACCG
301  CGCGCCTGAG CTTTCGGCTTC GCGGCGCGGT TCCTGCGAGG TAAACGGTCC
351  CATTTTGACG ACGTATTCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```

m265.pep
  1  MSVILPPTRA NAAFAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
 51  MLSSAVAAEV KRRCLMFI XFVNRGLENV DINKVSNNRQ PAVNTARTIP
101  RAXASASAAR SCEVNGPILT TYS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m265.g265	MSVILPPTRANA AFAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSAVAAEV					
m265.pep						
g265	MSVILPPTRAQA AFAWARLMILSCLPCWCAACPWSSSPCPSWWASAGAEMPNSAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265.pep	KRRCLMFI XFAFVNRGLENV DINKVSNNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
g265						
	70	80	90	100	110	
	KRRCLMFI -FALVNQGLKNGDINKVSNNRQPEVSTARTIPRACASASAARSCEANGPILT					
	70	80	90	100	110	
m265.pep	TYSX					
g265	TYSX					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1067>:

```
a265.seq
1   ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GGC GCGGCTG ATGATTTTGT CTTGTTTGCT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGTGC GGGGGCGGAA
151 ATGCCCATCA GTGCGGTTGC GCGGCGGGTC AAGAGAAGGC GTTTGAAGTT
201 CATTTTGTCT CCTGCGAAGT ATCTGGT... . . . .GGTGT TTGAAGGACG
251 TAAAGGCGGG ACATCAACCG GCGGTTAATA CCGCCCGAAC CATACCGCGC
301 GCCTGAGCTT CGGCCTCGGC GCGCGTTC TGCGAGGCAA ACGGTCCCAT
351 TTTGACGACG TATTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1068; ORF 265.a>:

```
a265.pep
1   MSVILPPTRA NAAFAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MPISAVAAAV KRRRLKFIFA PAKYLX..XC LKDKVAGHQ PAVNTARTIPR
101 A*ASASAARS CEANGPILTT YS*
```

m265/a265 79.7% identity in 123 aa overlap

	10	20	30	40	50	60
m265.pep	MSVILPPTRANAFAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSSAVAAEV					
a265	MSVILPPTRANAFAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAE MPI SAVAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265.pep	KRRCLMFIKFAFVNRGLNV DINKVSNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
a265	KRRRLKFI---FAPAKYLXXCLKDV KAGHPAVNTARTIPRAXASASAARSCEANGPILT					
	70	80	90	100	110	
m265.pep	TYSX					
a265	TYSX					
	120					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1069>:

```
g266.seq
1   agttcagacg gcatcgccgc cgacaatgcc caaacagaaa gcccattcatg
51  accgcatcca tgtacatcct tttggtcttg gcactcatct ttgccaacgc
101 ccccttcttc acgaccagac tggtcggcgt ggccgcgctc aagcgcaaac
151 atttcggaca ccacctgatc gagctggcgg cagggtttcgc gctgaccgcc
201 tctcttgccct acatcctcga atcccgtgcg ggagcgggtac acaatcaggg
251 ttgggagttt tacgccaccg tcgtctgcct gtacctcatt ttcgccttcc
301 cgtgtttcgt gcggcggtat ttttggcaca cgcgcaacag ggaataa
```

This corresponds to the amino acid sequence <SEQ ID 1070; ORF 266.ng>:

```
g266.pep
1   MQFRRHRRRQ CPNRKPIMTA SMYILLVLAL IFANAPFLT RLFVGAALKR
51  KHFGHHLIEL AAGFALTASL AYILES RAGA VHNQGW EFYA TVVCLYLIFA
101 FPCFVRRYFW HTRNRE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1071>:

```
m266.seq
1   ATGCCGTTCC GCAACGCGtT cAGACGGCAT CGCCGCCGAC AACGCCTAA
51  CAGAAAGCCC ACCATGACCG CATCCATGTA CATCCTTTTG GTCTTGGCAC
101 TCATCTTTGC CAACGCCCCC TTCCTCACGA CCAGACTGTT CGGCGTGGCC
151 rCACTCAAGC GCAAACATTT CGGACACCAC ATGATCGAGC TGGCGGCAGG
201 TTTGCGCTG ACCGCCGTTT TTGCCTACAT CCTsGAATCC CGTGCAGGAT
251 CCGTACACGA TCAGGGTTGG GAGTTTTATG CCACAGTCGT CTGCCTGTAC
301 CTGATTTTTG CGTTTCCATG TTTTGTGTGG CCGTATTTTT GGCACACGCG
351 CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

```
m266.pep
  1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
 51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng) from *N. gonorrhoeae*:

m266/g266

	10	20	30	40	50	60
m266.pep	MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH					
g266	MQFRHRRRQCPNRKPIMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH					
	10	20	30	40	50	

	70	80	90	100	110	120
m266.pep	MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX					
	:					
g266	LIELAAGFALTAVLAYILES RAGAVHNQGW EFYATVVCLY LIFAFPCFVRRYFWHTRNREX					
	60	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

```
a266.seq
  1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAAA
 51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTTG CTGCTTGCCT
101  TGATTTTTGC CAACGCCCCC TTCCTCACGA CCAAGCTGTT CGGCATCGTA
151  CCGCTCAAGC GCAAACATTT CGGACACCAC CTGATCGAGC TGGCGGCAGG
201  TTTCGCGCTG ACCGCGGTTT TGCCTACAT CCTCGAATCC CGTGCGGGAG
251  CGGTACACGA TCAGGGTTGG GAGTTTACG CCACCGTCGT CTGCCTGTAC
301  CTGATTTTTG CGTTCCCTG TTCGTGTGG CGGTATTTT GGCACACGCG
351  CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

```
a266.pep
  1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLFGIV
 51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

m266/a266 91.7% identity in 120 aa overlap

	10	20	30	40	50	60
m266.pep	MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH					
a266	MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTKLFGIVPLKRKHFGHH					
	10	20	30	40	50	60

	70	80	90	100	110	120
m266.pep	MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE					
	:					
a266	LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE					
	70	80	90	100	110	120

m266.pep	X
a266	X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:

g267.seq

1	atgcaagtcg	ccttttttct	cgccgtggta	ttcaaaaata	tgggtttcca
51	caatcgcac	ggtcgggcag	gcctcttcgc	agaaaccgca	gaagatgcac
101	ttggtcagg	cgatgtcgta	acgcttggtg	cggcgggtgc	cgtcttcgcg
151	ttcttcgat	tcgatgttga	tcgccattgc	cggacacacc	gcctcgcaca
201	atttacacgc	gatgcagcgt	tcctctccgt	tcggaaaacg	gcgttgcgcg
251	tgcagaccgc	ggaaacgcac	ggattgcggc	gtttctctct	cgggaaaata
301	aattgtgtct	ttgcgggcga	aaaagttttt	gagcgttacg	cccatgcctt
351	tgaccagttc	gccaaagcga	aaggttttta	ctaa	

g267.pep

1 MQVAFFLAVV FKNMGFHNRI GRAGLFAETA EDALGQVDVV TLGAAGAVFA
51 FFRFDVDRHC RTHRLAQFTR DAAFLSVRKT ALRVQTAETH GLRRFLFGKI
101 NCVFAGKKVF ERYAHAFDQF AKQKGFY*

m267.seq

1	GTGCAAGTCG	CCTTTTTTCT	CGCCGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGCATC	AGTCGGGCAT	GCCTCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TTGGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGGCGCGTAC	CGTCTTCACG
151	TTCTTCCGAT	TCGATGTTAA	TCGCCATTGC	CGGACACACT	GCCTCACACA
201	ACTTACACGC	GATACACCGC	TCTTCGCCGT	TCGGATACCG	CcGCTGCGCG
251	TGCACACCGC	GGAAACGCAC	GATTGCGCG	GTTTCTCTCT	CGGGGAAATA
301	AATTGTGTCT	TTGCGGGCGA	AAAGTTTTTT	GATCGTTACG	CCCATACCTT
351	TTACCAATTC	GCCAAGCAGA	AAGGTTTTTA	CTAA	

m267 . pep

1 VQVAFFLAVV FKNMGFHNRI SRACLEAETA EDALGQVDVV TLGAARTVFT
51 FFRFDVNRHC RTHCLTQLTR DTPLFAVRIP PLRVQTAETH GLRRFLFGEI
101 NCVFAGEKVF ERYAHTFYQF AKQKGFY*

ORF 267 shows 82.7% identity over a 127 aa overlap with a predicted ORF (ORF 267.ng) from *N. gonorrhoeae*:

m267/g267

		10	20	30	40	50	60
m267.pep		VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGQVDV	VTLGAARTVFTFFRFDVNRHC			
		:					
g267		MQVAFFLAVVFKNMGFHNRI	GRAGLFAETAEDALGQVDV	TLGAAGAVFAFFRFDVDRHC			
		:					
		10	20	30	40	50	60
		70	80	90	100	110	120
m267.pep		RTHCLTQLTRDTPLFAVRIP	PPLRVQTAETHGLRRFLFGE	INCVFAGEKVFERYAHTFYQF			
			: : :	: : :	: : :	: : :	: : :
g267		RTHRLAQFTRDAAFLSVRKT	ALRVQTAETHGLRRFLFGK	INCVFAGKKVFERYAHAFDQF			
			: : :	: : :	: : :	: : :	: : :
		70	80	90	100	110	120
m267.pep		AKQKGFIYX					
g267		AKQKGFIYX					

a267.seq

1	GTGCAAGTCG	CCTTTTTTCT	CGCCGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGCATC	GGTCGGGCAG	GCTTCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TTGGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGGCGCGTGC	CGTCTTCGCG
151	TTCTTCCGAT	TCGATGTTGA	TCGCCATTGC	GGGGCAAACG	GCTTCACACA
201	ATTTACACGC	GATGCAGCGT	TCCTCGCCGT	TTGGATAACG	GCCTTGCGCG
251	TGCAGACCGC	GGAAACGCAC	GGATTGCGGC	GTTTCTCTTT	CGGGAAAATA
301	AATCGTGTCT	TTGCGGGCAA	AAAAGTTTTT	GAGCGTTACG	CCCATACCTT
351	TTACCAATTC	GCCAAGCAGA	AAGGTTTTTA	CTAA	

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
a267.pep
  1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGQVDVV TLGAARAVFA
 51  FFRFDVDRHC GANGFTQFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101  NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGQVDVV	TLGAARTVFTFF	FRFDVNRHC		
a267	VQVAFFLAVVFKNMGFHNRI	GRAGFFAETAEDALGQVDVV	TLGAARAVFA	FFRFDVDRHC		
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTPLFAVRIP	PLRVQTAETHGLRRFL	FGEINCVFAGEKV	FERYAHTFYQF		
	:::					
a267	GANGFTQFTRDAAFLAVWIT	ALRVQTAETHGLRRFL	FGKINRVFAGKKV	FERYAHTFYQF		
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
  1  atgaaaaaaa atttaccgcg actggcattg gcaagtatgc tgattttgtc
 51  gggctgcgac cgtttgggaa taggcaaccc gttttccgga aaggaaat
101  cctgcggaag cgaagagact aaagagattt tggtaaact ggtccgagc
151  aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaaga
201  ccaagcattt gccgatatcg gcatatcgca tatccgcaga atggtcgaac
251  gtttgggcat aaccgtcgat gaagtccgaa ctaccgagaa aaccgacacg
301  tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccgcaga
351  tgttgctgat tatgccgtcg ccgccaacca atctataggc aacagccata
401  agaaaacgcc cgactttttt gaaccctact accgcaaaga aggcgcgtat
451  tatgtcaaaa ctatttctta cagcgtccag ccgacagacg acaaaagcaa
501  aatctttgcc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551  agctggtgtc tatggcactg attaaagagc cgttggacaa agcgaaacaa
601  aggaacgaaa aacttgaagc ggcagaagcc accgcgcagg aagcgagggg
651  ggcagaagaa gcggcggcgc agggagcatt gggtcgggag caggaagccg
701  cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751  gagcagtttt ggaaaggatt gcctcaaact gtacagaata agctgcaagc
801  ctgcgagaaa acatgggaaa gcggtatgga caagatctgt gccacaatg
851  cgaaagccga aggtgaaacg ccaaacggca taaaagtcag tgagttggcg
901  tgtaaaacgg cagaaaccga agcagcgttg gaagagctgc acaaccgtaa
951  aaaagccctt atcgacgaaa tggtcaggga agaggacaag aaagaactgc
1001 caaagcggct ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
  1  MKKNLPALAL ASMLILSGCD RLGIGNPFSG KEISCGSEET KEILVKLVRD
 51  NVEGETVKTF DDDAFKDQAF ADIGISHIRR MVERLGITVD EVRTTEKTD
101  SSKLKCEAAL KLDVPDDVVD YAVAANQSIG NSHKKTPDFF EPYYRKEGAY
151  YVKTISYSVQ PTDDKSKIFA ELSQAHDIIH PLSELVSMAL IKEPLDKAKQ
201  RNEKLEAAEA TAQEAREAE EAAQALGRE QEAARVSEWE ERYKLSRSEF
251  EQFWKGLPQT VQNKLQASQK TWKSGMDKIC ANNAKAEGET PNGIKVSELA
301  CKTAETEARL EELHNRKKAL IDEMVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
  1  ..ATGGCACTGA TTAAAGAGCC GTTGACAAA GTGAAACAAA GGAACGAAGA
```

614

```

51   ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCGGGAGC
101  AGGAAGCCGC CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCGCGC
151  AG.CAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201  GCTGCAACCn TCACAGAAAA CATGGAAGAG CGGGATGGAT AAAATCTGTG
251  CCAACAATGC GAAAGCTGAA GGTAAGACGC CAAACGGCAT AAAATTCAGC
301  GAACTGGCAT GCAAAACGGC GAAACCGAA GCACGCTTGG AAGAGCTGCA
351  CAACCGTAAA AAAGCCCTTA TCGACGAAAT GGyCAGGGAA GCGGACAmGA
401  AAGAACTGTC AAAGCGGCTs TGA

```

This corresponds to the amino acid sequence <SEQ ID 1084; ORF 268>:

```

m268.pep (partial)
1   ..MALIKEPLDK VKQRNEELEA AEEAAAEAL GREQEAARVS EWEERYKLSR
51  XQFEQFWKGL PQTVQNKLP SQKTWKSMD KICANNAKAE GKTPNGIKFS
101 ELACKTAKTE ARLEELHNRK KALIDEMXRE ADXKELSKRL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 268 shows 86.0% identity over a 150 aa overlap with a predicted ORF (ORF 268.ng) from *N. gonorrhoeae*:

m268/g268

```

                                10      20
m268.pep                      MALIKEPLDKVKQRNEELEAAE-----
                                |||:|||:|||:|||:|||:|||:|||:|||
g268      SVQPTDDKSKIFAELSQAHDIIHPLSELVSMALIKEPLDKAKQRNEKLEAAEATAQEARE
          160      170      180      190      200      210

                                30      40      50      60      70      80
m268.pep  --EAAAEALGREQEAARVSEWEERYKLSRSQFEQFWKGLPQTVQNKLPQSQKTWKSMD
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      AEEAAAEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTVQNKLPASQKTWKSMD
          220      230      240      250      260      270

                                90      100     110     120     130     140
m268.pep  KICANNAKAEKTPNGIKFSELACKTAKTEARLEELHNRKKALIDEMXREADXKELSKRLX
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      KICANNAKAEGETPNGIKVSELACKTAETEARLEELHNRKKALIDEMVREEDKKELPKRLX
          280      290     300     310     320     330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1085>:

```

a268.seq
1   ATGGCACTGA TTAAAGAGCC GTTGGACAAA GCGAAACAAA GGAACGAAGA
51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCGGGAGC
101 AGGAAGTCGA CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCGCGC
151 AGCGAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAAGCC TCACAGAAAA CATGGAAGAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTGAAACGC CAAACGGCAT AAAATTCAGC
301 GAACTGGCAT GCAAAACGGC GGAAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTC TCGACGAAAT GGCCAGGGAA GCGGACAAGA
401 AAGAACTGCC AAAGCGGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1086; ORF 268.a>:

```

a268.pep
1   MALIKEPLDK AKQRNEELEA AEEAAAEAL GREQEVDRVS EWEERYKLSR
51  SEFEQFWKGL PQTVQNKLQA SQKTWKSMD KICANNAKAE GETPNGIKFS
101 ELACKTAETE ARLEELHNRK KALLDEMARE ADKKELPKRL *

```

m268/a268 91.4% identity in 140 aa overlap

```

                                10      20      30      40      50      60
m268.pep  MALIKEPLDKVKQRNEELEAAEEAAAEALGREQEAARVSEWEERYKLSRXQFEQFWKGL
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a268      MALIKEPLDKAKQRNEELEAAEEAAAEALGREQEVDRVSEWEERYKLSRSEFEQFWKGL

```

615

	10	20	30	40	50	60
m268.pep	70	80	90	100	110	120
	PQTVQNKLPQSQKTWKS	GMKDICANNAKAEGKTP	NGIKFSE	LACKTAKTEAR	LEELHNRK	
a268	PQTVQNKLPQSQKTWKS	GMKDICANNAKAEGKTP	NGIKFSE	LACKTAKTEAR	LEELHNRK	
	70	80	90	100	110	120
m268.pep	130	140				
	KALIDEMXREADXKELSKRLX					
a268	KALLDEMAREADKKELPKRLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1087>:

m268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGTGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG CCGCCCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTAAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGAAAAC CGAAGCACGC TTGGAAGAGC
401 TGCACAACCG TAAAAAAGCC CTTATCGACG AAATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGTCAAAGCG GCTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1088; ORF 268-1>:

m268-1.pep

```

1  VQSRDGLHK FKHICSAAMA LIKEPLDKVK QRNEELEAAE EAAAEALGR
51  EQEAARVSEW EERYKLSRSE FEQFWKGLPQ TVQNKQASQ KTWKSGMDKI
101 CANNAKAEGK TPNGIKFSEL ACKTAKTEAR LEELHNRKKA LIDEMAREAD
151 KKELSKRL*

```

m268-1/g268 82.3% identity in 164 aa overlap

	10	20	30
m268-1.pep	VQSRDGLHKFKHICSAAMALIKEPLDKVKQRNE		
g268	KEGAYVVKTISYSVQPTDDKSKIFAELSQAHDIHPLSELVS--MALIKEPLDKAKQRNE		
	150	160	170
	180	190	200
m268-1.pep	40	50	60
	ELEAAE-----EAAAEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTVQN		
g268	KLEAAEATAQEAREAEAAAEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTVQN		
	210	220	230
	240	250	260
m268-1.pep	90	100	110
	KLQASQKTWKS	GMKDICANNAKAEGKTP	NGIKFSE
g268	KLQASQKTWKS	GMKDICANNAKAEGKTP	NGIKVSE
	270	280	290
	300	310	320
m268-1.pep	150	159	
	MAREADKKELSKRLX		
g268	MVREEDKKELPKRLX		
	330		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1089>:

a268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGCGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG CCGCCCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTGAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGAAAAC CGAAGCACGC TTGGAAGAGC

```

616

401 TGCACAACCG TAAAAAGCC CTTCTCGACG AAATGGCCAG GGAAGCGGAC
 451 AAGAAAGAAC TGCCAAAGCG GCTCTGA

This corresponds to the amino acid sequence <SEQ ID 1090; ORF 268-1.a>:

a268-1.pep

1 VQSRDGLHK FKHICSAAMA LIKEPLDKAK QRNEELEAAE EAAAEALGR
 51 EQEVDVRVSE EERYKLSRSE FEQFWKGLPQ TVQNKLOASQ KTWKSGMDKI
 101 CANNAKAEGE TPNGIKFSEL ACKTAETEAR LEELHNRKKA LLEDEMAREAD
 151 KKELPKRL*

a268-1/m268-1 95.6% identity in 158 aa overlap

	10	20	30	40	50	60
a268-1.pep	VQSRDGLHKFKHICSAAMALIKEPLDKAKQRNEELEAAEAAAQ	ALGREQEVDRVSEW				
m268-1	VQSRDGLHKFKHICSAAMALIKEPLDKVQKQRNEELEAAEAAAQ	ALGREQEAARVSEW				
	10	20	30	40	50	60
	70	80	90	100	110	120
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEGETP	NGIKFSEL				
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEGKTP	NGIKFSEL				
	70	80	90	100	110	120
	130	140	150	159		
a268-1.pep	ACKTAETEARLEELHNRKKALLDEMAREADKKELPKRLX					
m268-1	ACKTAKTEARLEELHNRKKALIDEMAREADKKELSKRLX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1091>:

g269.seq

1 atggtttggc gtgtgaattg cgcggcaacg gcggcgctga ttttttcgct
 51 cagcccttgg atttggcgcg tgggtggtgt gtggtcgcg tccggttttt
 101 cctgcaaac ttgcgccagc cttgacgcgt ccagtgcgcc ggcgttgccg
 151 gtttcgccgt gggactttat ccggaacacg gcttcgcccc aggtgtcggc
 201 ggctttgatg cacagtttta aaaccagggc tttggggcg tttctgcgc
 251 cgcccggtgc cattttgctg tccaatcgcg gggttaaaa accggtgtcg
 301 ttttaagtcg cgtccgtcca agtcgatacg agcgcgcttc tttgcctttc
 351 attgcggtct tcgtaa

This corresponds to the amino acid sequence <SEQ ID 1092; ORF 269.ng>:

g269.pep

1 MVWRVNCAAT AALIFSSSPW IWAVVWWSR SAFSCKPCAS LDASSAPALA
 51 VSPWDFIRNT ASPKVSALM HSFKTRALGR FSAPPVAILL SNRGVKKPLS
 101 FKSPSVQVDT SALLCLSLRS S*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1093>:

m269.seq

1 ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
 51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGTCTCGG TCGGCTTTGT
 101 CTTGCAAACC TTGCGCCaCG TGCCCGCGTC CAGCGCTGC GTTGATGGTT
 151 TCGCCGTGGG ACTTTATCCA AAACACGGCT TCGCCCAAGG TGTCGGCGGC
 201 TTTGATGCAC AGTTTTAAAA CCAGGGCTTT GGGGCGGTTT TCGTCGCCGC
 251 CTGTCGCCAT TTTGCTGTCC GAGCGCGGGG TAAAAAGCC GTTGTCGTTT
 301 AAATTTTCGT CCGTCCAAGT CGATACGAGC GCGCTTCTCT GCCTTTCGTT
 351 GCGGTCTTCG TAA

This corresponds to the amino acid sequence <SEQ ID 1094; ORF 269>:

m269.pep

1 MVWRVNCAAT AVLIFSSSPW IWAIVWWSR SALSCKPCAT CPRPAPALMV
 51 SPWDFIONTA SPKVSALMH SFKTRALGRF SSPPVAILLS ERGVKKPLSF
 101 KFSSVQVDT SALLCLSLRS *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng) from *N. gonorrhoeae*:

```

m269.pep    MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT    59
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g269        MVWRVNCAATAALIFSSSPWIWAAVWVWSRFAFSCPCASLDASSAPALAVSPWDFIRNT    60

m269.pep    ASPKVSAALMHSEFKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDTALLCLSLRS    119
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g269        ASPKVSAALMHSEFKTRALGRFSAAPPVAILLSNRGVKKPLSFKSPSVQVDTALLCLSLRS    120

m269.pep    SX    121
             ||
g269        SX    122

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

```

a269.seq
1  ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGGCGCGG TCTGCTTTGT
101 CTTGGAGGTT TTGCGCCAGC GTGCCCGCGT CCAGCGCGCC GCGTTGACG
151 GTTTCGCCGT GGGACTTTAT CCAGAACACG GCTTCGCCCA AGGTGTCGGC
201 GGCTTTGATG CACAGTTTAA AAACCAGGGC TTTGGGCGCG TTTTCGTCGC
251 CGCCTGTCGC CATTGCTGTC TCCGGGCGCG GGGTTAAAAA GCCGTTGTCG
301 TTAAATTTT CGTCCGTCCA AGTCGATACG AGCGCGCTTC TCTGCCTTTC
351 GTTGTGGTCT TCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1096; ORF 269.a>:

```

a269.pep
1  MVWRVNCAAT AVLIFSSSPW IWAAVWVWAR SALSWRFCAS VPASSAPALT
51 VSPWDFIQNT ASPKVSAALM HSEFKTRALGR FSSPPVAILL SGRGVKKPLS
101 FKFSSVQVDT SALLCLSLWS S*

```

m269/a269 90.1% identity in 121 aa overlap

```

              10      20      30      40      50      59
m269.pep    MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a269        MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSWRFCASVPASSAPALTVSPWDFIQNT
              10      20      30      40      50      60

              60      70      80      90      100     110     119
m269.pep    ASPKVSAALMHSEFKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDTALLCLSLRS
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a269        ASPKVSAALMHSEFKTRALGRFSSPPVAILLSGRGVKKPLSFKFSSVQVDTALLCLSLWS
              70      80      90      100     110     120

m269.pep    120
              SX
              ||
a269        SX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

```

g270.seq
1  atgaataaaa accgcaaatt actgcttgcc gcaactgetgc tgactgcctt
51 tgccgccttc aagctcggtt tgttgcaatg gtggcaggcg cagcagccgc
101 aagccgtggc ggcgcaatgc gatttgaccg agggttgcac gctgccggac
151 ggaagccgtg tccgcgccgc cgccgtttca accaaaaaac cgtttgatat
201 ttatatcgaa cacgcgccgc ccggcacgga acaggtcagc atcagcttca
251 gtatgaaaaa tatggatatg ggtttcaacc gctatatgtt cgagcggcaa
301 ccgtcgggga cttggcaggc agcacgcata cgccgtcccg tctgtgtcga
351 aggcaggcgc gattttacgg cggacattac aatcggcagc cggacatttc
401 agacggcatt taccgccgaa taa

```

This corresponds to the amino acid sequence <SEQ ID 1098; ORF 270.ng>:

618

g270.pep

```

1 MNKNRKLLLA ALLLTAFAAF KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
101 PSGTWQAARI RLPVCVEGRR DFTADITIGS RTFQTAFTAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1099>:

m270.seq

```

1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
51 TGCCGCCGTC AAGCTCGTTT TGTTGCAATG GTGGCAGGCG Ca. CAGCCGC
101 AAGCTGTGGC GGCGCAATGC GATTTGACCG AGGGTTGCAC GCTGCCGGAC
151 GGAAGCCGCG TCCGCGCCCG CGCGGTTTCA ACCAAAAAAC CGTTTGATAT
201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGT CGGACATTC
401 AGACGGCATT TACCGCCGAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1100; ORF 270>:

m270.pep

```

1 MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA XQPQAVAAQC DLTEGCTLPD
51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 270 shows 96.4% identity over a 140 aa overlap with a predicted ORF (ORF 270.ng) from *N. gonorrhoeae*:

m270/g270

	10	20	30	40	50	60
m270.pep	MNKNRKLLLAALLLIAFAAVKLVLLQWWQAXQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
g270	MNKNRKLLLAALLLTAFAAF KLVLLQWWQA QQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRI RLPICVEGRR					
g270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAARI RLPVCVEGRR					
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1101>:

a270.seq

```

1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
51 TGCCGCCGTC AAGCTCGTTT TGTTGCAATG GTGGCAGGCG CAGCAGCCGC
101 AAGCTGTGGC GGCGCAATGC GATTTGACCG AGGGTTGCAC GCTGCCGGAC
151 GGAAGCCGCG TCCGCGCCCG CGCGGTTTCA ACCAAAAAAC CGTTTGATAT
201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGC CGGACATTC
401 AGACGGCATT TACCGCCGAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1102; ORF 270.a>:

a270.pep

```

1 MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ

```

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101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

m270/a270 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRKL	LLAALLLIAFAAVKL	VLLQWQAXQPQAVAAQCDL	TEGCTLPDGS	SRVRAAAVS	
a270	MNKNRKL	LLAALLLIAFAAVKL	VLLQWQAXQPQAVAAQCDL	TEGCTLPDGS	SRVRAAAVS	
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPFDIYIEHAPAGTEQVSISFS	MKNMDMGFNRYMFERQPSGTWQAVRI	RLPICVEGRR			
a270	TKKPFDIYIEHAPAGTEQVSISFS	MKNMDMGFNRYMFERQPSGTWQAVRI	RLPICVEGRR			
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADITIGSRTFQTAFTAEX					
a270	DFTADITIGSRTFQTAFTAEX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

```

1  atgttcagtt cgcggatggc gaggatttgg gcgacggggg taacgttggtg
51  tatggtcagt ccgtgtccgg cgttgacgac caagcccaaa tcgccggcgca
101  aatgcgcgcc gttttggatg cgctcgaact gcctgatttg ttcggcggtgg
151  ctttgtgcgt cggcatatgc gccggtgtgc agctcgacaa cgggcgcgcc
201  gacatcacgg gcggcttggg tttgcctgtc gtcggcatcg ataaacaagg
251  acacgcgtat gcccggtcgc gtcaggattt tggcgaattc ggcgattttt
301  tcctgttgcg ccaatacgtc caaaccgcct tcggtcgtga tttcctgccg
351  tttttcaggc acgatgcaca cgtcttccgg catcacttta agcgcgtttt
401  cgagcatttc ttccgtcaac gccatttcaa ggttcaggcg cgtgcggatg
451  gcgtttttga cggcaaatac atccgcgtct ttgatgtggc ggcggtcttc
501  gcgcaggtgc atggtaatca ggtctgcacc gtgcgtttcg gcaaccagtg
551  ccgcctccac ggggctggga taa

```

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

g271.pep

```

1  MFSSRMARIW ATGVTLCMVS PCPALTTKPK SPAKCAPFWM RSNCLICSAW
51  LCASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILANSATF
101  SCCANTSKPP SVVISCRFSG TMHTSSGITL SAFSSISSVN AISRFRVRM
151  AFLTANTSAS LMWRRSSRRC MVIRSAPCVS ATSAASTGLG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

```

1  AwGTTcagtt CGCGGATGGC GAGGATTtGG GCGATGGGGG TAACGTTGTG
51  TATGGTCAGT CCGTGTCCGG CGTTGACGAC CAAGCCCAAA TCGCCGGCGA
101  AATGCGCGCC GTTTTGGATG CGCTCGAACT GCCTGATTtG TTCGGCGTGG
151  CTGCGCGCGT CGGCATACGC GCCTGTGTGC AGCTCGACAA CGGGCGCGCC
201  GACATCACGG GCGGCTTtGA TTTGCCTGTC GTCGGCATCG ATAAACAAAG
251  ACACGCGTAT GCCTGCGTCG GTCAGGATTt TGGTGAACCC GGCGATTtTT
301  TCCTGTtGCG CCAATACGTC CAAACCGCCT TCGGTCGTGA TTTCTGACG
351  TTTTTCAGGC ACGATGCACA CGTCTTCCGG CATCACTtTC AAAGCGTtTT
401  CCAACATTTC TTCCGTCAAC GCCATTtCAA GGTTcAGGCG CGTGCGGATG
451  GCGTtTTTGA CGGCAAACAC GTCCGCGTCT TTGATGTGGC GGCGGTCTTC
501  GCGCAGGTGC ATGGTAATCA AATCCGCACC GTGCGTtTCG GCAACCAGTG
551  CCGCCTCCAC GGGGCTGGGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

```

1  XFSSRMARIW AMGVTLCMVS PCPALTTKPK SPAKCAPFWM RSNCLICSAW
51  LRASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILVNPAIF
101  SCCANTSKPP SVVISXRFSG TMHTSSGITF KAfSNISSVN AISRFRVRM
151  AFLTANTSAS LMWRRSSRRC MVIKSAPCVS ATSAASTGLG *

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. gonorrhoeae*

ORF 271 shows 95.2% identity over a 189 aa overlap with a predicted ORF (ORF 271.ng) from *N. gonorrhoeae*:

m271/g271

	10	20	30	40	50	60
m271 . pep	XFSSRMARIWAMGVTL CMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
g271	MFSSRMARIWATGVTL CMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLCASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271 . pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNP AI FSCCANTS SKPPSVVISXRFSG					
g271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILANSA IF FSCCANTS SKPPSVVISCRFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m271 . pep	TMHTSSGITL SAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIR SAPCVS					
g271	TMHTSSGITL SAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIR SAPCVS					
	130	140	150	160	170	180
	190					
m271 . pep	ATSAASTGLGX					
g271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1107>:

a271 . seq

1	ATGTT	CAGTT	CGCGG	ATGGC	GAGGA	TTTGG	GCGAT	GGGGG	TAACG	TTGTG
51	TATGG	TCA	CGTGT	CCCGG	CGTTG	ACGAC	CAAGC	CCAAA	TCGCT	TGGCA
101	AATGC	GCGCC	GTTTT	TGGAT	CGCTC	GAACT	GCCTG	ATTTG	TTCGG	CGTGG
151	CTGCG	CGCGT	CGGCAT	ACGC	GCCTG	TGTGC	AGCTC	GACAA	CGGGC	CGCGC
201	GACAT	CACGG	GCGGCT	TGGA	TTTGC	CTGTC	GTCGG	CATCG	ATAAA	CAAGG
251	ACACG	CGTAT	GCCCG	CGTCG	GTCAG	GATTT	TGGTG	AATTC	GGCAAT	TTTG
301	TCTTG	TGCG	CCAAT	ACGTC	CAAGC	CGCCT	TCGGT	CGTGA	TTTCT	TGACG
351	TTTTT	CCGGC	ACGAT	GCACA	CGTCT	TCCGG	CATCA	CTTTA	AGCGC	GTTTT
401	CGAGC	ATTTT	TTCCG	TCAAC	GCCAT	TTCAA	GGTTC	CAGGC	CGTGC	GGATG
451	GCGT	TTTTT	GACG	AAAC	GTCCG	CGTCT	TTGAT	GTGGC	GGCGG	TCTTC
501	GCGC	AGGTGC	ATGGA	AATCA	GGTCG	GCACC	GTGCG	TTTCG	GCAAC	CAGTG
551	CCGC	CTCCAC	GGGGC	TGGGA	TAA					

This corresponds to the amino acid sequence <SEQ ID 1108; ORF 271.a>:

a271 . pep

1	MFSSRMARIW	AMGVTL	CMVS	PCPAL	TTKPK	SLAKCAP	FWM	RSNCLIC	SAW
51	LRASAYAPVC	SSTTGAPTSR	AAWICLSSAS	INKDTRMPAS	VRILVNSAIL				
101	SCCANTS	SKPP	SVVIS*RFSG	TMHTSSGITL	SAFSSISSVN	AI	SRFRVRM		
151	AFLTANTSAS	LMWRRSSRRC	MVIR	SAPCVS	ATSAASTGLG	*			

m271/a271 96.3% identity in 189 aa overlap

	10	20	30	40	50	60
m271 . pep	XFSSRMARIWAMGVTL CMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
a271	MFSSRMARIWAMGVTL CMVSPCPALTTKPKSLAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271 . pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNP AI FSCCANTS SKPPSVVISXRFSG					
a271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNSAILSCCANTS SKPPSVVISXRFSG					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIKSAPCVS					
a271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRSAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
a271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

g272.seq

```

1  atgactgcaa aggaagaact gttcgcatgg ctgcgccata tgaacaaaaa
51  caaaggttcc gacctgtttg tgacgacca tttcccgccc gctatgaagc
101 tggacggcaa aatcaccgcg atcacggacg aaccgctgac ggcggaaaaa
151 tgtatggaaa tcgccttttc gattatgagt gcgaagcagg cggaagaatt
201 ttcacgcgacc aacgagtgcg atttcgccat cagcctgccg gacaccagcc
251 gcttccgcgt caatgcgatg atacagcgcg gtgcgacggc gttggtattc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgccgcc
351 ggccttgaag gatgttgcgc tgaaaaaacg cgggctggtt atttttgtcg
401 gcggcaccgg ctcgggcaaa tcgacttcgc tcgcctcgct tatcgactac
451 cgcaatgaaa attcgttcgg acacatcatc accatcgaag atccgatcga
501 gtttgtccac gaacacaaaa actgcatcat taccagcgcg gaggtcggcg
551 tggacacgga aaactggatg gcggcggtga aaaatacgct gcgtcaggcg
601 ccggatgtga tccttatcgg cgaaatccgc gaccgtgaaa caatggacta
651 cgccatcgcc tttgccgaaa cggggcattt gtgtatggcg acgctgcacg
701 ccaacagcac caatcaggcg ctcgaccgca tcatcaactt cttccccgag
751 gagcggcgcg aacaattgct gacggatttg tcgctcaacc ttcaggcggt
801 tatttcgcaa cgcctcgttc cgcgagacgg cggcaaggcg aggggtggcg
851 cagtcgaggt gctgctcaat tcgcccctga tttcggagtt gattcacaac
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggatgccttg aaaaatgccg attccgcaca tgatttgcgt
1051 ttggcggtac agttgcgcag ccgcagggca caaagttccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

g272.pep

```

1  MTAKEELFAW LRHMNKNKGS DLFVTTTHFP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAM IQRGATALVF
101 RAITSKIPKF ESLNLPALK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSGFHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

m272.seq

```

1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAWCCAAAA
51  CAAAGGTTCC GACCTGTTCG TGACAACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACC CGC ATCACGGACG AACC GCTGAC GGCGGAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGCCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GCGCGACGGC GTTGGTATTC
301 GCTACGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 AGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCAGCGCG GAGGTCCGCC

```

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```

551 TGGATACGGA AACTGGATG GcGGCGTTGA AAAACACGCT GCGTCAGGCG
601 CCTGATGTCA TCCTTATCGG CGAAATCCGT GACCGCGAAA CAATGGACTA
651 CGCCATTGCC TTGCGCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTTG TCGCTCAACC TTCAGGCGTT
801 TATTTGCAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCTcGA TTTCGGAGTT GATTACAAC
901 GGCAACATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACC TTCGATCAAC ACCTTTACCA ATTGTATGAA AAAGGCGATA
1001 TTTCCCTGCA AGAAGCATTG AAAAATGCCG ATTCGCGACA CGATTTCGCT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCGCGCG CAaAGTTyCA GCCCCGATT
1101 GGnACTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1112; ORF 272>:

m272.pep

```

1  MTAKEELFAW LRHMxQNKGs DLFVTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVnam IQRGATALVF
101 RTITSKIPKF ESLNLPPVLK DVALKKRGLV IFVGGTGSGK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLcMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLyQLYE KGDISLQEAL KNADSAHDLR
351 LAVQLRSRRA QXSPDLXLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 272 shows 97.6% identity over a 370 aa overlap with a predicted ORF (ORF 272.ng) from *N. gonorrhoeae*:

m272/g272

	10	20	30	40	50	60
m272.pep	MTAKEELFAWLRHMxQNKGsDLFVTTHFPPAMKLDGKITRITDEPLTAEKcMEIAFSIMS					
	:					
g272	MTAKEELFAWLRHMKNKGsDLFVTTHFPPAMKLDGKITRITDEPLTAEKcMEIAFSIMS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m272.pep	AKQAEFSSTNECNFAISLPDTSRFRVnamIQRGATALVFRTITSKIPKFESLNLPPVLK					
	: :					
g272	AKQAEFSSTNECNFAISLPDTSRFRVnamIQRGATALVFRAITSKIPKFESLNLPPALK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m272.pep	DVALKKRGLVIFVGGTGSGKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIITQR					
g272	DVALKKRGLVIFVGGTGSGKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIITQR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m272.pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAIAFAETGHLcMATLHANSTNQA					
g272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAIAFAETGHLcMATLHANSTNQA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m272.pep	LDRIINFFPEERREQLLTDLsLNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
g272	LDRIINFFPEERREQLLTDLsLNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m272.pep	GNIHEIKEVMKKSTTLGMQTFDQHLyQLYEKGDISLQEALKNADSAHDLRLAVQLRSRRA					
	:					
g272	GNIHEIKEVMKKSTTLGMQTFDQHLyQLYEKGEISLQDALKNADSAHDLRLAVQLRSRRA					
	310	320	330	340	350	360

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```

          370
m272.pep  QSXSPDLXLLX
          || :||| |||
g272      QSSDPDLELLX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

```

a272.seq
1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51  CAAAGGTTCC GACCTGTTCC TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GCGGAAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGCAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG
551 TGGATACGGA AAACGATGAT GCGGCGTTGA AAAACACGCT GCGTCAGGCA
601 CCGGATGTGA TTCTGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGCAG
751 GAGCGGCGCG AACAATTGCT GACGGATTTG TCGCTCAACC TTCAGGCATT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCTGA TTTCGGAGTT GATTACAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACT TTCGACCAAC ACCTTTACCA ATTGTATGAA AAAGGCGAGA
1001 TTTCTTGCA GGATGCCTTG AAAAATGCCG ATTCCGCACA CGATTTCGCT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCAGGCG CAAAGTTCCG GTCCCATT
1101 GGAAGTGTCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

```

a272.pep
1  MTAKEELFAW LRHMNKNKGS DLFVTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAI IQRGATALVF
101 RAITSKIPKF ESLNLPVVK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYIAI FAETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLYQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDLELL *

```

m272/a272 97.6% identity in 370 aa overlap

```

          10      20      30      40      50      60
m272.pep  MTAKEELFAWLRHMNKNKGS DLFVTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
          ||||| :|||||
a272      MTAKEELFAWLRHMNKNKGS DLFVTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
          10      20      30      40      50      60

          70      80      90      100     110     120
m272.pep  AKQAEFSSTNECNFAISLPDTSRFRVNAI IQRGATALVFRTITSKIPKFESLNLPVVK
          ||||| :|||||
a272      AKQAEFSSTNECNFAISLPDTSRFRVNAI IQRGATALVFRITSKIPKFESLNLPVVK
          70      80      90      100     110     120

          130     140     150     160     170     180
m272.pep  DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR
          ||||| :|||||
a272      DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR
          130     140     150     160     170     180

```

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	190	200	210	220	230	240
m272.pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
a272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
	190	200	210	220	230	240
	250	260	270	280	290	300
m272.pep	LDRIINFFPEERREQLLTDLSNLQAFISQRLVPRDGGKGRVA AVEVLLNSPLISELIHN					
a272	LDRIINFFPEERREQLLTDLSNLQAFISQRLVPRDGGKGRVA AVEVLLNSPLISELIHN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m272.pep	GNIHEIKEVMKKSTTLGMQTFDQHL Y Q L Y E K G D I S L Q E A L K N A D S A H D L R L A V Q L R S R R A					
a272	GNIHEIKEVMKKSTTLGMQTFDQHL Y Q L Y E K G E I S L Q D A L K N A D S A H D L R L A V Q L R S R Q A					
	310	320	330	340	350	360
	370					
m272.pep	Q S X S P D L X L L X					
a272	Q S S G P D L E L L X					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1115>:

g273.seq

```

1  atgagctcttc aggcggtatt tatatacccc ccaagccgta ccgcacaata
51  caacgaaaat caggaaaacg gcggtaaagc tcataaacag ggacaaagcg
101 gcaaacacac cgaccgccgt caggatatag gcgtattcga ggccggaact
151 ccattcaccg ttttctgcc gtttctgtc gcttttgaaa taaaggatga
201 tgccggcaag cagcgcggca gccgcgccg acattggcat tgtgttcatt
251 gttgttcctt aacggttaaa aaccgcccg gccgtgcaac cgttttaagg
301 cgggaaattg caaaatttgt ttgcggggcg gtgccgctga aatcaaggcg
351 gtttgagaag tgtttccnac gcgcccgcc tatgtgccga aatattattt
401 gtcgctcacc tgcaaaatcg ccaagaacgc gctttgcgga atttccacgt
451 tgcccacttg tttcatacgg cgtttgctg ctttttgtt ttcaagcagt
501 ttttcttac gcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1116; ORF 273.ng>:

g273.pep

```

1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHTDRR QDIGVFEAGT
51  PFTVFLPFLV AFEIKDDAGK QRGSRARHWH CVHCCSLTVK NPPGRATVLR
101 REIAKFVCGR VPLKSRRFEK CFXRARPMCR NIICRSPAKS PRTRFAEFPR
151 CPLVSYGVCL LFVQAVFSY A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1117>:

m273.seq

```

1  ATGAGTCTTC AGGCGGTATT TATATACCCm CCAAGCCGTA CCGCACAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCAYAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCTGT CAGGATATAG GCGTATTCAA GGCCGGAAC
151 CCATTCCCCG TTTCTCTGCC GCTTCTTGTC GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCG ACATTAGCAT TGTGTTCATT
251 GTTGTTCCTT AATGCTTAAA AACCCGCTG TCCGTGCAAC CGTTTAAAG
301 CGGCAAAATG CAAAATTGT TTGCGGGCGC GTGCCCTGA AATCAGGGC
351 GTTTGAGGGG TGTTCCTGAC GCGCCGCCCT GTGTGCCGA GTTATTGTG
401 GCTCACCTGC AAAATCGCCA AGAACGCGCT TTGCGGAATT TCCACATTGC
451 CCACTTGTTT CATACGGCGT TTACCTGCCT TTTGtKtWTC AAGCAGTTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1118; ORF 273>:

m273.pep

```

1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHADRC QDIGVFKAGT
51  PFPVFLPLLV AFEIKDDAGK QRGSRARH*H CVHCCSLMLK NPPVRATVLR
101 RQIAKFVCGR VPLKSGRFEG CSRRALCAG VICRSPAKSP RTRFAEFPHC
151 PLVSYGVYLP FVXQAVFSYA *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 273 shows 86.0% identity over a 171 aa overlap with a predicted ORF (ORF 273.ng) from *N. gonorrhoeae*:

m273/g273

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGSGKHADRCQDIGVFKAGTPFPVFLPLL					
	: : :					
g273	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGSGKHTDRRQDIGVFEAGTPFTVFLPFLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m273.pep	AFEIKDDAGKQGRSRARHXHCVHCCSLMLKNPPVRATVLRRIAKFVCGRVPLKSGRFEG					
	: : :					
g273	AFEIKDDAGKQGRSRARHWHCVHCCSLTVKNPPGRATVLRREIAKFVCGRVPLKSRFEK					
	70	80	90	100	110	120
	130	140	150	160	170	
m273.pep	CSRRA-ALCAGVICRSPAKSPRTRFAEFPHCLVSYGVLPFVXQAVFSYAX					
	: : : :					
g273	CFXRARPMCRNIICRSPAKSPRTRFAEFPRCLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

a273.seq

```

1   ATGAGTCTTC AGGCGGTATT TGTATACCCC CCAAGCCGTA CCGCACAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCATAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCCGT CAGGATATAG GCGTATTCCA GACCGGAAC
151 CCATTCACCG TTTTCCTGCC GCTTTTGTG GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCCG ACATTAGCAT AATGTTTATT
251 GTTGTTCCTT AACGGTTAAA AACC CGCCCG TCCGTGCAAC CGTTTTTAAG
301 AGGCGGTAAA TCACAAAGTT TGTGGCGGA CGTGCTCTCT TACAATCAGG
351 GCGGTTTAAG GGGCATGATG CACTGCCCCG TGTGCCGGAT ATTATTTGTC
401 GCTCACCTGC AAAATTGCCA AGAACGCGCT TTGCGGGATT TCCACATTGC
451 CCACTTGTTT CATACGGCGT TTGCCTGCTT TTTGTTTTTC AAGCAGTTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

a273.pep

```

1   MSLQAVFVYP PSRTAQYNEN QENGGAHKQ GSGKHADRR QDIGVFQTGT
51  PFTVFLPLFV AFEIKDDAGK QGRSRARH*H NVHCCSLTVK NPPVRATVEK
101 RR*ITKFVGG RALLQSGRFK GHDALPRVPD IICRSPAKLP RTRFAGFPHC
151 PLVSYGVCLL FVFQAVFSYA *

```

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGSGKHADRCQDIGVFKAGTPFPVFLPLL					
	: : :					
a273	MSLQAVFVYPPSRTAQYNENQENGGAHKQGGSGKHADRRQDIGVFQTGTPTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m273.pep	AFEIKDDAGKQGRSRARHXHCVHCCSLMLKNPPVRATVL-RRQIAKFVCGRVPLKSGRFE					
	: : :					
a273	AFEIKDDAGKQGRSRARHXHNVHCCSLTVKNPPVRATVFKRRXITKFVGG RALLQSGRFK					
	70	80	90	100	110	120
	120	130	140	150	160	170
m273.pep	GCSRRAALCAGVICRSPAKSPRTRFAEFPHCLVSYGVLPFVXQAVFSYAX					
	: :					
a273	GHDALPRV-PDIICRSPAKLP RTRFAGFPHCLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1121>:

g274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCatCGCC AgcgTCGCTA TGTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAGGATG
101 GCAAGCATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTCCT CATTCTCTCC GATATGAATG CGGCAAAAGT
201 GTTTGTCTGGC ggCgagtTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTgt tcaaAACCCT
351 TCCGCCGGCC AACCCTGGT ATGTGCGCGT GGAaggacgCG GCAGGCGTGT
401 GGCAGCTCGA GAACAAATGG ATTACCAGCC AGGGCAATGC GGTCGATTG
451 ACCCCGATGG ACAAACCTTT CAATAATGCA GGAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1122; ORF 274.ng>:

g274.pep

```

1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLPPA NHWYVRVEDA AGVWRVENKW ITSQGNVAVDL
151 TPMDKLFNNA GSK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1123>:

m274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAGACG
101 GCAAACATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCTCC GATATGAATG CGGCAAAAGT
201 GTTTGTCTGGC GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTGT TCAAACCCT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGCAGCTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTCGATTG
451 ACCCCGATGG ACAAGCTTTT CAATAATACT GAAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1124; ORF 274>:

m274.pep

```

1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTSLPT NHWYVRVEDA AGVWRVENKW ITSQGNVAVDL
151 TPMDKLFNNT ESK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 274 shows 97.5% identity over a 163 aa overlap with a predicted ORF (ORF 274.ng) from *N. gonorrhoeae*:

g274/m274

	10	20	30	40	50	60
g274.pep	MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
m274	MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g274.pep	DMNAAKVFGGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLPPA					
m274	DMNAAKVFGGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTSLPT					
	70	80	90	100	110	120
	130	140	150	160		
g274.pep	NHWYVRVEDAAGVWRVENKWITSQGNVAVDLTPMDKLFNNAGSKX					
m274	NHWYVRVEDAAGVWRVENKWITSQGNVAVDLTPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

```
a274.seq
1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAGCATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCTCCC GATATGAATG CGGCAAAAGT
201 GTTTGTCGGC GGCGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GCGGGAATAT GAGGCGGTGT TCAAACCCCT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGCAGCGTCG GAACAAATGG ATTACCAGCC AAGGCAATGC GGTGATTTG
451 ACCCCGATGG ACAAACCTTT CAATAATACT GAAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

```
a274.pep
1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFVG GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNT ESK*
```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274.pep	MAGPIFVVIVASVAMFFVAQQHATDLVTDDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
a274	MAGPIFVVIVASVAMFFVAQQHATDLVTDDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m274.pep	DMNAAKVFVGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
a274	DMNAAKVFVGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
	70	80	90	100	110	120
	130	140	150	160		
m274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
a274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1127>:

```
g276.seq
1  atgatttttcg cgccatccat gacgatgatg cggtcggcgg attcgacggt
51  gggtcaggcgg tgggacgagc tgatgccggt gcggttttcc atcaggcggt
101 cgagcgcttg ttggacgagg cgttcggtt cgttgtccaa tgcgctggtg
151 gcttcgtcca ataataatat cggcgcgtct ttcaaatgg cgcgggcgat
201 ggcgacgcgt tgcgctgctc cgccggataa gttgctgccg ttcgatccga
251 tgggctggtg cagtcgagc ggggatgcgt cgatcaggct ttgcaggttg
301 gcggcttgga gggcggacag gacttcggct tcgcccgcgt cgggacggct
351 gtatcggacg ttttcaaaca ggggtgctgc aaacaggaat acgtcttggg
401 agacgagggc gaattgggag cgacggcagc cgagtttgat gtcggcgatg
451 tcgataccgt ctatgcagat gttgccgga gacggttcga caaagcgggg
501 cagaaggttg acgacggttg atttgccgct gccggaacgt ccgaccaggg
551 cgacgcgttc gccttgctc atgtcgaggt tgaagtgtc gagggctttg
601 atgccgtctg aacggtattc gacatcgacg ttgcggaagc tgatgcgccc
651 ttcgacacgc tgcggcgca gcgtgccttt gtctgttcg ggcggggtgt
701 cgagaaatgc acatacgccg tcggcggcga ggaacatcgt ctgcataggg
751 atgctgatgt tggcaaggct tttgatggg gcgtacattt gcagcatcgc
801 gacgatgaat gccataaatt cgccgatggt ggtgtag
```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

g276.pep

```

1  MILPPSMTMM RSADSTVVRR WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKRGRR LTTVDLPLPER PTRATRSPLC MSRLKLSRAL
201 MPSERYSTST LRKLMPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1129>:

m276.seq

```

1  ATGATTTTGC CGTCGTCCAT CACGATGATG CGGTCGGCCC CTTCGATGGT
51  GGTACAGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTCC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCTAA TGCGCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATG CGCGGGCAAT
201 GGCGACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGGGAGCTGT CAATCAGGCT TTGCAGGTTG
301 GCGGTTTGGA GGGCGAACAG GACTTCGGCT TCGCCGCGT CGGGACGGCT
351 GTATCGGACG TTTTCAAACA GGGTGTCTGC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGGC GAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTCTG ATGTCGAGGT TGAAGTTGTC GAGGGCTTTG
601 ATGCCGCTCT AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TGCGGTGCGA GCGTGCCCTT GTCCTGTTCT GGCGGGGTGT
701 CGAGAAATGC ACATACACCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTGATGT TGGCAAGGCT TTTGATGGGG GCGTACATTT GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1130; ORF 276>:

m276.pep

```

1  MILPSSITMM RSAPSMVVRR WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPPDKLLP FDPMGWCSPS GELSIRLCRL
101 AVWRANRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKRGSR LTTVDLPLPER PTRATRSPLC MSRLKLSRAL
201 MPSERYSTST LRKLMPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 276 shows 96.8% identity over a 278 aa overlap with a predicted ORF (ORF 276.ng) from *N. gonorrhoeae*:

m276/g276

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	:					
g276	MILPSSMTMMRSADSTVVRRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
	: : : : : : :					
g276	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKRGSRLLTTVDLPLPER					
	: : : : : : :					
g276	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKRGRRLLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPLCMSRLKLSRALMPSERYSTSTLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
	: : : : : : :					
g276	PTRATRSPLCMSRLKLSRALMPSERYSTSTLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240

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	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

a276.seq

```

1  ATGATTTTGC CGTCGTCCAT TACGATGATG CCGTCGGCCC CTTCGATGGT
51  GGTCAGGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCCAA TGCCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAAATGG CGCGGGCAAT
201 GGCAACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGTGATGCGT CGATCAGGCT TTGCAGGTTA
301 GCGGCTTGGA GGGCGGATAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 ATATCGGACG TTTTCAAACA GGGTGTCGTC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGGC AAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTG ACGACGGTG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTG ATGTCGAGGT TGAAGCCGTC GAGGGCTTTG
601 ATGCCGTCG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TCGGTGCGA GCGTGCTTT GTCTGTTCG GCGGGGTGT
701 CGAGAAATGC ACATACGCCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTAATGT TGGCAAGGCT TTTGATGGGG GCGTACATT GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

a276.pep

```

1  MILPSSITMM RSAPSMVRR WATMPVRES IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRPPDKLLP FDPMGWCS PS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLSMSAM
151 SIPSMQMLPA DGSTKGRSRL TTVDLPLPER PTRATRSPCL MSRLKPSRAL
201 MPSEYSTST LRKLMPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVRRWATMPVRESIRRSSACWTRRSDSLSNALVASSNNNIGAS					
a276	MILPSSITMMRSAPSMVRRWATMPVRESIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRPPDKLLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
a276	FKMARAMATRCRPPDKLLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLSMSAMSIIPSMQMLPADGSTKGRSRLTTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSLSMSAMSIIPSMQMLPADGSTKGRSRLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPCLMSRLKLSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVS RNAHTP					
a276	PTRATRSPCLMSRLKPSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVS RNAHTP					
	190	200	210	220	230	240
	250	260	270	279		
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					

630

250 260 270

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1133>:

```
g277.seq (partial)
1  ..atggtacacg tcgccgtagc ttacggtatt gccgtccggc gtttttgccc
51  aaacgaggtc atagacgttt tccacgcctt gcaggtagat cgccaagcgt
101 tcgatgccgt aggtaatttc gccgagtacg ggcgtagaat cgataaccgcc
151 gacttggttg aaataggtaa actgggttac ttccatgccg ttgagccaga
201 cttcccagcc caaaccaccac gcaccgaggg tggggttttc ccagtcgtct
251 tcgacaaagc ggatgtcgtg gactttggga tcgatgccca attcgcgcag
301 ggagtcgaga tagaggtcct ggatattggc gggggcgggg ttgaggcgga
351 cttggaattg gtaatagtgt tgcaggcggg tggggttggt gccgtagcgg
401 ccgtcttttg ggcggcggtt ggggtggacg taggcggcaa accaaggctc
451 gggggccgagc gcgcgcaggc aggtggcggg atgggatgtg ccggcaccga
501 cttccatgtc gaagggttgg atgacgggtg agcctttgtc tgcccagaag
551 gtttgcagtt tgaagatgat ttgttgaag gtaagcatgg cttattgttc
601 gataaaataa aggttttatt ttactgtttc catagccgct tgaatagatt
651 tatctcgaag acagcctga
```

This corresponds to the amino acid sequence <SEQ ID 1134; ORF 277.ng>:

```
g277.pep (partial)
1  ..MVHVAVAYGI AVRRFCPNEV IDVFHALQVH RQAFDAVGNF AEYGRAIDTA
51  DLLEIGKLG YFHAVEPDFPA QTPRTEGGVF PVVFDKADV DFGIDAQFAQ
101 GVEIEVLDIG GGGFEGDLEL VIVLQAVGVV AVAAVFGAAA GLDVGGKPLR
151 GAERAQAGGG MGCAGTDFHV EGLDDGAFAV CPEGLQFEDD LLEGKHGLLF
201 DKIKVLFYCF HSRLNRFISK TA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1135>:

```
m277.seq
1  ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAGTGG
101 CGCAGCAGCC AGTCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTGCTC
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA GGTGACGGTG TTGCCGTCGA
201 GCGTTTTTGC CCAAACGAGG TCGTAGACGT TTTCTACACC TTGCAAGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGCGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT AAAGTGGGTT ACTTCCATGC
351 CGTTGAGCCA GACTTCCAG CCCAAACCCC ACGCGCCGAG GGTGGGTTT
401 TCCAGTCGT CTTCGACAAA GCGGATGTCG TGGACTTTGG GATCGATGCC
451 CAATTCGCGC AGAGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGCAGGCG GTTGGGTTG
551 TCGCCGTAGC GGCCGTCTT GGGCGCGCG CTGGGTTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG GCAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGTT GGATGACGGT GCAGCCTTTG
701 TCTGCCAGA ATGTTTGCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GGCTTATGA
```

This corresponds to the amino acid sequence <SEQ ID 1136; ORF 277>:

```
m277.pep
1  MPRFEDKLVG RQEGGVVFFG KQAFGLRFVV VELAQQPVGI AVFEVVGGLL
51  DFVLVVHVAV GDGVAVERFC PNEVVDVFT LQVHRQAFDA VGDFAEYGRA
101 VDAADLLEIG KLG YFHAVEP DFPAQTPRAE GGVPVVFDA ADVVDFGIDA
151 QFAQRVEIEV LDIGSGLEG DLELVIVLQA VGVVAVAAVF GAAAGLDVGG
201 KPRLGAECAQ AGGGMGCAGT DFHVEGLDDG AAFVCPCLQ FEDDLLEGKH
251 GL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 277 shows 90.0% identity over a 221 aa overlap with a predicted ORF (ORF 277.ng) from *N. gonorrhoeae*:

g277/m277

g277.pep

10 20 30
MVHVAVAYGI AVRRFCPNEV IDVFHALQVH

```

m277      GLRFVVVELAQQFVGIAVFEVVGGLLDFVLVVHVAVGDBGVAVERFCPNEVVDVFTLQVH
           30          40          50          60          70          80

           40          50          60          70          80          90
g277.pep  RQAFDAVGNFAEYGRAIDTADLLEIGKLGYPHAEVDFPAQTPTREGGVFPVVDKADV
           |||||:|||||:|:|||||||||||||||||||||:|||||
m277      RQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAEVDFPAQTPRAEGGVFPVVDKADV
           90          100         110         120         130         140

           100         110         120         130         140         150
g277.pep  DFGIDAQFAQGVIEIVLDIGGGFEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGKPR
           ||||| |||||:|:|||||||||||||||||||||
m277      DFGIDAQFAQRVEIEVLDIGGSGLEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGKPR
           150         160         170         180         190         200

           160         170         180         190         200
g277.pep  GAERAQAGGGMGCAGTDFHVEGLDDGAAFVCPEGLQFEDDLLEGKHGLL
           || |||||
m277      GAECAQAGGGMGCAGTDFHVEGLDDGAAFVCPECLQFEDDLLEGKHGLX
           210         220         230         240         250

```

```
a277.seq
  1  ATGCCCCGCT  TTGAGGACAA  GCTCGTAGGC  AGGCAGGGCG  AGGGCGGCGT
51  TTTCTTCGGC  AAGCAGGCGT  TTGGCTTGCG  CTTCGTAGTC  GTTGAAGTGG
101 CGCAGCAGCC  AATCGGCATC  GCTGTATTCG  AAGTTGTAGG  TGGATTGTTC
151 GACTTCGTTT  TGGTGGTACA  CGTCGCCGTA  AGTTACTGTA  TTAACCGTCCA
201 GCGTTTTTTC  CCAAACGAGG  TCATAGACGT  TTTCCACGCC  TTGCAGGTAC
251 ATCGCCAAGC  GTTCGATGCC  GTAGGTGATT  TCGCCGAGTA  CGGGGGTGCA
301 GTCGATGCCG  CCGACTTGTT  GGAAATAGGT  GAACTGGGTT  ACTTCCATAC
351 CGTTGAGCCA  GACTTCCAG  CCCAAACCCC  ACGCGCCGAG  GGTGGGGTTT
401 TCCCAGTCGT  CTTCGACAAA  GCGGATGTCT  TGCACTTTGG  GGTTCGATGCC
451 CAATTGCGGC  AGGGAGTCGA  GATAGAGGTC  TTGGATATTG  GCGGGAGCGG
501 GCTTGAGGGC  GACTTGGAAT  TGGAATAGT  GTTGCAGGCG  GTTGGGGTTG
551 TCGCCGTAGC  GACCGTCTTT  GGGGCGGCGG  CTGGGTGGA  CGTAGGCGGC
601 AAACCAAGC  TCGGGGCCGA  GTGCGCGCAG  ACAGGTGGCG  GGATGGGATG
651 TGCCGGCACC  GACTTCCATG  TCGAAGGGTT  GGATGACGGT  GCAGCCTTTG
701 TCTGCCCAGA  ATGTTTGCAG  TTTGAAGATG  ATTGTGTTGA  AGGTAAGCAT
751 GGCTTATGA
```

a277.pep

1	MPRFEDKLVG	RQEGGVVFFG	KQAFGLRFVV	VELAQQPIGI	AVFEVVGGLF
51	DFVLVVHVAV	SYCITVQRFC	PNEVIDVFHA	LQVHRQAFDA	VGDFAEYGGA
101	VDAADLLEIG	ELGYFHTVEP	DPAQTPRAE	GGVFPVVFDK	ADVVFHGVDA
151	QFAQGVEIEV	LDIGGSGLEG	DLELVIVLQA	VGVVAVATVF	GAAAGLDVGG
201	KPRLGAECAQ	TGGGMGCAGT	DFHVEGLDDG	AAFVCPECLQ	FEDDLLEGKH
251	GL*				

	10	20	30	40	50	60
m277.pep	MPRFEDKLVGRQGE GGV FFGKQAFGLRFV VV ELAAQ Q PVGI AV FEV V GGLLDFVL V VHVAV					
a277	MPRFEDKLVGRQGE GGV FFGKQAFGLRFV VV ELAAQ Q PIGI AV FEV V GGLLDFVL V VHVAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m277.pep	GDGVAVERFCPNEV VD VFYTLQVHRQAFDAVGDFAEYGRAVDAADLLEIGKLG Y FHAVEP					
	: :					
a277	SYCITVQRFCPNEV ID VFHALQVHRQAFDAVGDFAEYGGAVDAADLLEIGELGY F HTVEP					
	70	80	90	100	110	120
	130	140	150	160	170	180

632

```

m277.pep    DFPAQTPRAEGGVFPVVFDDKADVDFGIDAQFAQRVEIEVLDIGGSGLEGDLVLVILQA
            |||||
a277        DFPAQTPRAEGGVFPVVFDDKADVDFGIDAQFAQRVEIEVLDIGGSGLEGDLVLVILQA
            130      140      150      160      170      180

            190      200      210      220      230      240
m277.pep    VGVVAVAAVFGAAAGLDVGGKPRLLGAECAQAGGGMGCAGTDFHVEGLDDGAAAFVCECLQ
            |||||
a277        VGVVAVATVFGAAAGLDVGGKPRLLGAECAQAGGGMGCAGTDFHVEGLDDGAAAFVCECLQ
            190      200      210      220      230      240

            250
m277.pep    FEDDLLEGKHGLX
            |||||
a277        FEDDLLEGKHGLX
            250

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1139>:

g278.seq (partial)

```

1  ttgctgcaa tcacgcccg tgcatgtttt tcgacagggg cgggtcaaagt
51  tgtattaatc ggacctttgc cgtcgatagg ccgacccaat gcatcgacga
101 cgcgtccgac caattcgcgt ccgaccggca cttctaaaat acggccggta
151 caggtaaccg tgcgccttc tttaatatgt tcgtactcgc ccaacactac
201 ggaccgcagc gagtgcgct ccaggttcat cgccaagcct aaagtgttac
251 ccgggaattc gagcatctca ccttgcatg catctgacaa accatggatg
301 cgaacgatac cgtcagttac cgaaatcacc gtaccacggg tactcacttc
351 ggcatttaca gacagatttt cgatcttggc tttaatcaga tcgctaattt
401 cagcaggatt aagctgcatg aaaactctcc taattcgtca tagtcgtgta
451 caaagcactc agtttgctt gtacagacaa atccaaaacc tgatcaccca
501 cttcaacttt ta...

```

This corresponds to the amino acid sequence <SEQ ID 1140; ORF 278.ng>:

g278.pep (partial)

```

1  LRAITPGAIF STGAVKVLI GPLPSIGRPN ASTTRPTNSR PTGTSKIRPV
51  QVTVSPSLIC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVLTSFT DRFSILALIR SLISAGLSCM KTLIRHSRV
151 QSTQFALYRQ IQNLITHFNF...

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1141>:

m278.seq..

```

1  TTGCGCGCAA TCACGCCCGG TCGATTTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CCGTCCGAC CAGTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTGCGCTTC TTTAATGTGT TCGTACTCGC CCAACACTAC
201 GGCGCCGACG GAGTCGCGCT CCAGGTTTAT CGCCAAGCCG AAAGTGTTC
251 CCGGGAATTC GAGCATCTCA CCTTGCATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATTACC GTACCACAGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTGCTTGT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTCAACTTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCACCA ACTCGCCGAC
601 CTGTTTGTCT GTCAACGGAT AGGCACTGTA AATGACGGCA GATTGTATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1142; ORF 278>:

m278.pep

```

1  LRAITPGAIF SIGAVKVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLMC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPQVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRDFD DRDFQLAVET LIQHLHLAD
201 LFVGQRIGTV NDGRFDMVE*

```

Computer analysis of this amino acid sequence gave the following results:

633

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 278 shows 95.9% identity over a 170 aa overlap with a predicted ORF (ORF 278.ng) from *N. gonorrhoeae*:

g278/m278

	10	20	30	40	50	60
g278.pep	LRAITPGAIFSTGAVKVVLI	GPLPSIGRPNASTTRPTNSRPTGT	SKIRPVQVT	VSPSLIC		
m278	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGT	SKIRPVQVT	VSPSLMC		
	10	20	30	40	50	60
	70	80	90	100	110	120
g278.pep	SYS	PNTTAPTESRSR	FIAPKVLPGNSSIS	PCIASDKPMMRTIP	SVTEITVPRVLTSAFT	
m278	SYS	PNTTAPTESRSR	FIAPKVLPGNSSIS	PCIASDKPMMRTIP	SVTEITVPRVLTSAFT	
	70	80	90	100	110	120
	130	140	150	160	170	
g278.pep	DRFSILALIRSLISAGLSCMK	TLLIRHSRVQSTQFALYRQ	IQNLI	THFNF		
m278	DRFSILALIKSLISAGLSCMK	TLLIRHSRVQSTQFALYRQ	IQNLI	THFNFY	AAANQLRFDF	
	130	140	150	160	170	180
m278	DRDFQLAVETLIQHLHLQ	LADLFV	GQRIGTVNDGRFDMVE*			
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ.ID 1143>:

a278.seq

```

1   TTGCGCGCAA TCACGCCCCG TGCGATTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATATGT TCGTGCTCGC CCAACACTAC
201 GGCGCCGACG GAGTCGCGCT CCAGGTCAT  CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATCACC GTACCACGGG TACGCAC TTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTCGCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTTCAGC ATTTGCGCCA ACTCGCCGAC
601 CTGTTTGTCG GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

a278.pep

```

1   LRAITPGAIF SIGAVKVVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLIC SCS
```

m278/a278 98.2% identity in 219 aa overlap

	10	20	30	40	50	60
m278.pep	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGT	SKIRPVQVT	VSPSLMC		
a278	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGT	SKIRPVQVT	VSPSLIC		
	10	20	30	40	50	60
	70	80	90	100	110	120
m278.pep	SYS	PNTTAPTESRSR	FIAPKVLPGNSSIS	PCIASDKPMMRTIP	SVTEITVPRVLTSAFT	
a278	SCSPNTTAPTESRSR	FIAPKVLPGNSSIS	PCIASDKPMMRTIP	SVTEITVPRVLTSAFT		
	70	80	90	100	110	120

634

	130	140	150	160	170	180
m278.pep	DRFSILALIKSLISAGLSCMKTLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRDFD					
a278	DRFSILALIKSLISAGLSCMKTLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRDFD					
	130	140	150	160	170	180
	190	200	210	220		
m278.pep	DRDFQLAVETLIQHLQLADLFVQGRIGTVNDGRFDMVEX					
a278	DRDFQLAVETLIQHLQLADLFVQGRIGTVNDGRFDMVEX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1145>:

g279.seq

```

1  atgacgcgga tttgcggctg cttgatttca acggttttga gtgtttcggc
51  aagtttgctg gcggcgggtt tcatcaggct gcaatgggaa ggaacggata
101 ccggcagcgg cagggcgcggt ttggctccgg cttctttggc ggcagccatg
151 gtgcgtccga cggcgggcggt gttgcctgca atcacgactt gtccgggcga
201 gttgaagttg acggcttcga ccacttcgcc ctgtgcgcat tcggcacaaa
251 tctgcctgac ctgttcattc tccaaacca aaatggcgcg cattgcgcct
301 acgccttgcg gtacggcgga ctgcatcagt tcggcgcgca ggcggacgag
351 tttgacggca tcggcaaaat ccaatgcttc ggcgcgaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgtttt gccgccact
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 1146; ORF 279.ng>:

g279.pep

```

1  MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTCSS SKPKMAAIAP
101 TPCGTADCIS SARRRSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1147>:

m279.seq

```

1  ATAACGCGGA TTTGCGGCTG CTTGATTTC ACGGTTTTC GGGCTTCGGC
51  AAGTTTGTCT GCGGCGGGTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGGCAGCGG CAGGGCGCGT TTGGCACCGG CTTCTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGGCGGCGGC GTTGCCTGCA ATCACGATTT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACTTCGCT TTGGGCGGCT TCGGCACAAA
251 TGGCTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA GGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT TCAATGCGCC GGCGGCAACG AGTGCGGTGT
401 ATTCGCCGAG GCTGTGTCCG GCAACGGCGG CAGGCGTTT GCCGCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1148; ORF 279>:

m279.pep

```

1  ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAQMALTCSS SKPRIAAIAP
101 TPCGTADCIS SARRRSLTA SAKFNAPAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
	:	:	:	:	:	:
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120

635

```

m279 . pep      ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRSLTA
                || ||||| ||||| ||| : ||||| ||||| : ||||| ||||| ||||| ||||| |||||
g279            ITTCPGELKLTASTTSPCADSAQICLTCSSSKPKMAAIAPTPCGTADCISSARRRSLTA
                70      80      90      100     110     120

                130      140      150
m279 . pep      SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX
                ||| || ||||| ||||| ||||| ||||| : |||
g279            SAKSNASAATSAVYSPRLCPATAAGVLPPTSX
                130      140      150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1149>:

```

a279 . seq
  1  ATGACNCNGA TTTGCGGCTG CTTGATTTC ACGGTTTNA GGGCTTCGGC
 51  GAGTTTGTG GCGGCGGGTT TCATGAGGCT GCAATGGGA GGTACNGACA
101  CNGGCAGCG CAGGCGCGCT TTGGCGCCG CTTCTTTGG GCAAGCATA
151  GCGCGCTCGA CGGCGGCGGC ATTGCCTGA ATCACGACT GTCCGGGCGA
201  GTTGAAGTG ACGGCTTCAA CCACTTCAT CTGTGCGGA TCGGCGCAA
251  TTTGTTTAC CTGTTTCAT TCCAAGCCG GAATCGCCG CATTGCGCC
301  ACGCCTTGCG GTACGGCGGA CTGCATCAG TCGGCGCGC NGCGCACGAG
351  TTTGACCGCG TCGGCAAAAT CCAATGCGC GCGGCAACN AGTGCGGTGT
401  ATTCGCCGAN GCTGTGTCC GCAACGCGG CAGGCGTTT GCCGCCGCT
451  TCCGAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1150; ORF 279.a>:

```

a279 . pep
  1  MTXICGCLIS TVXRASASLS AAGFMRLQWE GTDTGSGRAR LAPASLAASI
 51  ARSTAAALPA ITTCPGELKL TASTTSSCAD SAQICFTCSS SKPRIAAIAP
101  TPCGTADCIS SARXRTSLTA SAKSNAPAAT SAVYSPXLCP ATAAGVLPPA
151  SE*

```

m279/a279 88.2% identity in 152 aa overlap

```

                10      20      30      40      50      60
m279 . pep      ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA
                :| ||||| ||||| ||||| : ||||| ||||| ||||| : || |||||
a279            MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRARLAPASLAASIARSTAAALPA
                10      20      30      40      50      60

                70      80      90      100     110     120
m279 . pep      ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRSLTA
                || ||||| ||||| ||| : ||||| ||||| ||||| ||||| ||||| |||||
a279            ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTPCGTADCISSARRRSLTA
                70      80      90      100     110     120

                130      140      150
m279 . pep      SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX
                ||| ||||| ||||| ||||| ||||| : |||
a279            SAKSNAPAATSAVYSPXLCPATAAGVLPPASEX
                130      140      150

```

Expression of ORF 279

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in *E. coli* as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in *E. coli*. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided herein.

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1151>:

g280.seq

```

1  atgaaacacc tcaaacttac ccttattgcc gcattgctgg ccaccgccgc
51  aactgccgca ccccttcggt ttgtaaccag tttcagcatt ttaggcgacg
101 tagccaaaca aatcggcggt gagcgcgtag ccgtacaaag cctcgtcgga
151 gccaaaccaag atactcatgc ctatcacatg accagtggcg acattaaaaa
201 aatccgcagt gcaaaactcg tcctgtctaa cggcttgga cttgaagccg
251 ccgacatcca acgcgcgctc aaacagagca aagtatccta tgccgaagcg
301 accaaaggca tccaaccctt caaagccgaa gaagaaggcg gacaccatca
351 cgaccaccat cagcaccacg atcatgacca cgaaggacac caccacgacc
401 acggcgaata tgacccccac gtctggaacg accctgttct tatgtccgac
451 tatgcccata acgtcgctga aaccctgata aaggccgatc ccgaaggcaa
501 agtttattat caacaacgct tgggcaacta ccaaatgcag cttaaaaaac
551 tgacacgca cgcacaagcc gcatttaatg ccgtccctgc cgccaaacgc
601 aaagtcctga ccgggcacga cgcattttcc tacatgggca accgctacaa
651 catcagcttc atcgccccgc aaggcgtgag cagcgaagcc gagccgtccg
701 ccaacaagt cgccgccatc atccggcaaa tcaaacgca aggcatacaa
751 gccgtattta ccgaaaatat caaagacacc cgcatggttg accgcatcgc
801 caaagaaacc ggcgtaacg tcagcggcaa actgtattcc gacgcactcg
851 gcaacgcgcc cgcagacacc tacatcggca tgtaccgcca caacgtcgaa
901 gccttgacca acgcgatgaa gcaataa

```

This corresponds to the amino acid sequence <SEQ ID 1152; ORF 280.ng>:

g280.pep

```

1  MKHLKLTIA ALLATAATAA PLPVVTSFSI LGDVAKQIGG ERVAVQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADIQRAV KQSKVSYAEA
101 TKGIQPLKAE EEGGHHHDH HDHDHDHEGH HHDHGEYDPH VWNDPVLMSD
151 YAQNVAETLI KADPEGKVYY QQRLGNYQMQ LKKLHSDAQA AFNAVPAKR
201 KVLTHGDAFS YMGNRYNISF IAPQVSSEA EPSAKQVAI IRQIKREGIK
251 AVFTENIKDT RMDRIAKET GNVVSGKLYS DALGNAPADT YIGMYRHNVE
301 ALTNAMKQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1153>:

m280.seq

```

1  ATGAAACACC TCAAACCTCAC CTTATTGCC GCATTGCTGA CCGCCTCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTTACGATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGTGGCG ACATTAAAAA
201 AATCCGCACT GCAAACTCG TCCTGCTCAA CGGCTTAGGA CTTGAAGCTG
251 CCGATGTGCA ACGCGCGTCA AAACAAAGCA AAGTATCCTA TACCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCACG AAGGACACCA CCATGACCAC GGCGAATATG
401 ACCCGCACGT CTGGAACGAC CCCGTCCTTA TGTCCGCTA TGCCCAAAAC
451 GTTGCCAAAG CCCTGATAAA GGCCGATCCC GAAGGCAAAG TTTATTATCA
501 ACAACGCTTG GGCAACTACC AAATGCAGCT CAAAAAACTG CACAGCGACG
551 CACAAGCCGC ATTTAATGCC GTCCCTGCTG CCAAACGCAA AGTCCTGACC
601 GGGCACGATG CCTTTTCCTA TATGGGCAA CGTTACCATA TCGAATTCAT
651 CGCCCCGCAA GGCGTGAGCA CGGAAGCCGA GCCTTCGGCC AAACAAGTCG
701 CCGCCATCAT CCGACAAATC AAACGCGAAG GCATCAAAGC CGTCTTACC
751 GAAAACATCA AGGACACCCG TATGGTTGAC CGTATCGCCA AAGAAACCGG
801 TGTCAACGTC AGCGGCAAAC TGTATTCCGA CGCACTCGGC AACCGCCCCG
851 CAGACACCTA CATCGGAATG TACCGCCACA ACATCAAAGC CTTGACCAAC
901 GCGATGAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1154; ORF 280>:

m280.pep

```

1  MKHLKLTIA ALLTASATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADVQRAV KQSKVSYTEA
101 TKGIQPLKAE EEGGHHHDH HDHEGHHHDH GEYDPHVWND PVLMSAYAQN
151 VAKALIKADP EGKVVYQQL GNYQMLKKL HSDAQAAFNA VPAKRKVL

```

637

201 GHDAFSYMGK RYHIEFIAPQ GVSSEAEPSA KQVAIIIRQI KREGIKAVFT
 251 ENIKDTRMVD RIAKETGVNV SGKLYSDALG NAPADTYIGM YRHNKALTN
 301 AMKQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 280 shows 93.8% identity over a 308 aa overlap with a predicted ORF (ORF 280.ng)
 from *N. gonorrhoeae*:

m280/g280

	10	20	30	40	50	60
m280.pep	MKHLKLTIAALLTASATAAPLPVVTFSFSILGDVAKQIGGERVSIQSLVGANQDTHAYHM					
	::					
g280	MKHLKLTIAALLATAATAAPLPVVTFSFSILGDVAKQIGGERVAVQSLVGANQDTHAYHM					
	10	20	30	40	50	60
	70	80	90	100	110	119
m280.pep	TSGDIKKIRSAKLVLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE EEGHHHDH-					
	::					
g280	TSGDIKKIRSAKLVLLNGLGLEAADVQRAVKQSKVSYAEATKGIQPLKAE EEGHHHDH					
	70	80	90	100	110	120
	120	130	140	150	160	170
m280.pep	---DHDHEGHHHDHGEYDPHVWNPVLM SAYAQNVAKALIKADPEGKVYYQQLGNYQMQ					
	::					
g280	HDHDHDHEGHHHDHGEYDPHVWNPVLM SDYAQNVAETLIKADPEGKVYYQQLGNYQMQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGVSEAEP SAKQVAAI					
	::					
g280	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFSYMGNRYNISFIAPQGVSEAEP SAKQVAAI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	::					
g280	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNV					
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
g280	ALTNAMKQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq

```

1  ATGAAACACC CCAAACCTCAC CCTTATCGCC GCATTGCTGA CCAC TGCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTT CAGCATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACC AAG ATACGCACGC CTATCATATG ACCAGCGCGC ACATTAAAAA
201 AATCCGCAGT GCAAACTCG TCCTGATTAA CGGCTTAGGA CTTGAAGCTG
251 CCGACATCCA ACGTGCCGTC AAACAGAGCA AAGTATCCTA TGCCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCACG ACCATGACCA CGAAGGACAC CACCACGACC
401 ACGGCGAATA TGACCCCCAC GTCTGGAACG ACCCGTCCT TATGTCGCC
451 TATGCCCAAA ACGTCGCCGA AGCCCTGATA AAGGCCGACC CCGAAGGCAA
501 AGTTTATTAT CAACAACGCT TGGGCAACTA CCAAATGCAG CTCAAAAAAC
551 TGCACAGTGA CGCACAAGCC GCATTTAATG CCGTCCCTGC CGCCAAACGC
601 AAAGTCCTGA CCGGGCACGA TGCCTTTTCC TATATGGGCA AACGTTACCA
651 TATCGAATTC ATCGCCCCAC AAGGTGTGAG CAGCGAAGCC GAGCCTTCAG
701 CCAAACAAGT CGCCGCCATC ATCCGACAAA TCAAACGCGA AGGCATCAAA
751 GCCGTATTTA CCGAAAATAT CAAAGACACC CGCATGGTTG ACCGCATCGC

```

638

801 CAAAGAAACC GGTGTCAACG TCAGCGGCAA ACTGTATTCC GACGCACTCG
 851 GCAACGCACC CGCAGACACC TACATCGGCA TGTACCGCCA CAACATCAAA
 901 GCCTTAACCA ACGCGATGAA GCAATAA

This corresponds to the amino acid sequence <SEQ ID 1156; ORF 280.a>:

a280.pep
 1 MKHPKLTLIA ALLTTAATAA PLPVVTSFSI LGDVAQIGG ERVSIQSLVG
 51 ANQDTHAYHM TSGDIKKIRS AKLVLINGLG LEAADIQRAV KQSKVSYAEA
 101 TKGIQPLKAE EEGGHHHDHD HDHDHDHEGH HHDHGEYDPH VWNDFVLMSA
 151 YAQNVAEALI KADPEGKVYY QQRLGNYQMQ LKKLHSDAQA AFNAVPAAKR
 201 KVLTGHDFAFS YMGKRYHIEF IAPQGVSSSEA EPSAKQVAAI IRQIKREGIK
 251 AVFTENIKDT RMVDRIAKET GVNVSGLKLYS DALGNAPADT YIGMYRHNK
 301 ALTNAMKQ*

m280/a280 96.4% identity in 308 aa overlap

	10	20	30	40	50	60
m280.pep	MKHLKLTLIAALLTASATAAPLPVVTSFSILGDVAQIGGERVSIQSLVGANQDTHAYHM					
a280	MKHPKLTLIAALLTTAATAAPLPVVTSFSILGDVAQIGGERVSIQSLVGANQDTHAYHM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m280.pep	TSGDIKKIRS AKLVLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE EGGHHHDHD					
a280	TSGDIKKIRS AKLVLLNGLGLEAADVQRAVKQSKVSYAEATKGIQPLKAE EGGHHHDHD					
	70	80	90	100	110	120
	130	140	150	160	170	
m280.pep	HDH---EGHHHDHGEYDPHVWNDFVLMSAYAQNVAKALIKADPEGKVYYQQRLGNYQMQ					
a280	HDHDHDHGEHHHDHGEYDPHVWNDFVLMSAYAQNVAEALIKADPEGKVYYQQRLGNYQMQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQA AFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGVSSSEA EPSAKQVAAI					
a280	LKKLHSDAQA AFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGVSSSEA EPSAKQVAAI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIK AVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
a280	IRQIKREGIK AVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
a280	ALTNAMKQX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1157>:

g281.seq
 1 atgcactacg ccctcgcatc cgtcttctgc ctgtccctca ggcgcgcacc
 51 cgtcgccgta ttctcgtca tgcgcgctat gagcctgata ggcgacgcat
 101 tgagccacgc cgtcctgccc ggtgccgccg tcggtacat gtttgccggc
 151 ttgagcctgc ccgctatggg tgtgggcggg tttgccgccg gtatgctgat
 201 ggcgctgctt gccggactcg tcagccgctt taccaccctg aaagaagatg
 251 ccaactttgc cgccttttac ctgagcagcc tcgccatcgg cgtaatcctc
 301 atcagcaaaa acggcagcag cgtcgattta ctccacctcc ttttcggatc
 351 tgtgcttgcc gtcgatattc ccgcactgca actcatcgcc gccgtctccg
 401 gcctcacgct cattaccctt gccgtcatct accgccccct ggtgctagaa
 451 agcatagacc cccttttctt caagtccgct aacggcaag gcgggctttg

639

```

501 gcacgtcatt ttcctcatcc tcgtcggttat gaacctcgta tccggcttcc
551 aagctctcgg catcctgatg tcggtcggaa ttatgatgct gcccgccatt
601 accgcccgtt tatgggcaag aaatatgggg acgctcattc tgttgctcgt
651 cctcatcgcc cttttttgcg gtttgatcgg gctgctcatt tctaccaca
701 tcgaaatccc ttccggcccc gccatcatcc tctgttgag cgctctttat
751 cttttttccg tcatactcgg caaagaaggc ggcattctgc ccaaagtgtt
801 caaaaaccac cgccaccaca ccacctga

```

This corresponds to the amino acid sequence <SEQ ID 1158; ORF 281.ng>:

g281.pep

```

1  MHYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51  LSLPAMGVGG FAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVIL
101 ISKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSGLTLITL AVIYRPLVLE
151 SIDPLFLKSV NGKGGWLWHVI FLVLVVMNLV SGFQALGILM SVGIMMLPAI
201 TARLWARMNG TLILLSVLIA LFCGLIGLLI SYHIEIPSGP AIILCCSVLY
251 LFSVILGKEG GILPKWFKNH RHHTT*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1159>:

m281.seq (partial)

```

1  ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
51  CGTCGGCGTA TTCCTCGTCA TGCGCCGTAT GAGCCTGATA GGCGACGCAT
101 TGAGCCACGC CGTCTGCCCC GGTGCCGCCG TCGGCTACAT GTTTGCCGGC
151 TTGAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGCAG GCATGCTGAT
201 GGCAGTGTCT GCCGGACTCG TCAGCCGCTT CACCACCCTG AAAGAAGATG
251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG CGTAGTCCTC
301 GTCAGCAAAA ACGGGAGCAG CGTCGATTG CTCCACCTCC TTTTCGGCTC
351 TGTAATTGCC GTCGATATTC CTGCCCTGCA GCTCATCGCC GCCGTCTCCA
401 GCCTCACGCT CATTACCCTT GCCGTCATCT ACCGCCCGCT CGTACTCGAA
451 AGCATCGACC CCCTGTTTCT CAAATCCGTC GGCGGCAAAG GCGGGCTTTG
501 GCACGTCCTC TTTCTCGTCC TGGTCGTCAT GAACTCGTA TCCGGCTTTC
551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TCATGATGCT GCCAGCCATT
601 ACCGCCCGCC TGTGGGCGAA GCATATGGGC GCACTCATCC TCCTATCCGT
651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
701 TCGAAATTCC TTCCGGTCCC GCCATCATCC TCTGTTGCAG CGTCCTTTAT
751 CTCTTTTCCG TCATACTCGG CAAAGAAGGC GGCATTCTGA CC..

```

This corresponds to the amino acid sequence <SEQ ID 1160; ORF 281>:

m281.pep (partial)

```

1  MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51  LSLPAMGLGG VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL
101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSSLTLITL AVIYRPLVLE
151 SIDPLFLKSV GKGGLWHVL FLVLVVMNLV SGFQALGILM SVGLMMLPAI
201 TARLWAKHMG ALILLSVLTA LLCGLSGLLI SYHIEIPSGP AIILCCSVLY
251 LFSVILGKEG GILT..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 281 shows 93.5% identity over a 263 aa overlap with a predicted ORF (ORF 281.ng) from *N. gonorrhoeae*:

m281/g281

```

              10      20      30      40      50      60
m281.pep    MRYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLPGAAVGYMFAGLSLPAMGLGG
              |:|||||
g281         MHYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLPGAAVGYMFAGLSLPAMGVGG
              10      20      30      40      50      60

              70      80      90      100     110     120
m281.pep    VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA
              |||:|||||
g281         FAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVILISKNGSSVDLLHLLFGSVLA
              70      80      90      100     110     120

              130     140     150     160     170     180
m281.pep    VDIPALQLIAAVSSLTLITLAVIYRPLVLESIDPLFLKSVGGKGGWLWHVLFLVLVVMNLV

```

	: : :
g281	VDIPALQLIAAAVSGLTTLITLAVIYRPLVLESIDPLFLKSVNGKGGLWHVIFLILVVMNLV
	130 140 150 160 170 180
	190 200 210 220 230 240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP
	: : :
g281	SGFQALGIILMSVGIMMLPAITARLWARNMGTLILLSVLIALFCGLIGLLISYHIEIPSGP
	190 200 210 220 230 240
	250 260
m281.pep	AII LCCSVLYLF SVILGKEGGILT
	:
g281	AII LCCSVLYLF SVILGKEGGILPKWFKNHRHHTTX
	250 260 270

```
a281.seq
1 ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
51 CGTCGGCGTA TTCTCTCGTA TGCGCCGTAT GAGCCTGATA GGCGACGCAT
101 TGAGCCACGC CGTCTTGCCC GGTGCCGCCG TCGGCTACAT GTTTGCCGGC
151 TTAAGCCTGC CGCCCATGGG TTTGGGCGGC GTAGCCGCAG GTATGCTGAT
201 GGCACGTGCTT GCCGGACTCG TCAGCCGCTT CACCACCCTG AAAGAAGATG
251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG TGTAGTCCTC
301 GTCAGCAAAA ACGGCAGCAG CGTCGATTTG CTCCACCTCC TTTTCGGCTC
351 CGTACTTGCC GTCGATATTC GTCGCCCTGA ACTCATCGCC GCCGTATCCA
401 CCCTCACACT GCTTACCCTT CGCGTCATCT ACCGCCCGCT CGTACTCGAA
451 AGCATCGACC CCCTGTTTCT CAAATCTGTC GGCGCCAAAG CGGGCTTTTG
501 GCACGTCCTC TTTCTCGTCC TGGTCGTCAT GAACCTCGTA TCCGGCTTTC
551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TTATGATGCT GCCAGCCATT
601 ACCGCCCGCC TATGGGCGAA GCACATGGGC GACTCATCC TCCTATCCGT
651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
701 TCGAAATTCC TTCCGGTCCG GCCATCATCC TCTGTTGCAG CGTCCTTTAT
751 CTCTTTTCCG TCATACTCCG CAAAGAAGCC GGCATTCTGA CCAATGGCT
801 CAAAAACCAC CGCCACCACA CCACCTGA
```

a281.pep

1	<u>MRYALASVFC</u>	<u>LSLSAAPVGV</u>	FLVMRRMSLI	GDALSHAVLP	GAAVGYMFAG
51	LSPAMGLGG	VAAGMLMALL	AGLVSRFTTL	KEDANFAAFY	LSSLAIGVVL
101	VSKNGSSVDL	LHLLFGSVLA	VDIPALQLIA	AVSTLTLLTL	AVIYRPLVLE
151	SIDPLFLKSV	GKGGLLWHVL	FLVLVVMNLV	SGFOALGTLM	SVGLMMLPAI
201	TARLWAKHMG	ALILLSVLTA	LLCGLSGLLI	SYHIEIPSGP	<u>AIILCCSVLY</u>
251	LFSVILKKEG	GILTKWLKNN	RHHTT*		

	10	20	30	40	50	60
m281.pep	MRYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLPGAAVGYMFAGLSLPAMGLGG					
a281	MRYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLPGAAVGYMFAGLSLPAMGLGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m281.pep	VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA					
a281	VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m281.pep	VDIPALQLIAAVSSLTLT LAVIYRPLVLESIDPLFLKSVGGKGGLWHVFLVLVVMNLV					
a281	VDIPALQLIAAVSTLTLLT LAVIYRPLVLESIDPLFLKSVGGKGGLWHVFLVLVVMNLV					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281.pep	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILTKWLKNHRHHTTX					
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

g282.seq

```

1  atgggattgg gtatggaaat cggcaagctg atttgtggctc ttttggtgct
51  gatcaatccg tttagcgcgt tgctgcttta ccttgacctg accaacggac
101 acagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 tttgccgtga ttgcggtatt tgcgctgata ggcggtgcgc tattgaaggt
201 tttgggcatc agcgtcgggt cgtttcagggt cggcggcggg attttggtgc
251 tgctgatcgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 aatctcggcg cgcagccgga aacggggcaa gcgcgccccg cccgcaatgc
351 aggggagcatt gccgtcgtgc ccatcgccat accgatcacc atcggtccgg
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatatacgcgc tgattatcgc ggccggtttg gtggtcagtg cgatttggtta
501 tgccatttta atcgttgccg ggaaggtcag ccgcctgctg ggcgcgacgg
551 ggctgacgat tttaaaccgc attatgggta tgatgctggc ggcggtatcg
601 gtggagatta ttgtgtcggg actgaaaacg atattccgcg aactggcagg
651 ttga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

g282.pep

```

1  MGLGMEIGKL IVALLVLINP FSALSLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYS
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMLLAAS
201 VEIIVSGLKT IFPQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

m282.seq

```

1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCCTGATC GGCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CCGCGGCGGG ATTTTGGTGC
251 TGCTGATCGC CATTTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCTGTC CCATCGCCAT ACCGATCACC ATCGGCCCCG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CCGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTTGTTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGCGCGACGG
551 GGCTGACGAT TTTAAACCGC ATTATGGGTA TGATGCTGGC GGCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAACG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

m282.pep

```

1  MGLGMEIGKL IVAFLVLINP FSALSLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMLLAAS
201 VEIIVSGLKT IFPQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 282 shows 98.6 % identity over a 217 aa overlap with a predicted ORF (ORF 282.ng) from *N. gonorrhoeae*:

m282/g282

	10	20	30	40	50	60
m282.pep	MGLGMEIGKLIVAFVLVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	:					
g282	MGLGMEIGKLIVALLVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m282.pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	:					
g282	GGALLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282.pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	:					
g282	AVVPIAIPITIGPGGISTVIIYASAAKTYSDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
	190	200	210			
m282.pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
g282	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1167>:

a282.seq

1	ATGGGATTGG	GCATGGAAAT	CGGCAAGCTG	ATTGTGGCTT	TTTTGGTGC
51	GATTAATCCG	TTTAGCGCGT	TGTCGCTTTA	CCTTGACCTG	ACCAACGGGC
101	ACAGCACGAA	GGAGCGCAGG	AAGGTCGCGC	GGACGGCCGC	CGTTGCCGTG
151	TTTGCCGTGA	TTGCGGTATT	TGCGCTGATC	GGCGGTACGC	TGCTGAAGGT
201	TTTGGGCATC	AGCGTCGGTT	CGTTTCAGGT	CGGCGGCGGA	ATTTTGGTGT
251	TGCTGATTGC	CATTTTCGATG	ATGAACGGCA	ACGACAATCC	CGCCAAGCAG
301	AATCTCGGCG	CGCAGCCGGA	AACGGGGCAG	GTGCGCCCCG	CCCGCAATGC
351	CGGAGCGATT	GCCGTCGTGC	CCATCGCCAT	ACCGATCACC	ATCGGCCCGG
401	GCGGTATTTT	GACCGTGATT	ATTTACGCTT	CGGCGGCTAA	AACATACGGC
451	GACATCGCGT	TGATTATCGC	GGCCGGTTTG	GTGGTCAGTG	CGATTTGTTA
501	TGCCATTTTA	ATCGTTGCCG	GSAAGGTCAG	CCGCTTGCTG	GGTGCGACGG
551	GGTGACGAT	TTTAAACCGT	ATCATGGGTA	TGATGCTGGC	GGCGGTATCG
601	GTGGAGATTA	TTGTGTCGGG	ACTGAAAATG	ATATTCGCCG	AAC TGGCAGG
651	TTGA				

This corresponds to the amino acid sequence <SEQ ID 1168; ORF 282.a>:

a282.ppt

1	<u>MGLGMEIGKL</u>	<u>IVAFLVLINP</u>	<u>FSALSPLYDL</u>	<u>TNGHSTKERR</u>	<u>KVARTA</u>	<u>AAVAV</u>
51	<u>FAVIAVFALI</u>	<u>GGTLLKVLGI</u>	<u>SVGSFQVGGG</u>	<u>ILVLLIAISM</u>	<u>MNGNDN</u>	<u>PAKQ</u>
101	<u>NLGAQPETGQ</u>	<u>VRPARNAGAI</u>	<u>AVVPIAIPIT</u>	<u>IGPGGISTVI</u>	<u>IYASAAKTYG</u>	
151	<u>DIALIIAAGL</u>	<u>VVSAICYAIL</u>	<u>IVAGKVSRLI</u>	<u>GATGLTIILNR</u>	<u>IMGMM</u>	<u>LA</u>
201	<u>VEIIVSGLKM</u>	<u>IFPQLAG*</u>				

m282/a282 99.1% identity in 217 aa overlap

```

              10      20      30      40      50      60
m282.pep      MGLGMEIGKLIVAFVLINPFSALSLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI
              |||||
a282           MGLGMEIGKLIVAFVLINPFSALSLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI
              10      20      30      40      50      60

```

643

	70	80	90	100	110	120
m282.pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
a282	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQVRPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282.pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
a282	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
	190	200	210			
m282.pep	GATGLTILNRIMGMMMLAAVSVEIIVSGLKTIFPQLAGX					
a282	GATGLTILNRIMGMMMLAAVSVEIIVSGLKMIFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

```

g283.seq
1   atgaactttg ctttatccgt catcacattt accctcgctt ctttcctgcc
51  cgtcccgccg gccggaaccg ccgtctttac ttggaaagac ggcggcggca
101 acagctattc ggatgtgccg aaacagcttc atcccgacca gagccaaatc
151 ctcaacctgc ggacgctcca aaccaaaccg gcggtcaagc ccaaaccctgc
201 cgtcgatacg aatgcggaag gtgcgaagga aaacgaaaag gatatcgccg
251 agaaaaacgg gcagcttgag gaagaaaaga aaaaaattgc cgaaaccgaa
301 cggcagaaca aagaagaaaa ctgccggatt tcaaaaatga acctgaaggc
351 ggtgggaaac tcaaatgcga aaaacaagga tgatttgatc cgtaaataca
401 ataacgccgt aaacaaatac tgccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

```

g283.pep
1   MNFALSVITF TLASFLPVPP AGTAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRTLQTKP AVKPKPAVDT NADSAKENEK DIAEKNGQLE EEKKKIAETE
101 RQNKEENCRI SKMNLKAVGN SNAKNKDDLI RKYNNVANKY CR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

```

m283.seq
1   ATGAACCTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCC
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GGCGGCGGCA
101 ACAGCTATTC GGATGTACCG AAACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAAACCTGC GGACGCGCCA AACCAAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCGACA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAAGA AGAAAACCTGC CGGATTTCOA AAATGAACCT
351 GAAGGCGGTG GGAAATTCAA ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

```

m283.pep
1   MNFALSVIML TLASFLPVPP AGAAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRTQTKP AVKPAQADAG KRTDGAQEN NPDTAEKNRQ LEEKKRIAE
101 TERQNKEENC RISKMNLKAV GNSNAKNKDD LIRKYNNAVN KYCR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

	10	20	30	40	50	60
m283.pep	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTLQTKP					
	: : : : :					
g283	MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTLQTKP					
	10	20	30	40	50	60

	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRI SKMNLKAV					
	: : : : : :					
g283	AVKPKPA-VDTNAD-SAKENEKDIAEKNQGLEEEKKKIAETERQNKEENCRI SKMNLKAV					
	70	80	90	100	110	
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNAVNKYCRX					
g283	GNSNAKNKDDLIRKYNNAVNKYCRX					
	120	130	140			

```
a283.seq
1  ATGAACCTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCTGCC
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GGCGCGGCA
101 ACAGCTATTC GGATGTACCG AAACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAAACCTGG GGACGCGCCA AACCAAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGCG ACAGGAAAAA AATCCCAGCA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAAGA AGAAAACTGC CGGATTTCAA AAATGAACCT
351 GAAAGCGGTG GGAAATTCAA ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA
```

a283.pep

1	MNFALSVIML	TLASFLPVPP	AGAAVFTWKD	GGGNSYSQVP	KQLHPDQSQI
51	LNLRTQTQTP	AVKPAQADAG	KRTDGAAQEN	NPDTAEKNRQ	LEEEKKRIAE
101	TERQNKEENC	RISKMNLIKAV	GNSNAKNKDD	LIRKYNNAVN	KYCR*

	10	20	30	40	50	60
m283.pep	MNFALSVIMLTLASFLVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTRQTKP					
a283	MNFALSVIMLTLASFLVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTRQTKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRI SKMNLKAV					
a283	AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRI SKMNLKAV					
	70	80	90	100	110	120
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNAVNKYCRX					
a283	GNSNAKNKDDLIRKYNNAVNKYCRX					
	130	140				

```
g284.seq.
  1  atgccgtctg aaactcgaaa tcggtttcag acggcattgg tttagcgggc
 51  aggttggggc ttagcggctc ttgtaacggc attcgctttt gcctgcaaaa
101  gagtcgccgg ctttgcgctt gcctttgaag ccttcgccgg tttttttgaa
151  actgtctttc ttaaagcctt ctttcttgaa accttcgccg cgcgttttgc
201  cgccgaagcc ttctttgccc ggtttatgat cgccgcgccg gccgccggat
251  ttctatctgc ccagccgcc tttgcctttc ggcttgccgc ctgcggattt
301  gcgtttgcgg gccggctcca tgcttcgat ggtcagttcg gccagtttgc
351  ggtaattgta tttttcgatt ttgtggactt tgacgtattc gttcacttcg
401  gcaaacgtaa tcgcaatacc cgtgcggcct gcgcggccgg tgcgccgat
451  gcggtggacg tagtcttccg cctgtttcgg caggtcgtag tttatgacgt
```

645

```

501  gggtaaatggt  cggtagctca  ataccgcgtg  cggcaacgtc  ggtggcaacc
551  aaaattttgc  agcggccttt  acgcaaatac  gtcagcgtgc  ggttgcgcca
601  gccctgcggc  atatcgccgt  gcaggcagtt  ggccgcgaaa  cctttttcgt
651  acaattcatc  cgcgatgact  tcggtcatcg  ctttggtgga  cgtgaaaatc
701  acacattggt  cgatgttggc  atcgcgcagg  atgtggtcga  gcaggcgggt
751  tttgtggcgc  atatcgctgc  agtacaacaa  ctgctcttcg  attttgcctt
801  ggccgtccac  gcgttcgact  tcgataatct  cagagtcttt  ggtcagtttg
851  cgccgcagtt  tgccgactgc  gccgtcccaa  gtggcggaga  acaataaa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

g284.pep

```

1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRVAGFAF AFEAFAGFFE
51  TVFLKAFFLE TFAARFAAEA FFAREMIAAP AAGFPIAPAA FAFRLAACGF
101 AFAGRLHAFD GQFGQFAVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDVVGNG RYVNTACGNV GGNQNFAAAF TQIRQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHRRFG RENHTLVSVG IAQDVVEQAV
251 FVAHIVAVQQ LLFDFALAVH AFDFDNFRVF GQFARQFADC AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

m284.seq..

```

1  ATGCCGTCTG AAACTCGAAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
51  AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCGG CTTTGCCTTT GCCTTTGAAG CCTTCGCCGG TTTTTTTGAA
151 ACCGTCTCTC TTAAAGCCTT CTTTCTTGAA ACCTTCGCCG CGCGTTTTGC
201 CGCCGAAGCC TTCTTTGCTC GGTTTATGAT CGCCGCGCCA ACCGCCGGAT
251 TTACGATCGC CCCAGCCGCC TTTGCCTTTC GGCTTGCCGC CTGCGGATTT
301 GCGTTTGCGG GTCGTTTCCA TGCCTTCGAT GGTCAGTTTC GGCAGTTTTT
351 GGTAAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTGCGGCCT GCGCGGCCGG TGCGCCCGAT
451 GCGGTGGACG TAGTCTTCCG CCTGTTTCGG CAGGTCGTAG TTGATAACGT
501 GGGTAATGGT CGGTACGTCG ATACCGCGTG CGGCAACATC GGTGGCAACC
551 AAAATTTTGC AGCGGCCTTT ACGCAAATCC ATCAGCGTGC GGTGCGCCA
601 GCCTTGCGGC ATATCGCCGT GCAGGCAGTT TGCGGCGAAA CCTTTTTCTG
651 ACAGTTCATC CGCAATGACT TCGGTCATGG CTTTGGTGGA CGTGAAAATC
701 ACCGATTGAT CGATATTGGC ATCGCGCAAG ATATGATCGA GCAGGCGGTT
751 TTTGTGGCGC ATATCGTTCG AGTACAGCAG TTGTTCTTCG ATTTTGCCTT
801 GATCGTCCAC GCGTTCGACT TCGATGATTT CAGGGTCTTT GGTCAAGTTT
851 CGGCCAGTT TGCCGACCGC GCCGTCCCAA GTGGCGGAGA ACAACAAGT
901 CTGACGGTCG CTCGGCGTTG CTTCCACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAATCAG CACTTCCAAA
1001 CGTTCAAAAT CAACTTTGCC GCTTTGCATC AGGTCCATCA GACGGCCCGG
1051 CGTGGCGACA ATCAGATCGA CCGGTTTGCT CAGGGCACGG GTTTGGTAGC
1101 CGAAAGACGC GCCGCCGACG ATGCTGACGG TGCGGAACCA ACGCATATTT
1151 TTGGCATACG CCAGCGCGTT TTTCTCGACT TGAGCCGCCA GTTCGCGGGT
1201 CGGGGTCAAC ACCAAAGCAC GCGGGCCTTT GCCCGGTTT TCGCTGCGTT
1251 TGGTCAGTTT TTGCAAAGTC GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

m284.pep

```

1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE
51  TVSLKAFFLE TFAARFAAEA FFAREMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRHFHAFD GQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDNVGNG RYVDTACGNI GGNQNFAAAF TQIHQRAVAP
201 ALRHIAVQAV CGETFFVQFI RNDFGHGFGG RENHALIDIG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALIVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVARRCFHD GFDVVDKAHI QHTVGFVQNG HFQTFKINFA ALHQVHQFAR
351 RGDNQIDRFA QGTGLVAERR AADDADGAEP THIFGIRQRV FLDLSRQFAG
401 RGQHQSTRAF ARFFAAGQF LQSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

646

	10	20	30	40	50	60
m284 . pep	MPSETRNR FQTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
g284	MPSETRNR FQTALVYAAGWGLAVFVTAFAFACKRVAGFAFAFEAFAGFFETVFLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284 . pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAFAGRFHAFDGGQFGQFSVNV					
g284	TFAARFAAEAFFARFMIAAPAAGFPIAPAAFAFRLAACGFAFAGRLHAFDGGQFGQFAVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284 . pep	FFDFVDFDVFVHFGKRNRNTRAACAAGAPDAVDVVERLFRQVVVDVNGNGRYVDTACGNI					
g284	FFDFVDFDVFVHFGKRNRNTRAACAAGAPDAVDVVERLFRQVVVDVNGNGRYVNTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284 . pep	GGNQNFAAFTQIHQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
g284	GGNQNFAAFTQIRQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHRFGGRENHTLVDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284 . pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS					
g284	IAQDVVEQAVFVAHIVAVQQLLDFALAVHAFDFDNFRVFGQFARQFADCAVPSGGEQX					
	250	260	270	280	290	
	310	320	330	340	350	360
m284 . pep	LTVARRCFHDGFDVVDKAHIQHTVGFVQNHQFQTFKINFAALHQVHQATARRGDNQIDRFA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1179>:

```

a284 . seq
1   ATGCCGCTCTG  AAACGCGAAA  TCGGTTTCAG  ACGGCATTGG  TTTATGCGGC
51  AGGTTGGGGC  TTAGCGGTCT  TTGTAACGGC  GTTCGCCTTT  GCCTGCAAAA
101 GAATCGCCGG  CTTTGCCTTT  GCCTTTGAAG  CCTTCGCCGG  TTTTTTTGAA
151 ACCGTCTCTC  TTAAAGCCTT  CTTTCTTGAA  ACCTTCGCCG  CGCGTTTTGC
201 CGCCGAAGCC  TTCTTTGCTC  GGTATTATGAT  CGCCGCGCCA  ACCGCCGGAT
251 TTACGATCGC  CCCAGCCGCC  TTTGCCTTTC  GGCTTGCCGC  CTGCGGATTT
301 GCGTTTGCGG  GTCGGTTCCA  TGCCTTCGAT  GGTCAGTTCG  GGCAGTTTTC
351 GGTTAATGTA  TTTTTCGATT  TTGTGGACTT  TGACGTATTC  GTTCACTTCG
401 GCAAACGTAA  TCGCAATACC  CGTGCGCCCT  GCGCGGCCGG  TGCGCCCGAT
451 GCGGTGGACG  TAGTCTTCCG  CCTGTTTCGG  CAGGTCGTAG  TTGATAACGT
501 GGGTAATGGT  CGGTACGTCG  ATACCGCGTG  CGGCAACGTC  GGTGGCAACC
551 AAAATTTTGC  AGCGGCCTTT  GCGCAAATCC  ATCAGCGTGC  GGTTCGCGCA
601 GCCTTGCGGC  ATATCGCCGT  GCAGGCAGTT  GGCGGCGAAA  CCTTTTTCGT
651 ACAATTCAAT  CGCGATGACT  TCGGTCATGG  CTTTGGTGGA  CGTGAAATC
701 ACGCATTGAT  CGATGTCGGC  ATCGCGCAAG  ATATGATCGA  GCAGGCGGTT
751 TTTGTGGCGC  ATATCGTCGC  AGTACAGCAG  TTGTTCTTCG  ATTTTGCCTT
801 GGTCGTCCAC  GCGTTCGACT  TCGATGATTT  CAGGTCCTTT  GGTCAGTTTG
851 CGCGCCAGTT  TGCCGACCGC  GCCGTCCCAA  GTGGCGGAGA  ACAACAAAGT
901 CTGACGGTCT  TCCGGCGTGG  CTTGACGAT  GGTTTCGATG  TCGTCGATAA
951 AGCCCATATC  CAACATACGG  TCGGCTTCGT  CCAAATCAG  CACTTCCAAG
1001 CGGGCGAAAT  CGACTTTGCC  GCTTTGCATC  AAGTCCATCA  GACGGCCCGG
1051 CGTGGCGACA  ATCAGATCGA  CCGGTTTGCT  CAGGGCGCGG  GTTTGGTAGC
1101 CGAACGATGC  ACCACCGACG  ATGCTGACGG  TACGGAACCA  ACGCATATTT
1151 TTGGCATACG  CCAGCGCGTT  TTTCTCGACT  TGAGCCGCCA  ATTCGCGGGT
1201 CGGCGTCAAC  ACCAACGCGC  GCGGGCCTTT  GCCCGGTTTT  TCGCTGCGTT
1251 TGGTCAGTCG  CTGCAAAGTC  GGTA

```

This corresponds to the amino acid sequence <SEQ ID 1180; ORF 284.a>:

```

a284 . pep
1   MPSETRNR FQ TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE

```

647

```

51 TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRHFHAFD GQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRFLR QVVVDNVGNG RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHGFGG RENHALIDVG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALVVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVFRRGFDD GFDVVDKAHI QHTVGFVQNG HFQAGEIDFA ALHQVHQTAR
351 RGDNQIDRFA QGAGLVAERC TTDDADGTEP THIFGIRQRV FLDLSRQFAG
401 RRQHQRRARAF ARFFAAGQS LQSR*

```

m284/a284 94.8% identity in 424 aa overlap

```

              10      20      30      40      50      60
m284.pep      MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE
              |||||
a284          MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE
              10      20      30      40      50      60

              70      80      90      100     110     120
m284.pep      TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV
              |||||
a284          TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV
              70      80      90      100     110     120

              130     140     150     160     170     180
m284.pep      FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVVFRFRQVVVDNVGNRYVDTACGNI
              |||||
a284          FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVVFRFRQVVVDNVGNRYVDTACGNV
              130     140     150     160     170     180

              190     200     210     220     230     240
m284.pep      GGNQNFAAAFTQIHQRAVAPALRHIAVQAVCGGETFFVQFIRNDFGHGFGGRENHALIDIG
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a284          GGNQNFAAAFAQIHQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHGFGGRENHALIDVG
              190     200     210     220     230     240

              250     260     270     280     290     300
m284.pep      IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFFDDFRVFGQFARQFADRAVPSGGEQQS
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a284          IAQDMIEQAVFVAHIVAVQQLFFDFALVVHAFDFFDDFRVFGQFARQFADRAVPSGGEQQS
              250     260     270     280     290     300

              310     320     330     340     350     360
m284.pep      LTVARRCFHDGFDVVDKAHIQHTVGFVQNGHFQTFKINFAALHQVHQTARRGDNQIDRFA
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a284          LTVFRRGFDDGFDVVDKAHIQHTVGFVQNGHFQAGEIDFAALHQVHQTARRGDNQIDRFA
              310     320     330     340     350     360

              370     380     390     400     410     420
m284.pep      QGTGLVAERRAADDADGAEPHTHIFGIRQRVFLDLSRQFAGRGQHQSRAFFFAAFGQF
              ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a284          QGAGLVAERCTTDDADGTEPHTHIFGIRQRVFLDLSRQFAGRRQHQRRARAFARFFAAGQS
              370     380     390     400     410     420

m284.pep      *LQSRX
              ||||
a284          LQSRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1181>:

```

g285.seq
1  atgaccgata ccacaccgac agataccgat ccgaccgaaa acggcacgcg
51 caaaatgccg tctgaacacc gccccgcccc gccggcaaaa aaacgccgcc
101 cgctgctgaa gctgtcggcg gcactgctgt ctgtcctgat tttggcagta

```

151	tgtttctctcg	gctggatcgc	cggtagcgaa	gcaggtttgc	gcttcgggct
201	gtaccaaatac	ccgtcctggt	tcggcgtaaa	catttcctcc	caaaacctca
251	aaggcacact	gctcgacggc	ttcgacggcg	acaactggtc	gatagaaacc
301	gagggggcag	accttaaaat	cagccgcttc	cgcttcgcgt	ggaaaccgctc
351	cgaactgatg	cgccgcagcc	tgcacatcac	cgacatctcc	gccggcgaca
401	tcgccatcgt	aaccaaaccg	actccgccta	aagaagaacg	cccgcctcaa
451	ggcctgcccc	acagcataga	cctgcccgcg	gctgtctatc	tcgaccgctt
501	cgagacgggc	aaaatcagca	tgggcaaaac	ctttgacaaa	caaaccgtct
551	atctcgaacg	cctcaacgcg	gcataccggt	acgaccgtaa	agggcaccgc
601	ctcgacctga	aggccgcgga	cacgcctggg	agcagttcgt	cggggtcagc
651	ctcggtcggc	ttgaaaaaac	cgtttgccct	cgataccgcc	atttacacca
701	aaggcggatt	cgaaggcgaa	accatacaca	gtacggcgcg	gctgagcggc
751	agcctgaagg	atgtgcgcgc	cgaactgacg	atcgacggcg	gcaatatccg
801	cctctcggga	aaatccgtca	tccaccggtt	tgcggaatca	ttggataaaa
851	cattggaaga	agtactggtc	aaaggattca	acatcaatcc	gtccgccttc
901	gtgccttccc	tgcccgatgc	cgggctgaat	ttcgacctga	ccgccatccc
951	gtcgttttca	gacggcatcg	cgctggaagg	ctcgtctgat	ttggaaaaca
1001	caaagccgg	ctttgccgac	cgcaacggca	tccccgtccg	tcagggttttg
1051	ggcggccttg	tcataccggca	ggacggcacg	gtgcataatc	gcaatacgtc
1101	cgccgccttg	ctcggacggg	gcggcatcag	gctgtcgggc	aaaatcgaca
1151	ccgaaaaaga	catccttgat	ttaaataatag	gcatcaactc	cgtcggcgcg
1201	gaagacgtgc	tgcaaacgcg	gttcaaaggc	aggttggacg	gcagcatcgg
1251	catcggcggc	acgaccgcct	cgcccaaaat	ctcttggaac	ctcggcacccg
1301	gcacggcacg	cacggacggc	agcctcccca	tcgcaagcga	ccccgaaac
1351	gaacagcgga	aactggtggt	cgacaccgtc	aacatctccg	ccggggaagg
1401	cagcctgacc	gcgcaaggct	atctcgagct	gtttaaagac	cgctgctca
1451	agctggacat	ccgttcccgc	gcattcgacc	cttcgcgcgt	cgatccgcaa
1501	tttcgggcag	gcaatatcaa	cggttcgatt	catcttgccg	gtgaactggc
1551	aaaagagaaa	tttacgggca	aaatgcgttt	tttgcccggg	acgttcaacg
1601	gcgtgccgat	tgccggcagc	gccgacattg	tttacgagtc	ccgccacctt
1651	ccgcgcgccg	ccgtcgattt	gcggttgggg	cggaacatcg	tcaaaacaga
1701	cggcggcttc	ggcaaaaaag	gcgaccggct	taacctcaat	atcaccgcac
1751	ccgattttatc	ccgtttcggg	ttcggactcg	cggggtcttt	aaatgtacgc
1801	ggacaccttt	ccggcgattt	ggacggcggc	atccgaacct	ttgaaaccga
1851	ccatttcggc	acggcgcgca	acttacacat	cggcaaaagc	gcagacatcc
1901	gttcgctcga	ttttaccctc	aaaggctcac	ccggcacaag	ccgcccgatg
1951	cgcgccgata	tcaagggcgg	ccgcctttcc	ctgtcgggcg	gcgcgcggt
2001	tgctgatacc	gccggcctga	cgctggaagg	tacgggcgcg	cagcaccgca
2051	tccgcacaca	cgccgccatg	acgctggacg	gcaaacggtt	caaactcgat
2101	ttggacgctt	caggcggcat	caacagggaa	cttaccgat	ggaaaggcag
2151	catcggcatc	ctcgacatcg	gcggcgcat	caacctcaag	ctgcaaaacc
2201	gtatgacgct	cgaagccggt	gcggaacacg	tggcggcgaag	tgccgcaaat
2251	tggcaggcaa	tgggcggcag	cctcaacctg	caacactttt	cttgggacag
2301	gaaaccgggc	atatcggcaa	aaggcggcgc	acgcggcctg	cacatcgccg
2351	agttgcacaa	tttcttcaaa	ccgcccttcg	aacacaatct	ggtttttaa
2401	ggcgactggg	atgtgcgcta	cgggcacaac	gcgcgcggct	acctcaatat
2451	cagccggcaa	agcggcgatg	ccgtattgcc	cggcgggcag	gctttggggt
2501	tgaacgcatt	ttccctgaaa	acgcgctttc	aaaacgaccg	catcggaatc
2551	ctgcttgacg	gcggcgcgcg	tttcggacgg	attaacgcgc	atttgggcat
2601	cggcaacgcc	ttcggcgcca	atatggcaaa	tacaccgctc	ggcggcagga
2651	ttacagcctc	ccttcccgcg	ttgggcgcgt	tgaagccctt	tctgcccgcg
2701	gccgcgcaaa	acattaccgg	cagcctgaat	gcctccgcgc	aaatcggcgg
2751	acgggtaggc	tctccgtccg	tcaatgccgc	cgtaacgggt	agcagcaact
2801	acgggaaaat	caacgggcaat	atcaccgtcg	ggcaaaagccg	ctccttcgat
2851	accgcacctt	tgggcggcag	gctcaacctg	accgttgccg	atgccgaagc
2901	attccgcaac	ttcctaccgg	tcggacaaac	cgtaaaaggc	agcctgaatg
2951	ccgcgtaaac	cctcggcggc	agcatcgccg	acccgcactt	ggcgggcagt
3001	atcaacggcg	acaagctcta	ttaccgcaac	caaaccgaag	gcatcatctt
3051	ggacaacggc	tcgctgcgtt	cgcatattgc	aggcaggaaa	tgggtaatcg
3101	acagcctgaa	attccggcac	gaagggacgg	cggaactctc	cggcacggtc
3151	agcatggaaa	acagcgtgcc	cgatgtcgat	atcggcgcgg	tgttcgacaa
3201	ataccgcatac	ctgtcccgcg	ccaaccgcgc	cctgacgggt	tccggcaaca
3251	cccgcctgcg	ctattcgccg	caaaaaggca	tatccgttac	cggtatgatt
3301	aaaactgatac	aggggctggt	cggttcgcaa	aaatcctcga	tgccgtccgt
3351	cggcgacgat	gtcgtcgtat	tgggcgaagt	caagaaagag	gcggcgcgat
3401	cgctccccgt	caatatgaac	ctgactttag	acctcaatga	cggcatccgc

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3451 ttctccggct acggcgcgga cgttaccata ggcggcaaac tgaccctgac
3501 cgcgcaaccg ggcggaaatg tgcgtggggt gggcacggtc cgcgtcatca
3551 aagggcggtta caaagcatat gggcaggatt tagacattac caaaggcaca
3601 gtctcctttg tcggcccgtc caacgacccc aacctgaaca tccgcgccga
3651 acgcccgcctt tccccgcgtg gtgcggggcg ggaatattg ggcagcctca
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaaaaagac
3751 aagctctcct ggctcatcct caaccgtgcc ggcagcggca gcagcggcga
3801 caatgccgcc ctgtccgcag ccgcaggcgc gctgcttgcc gggcaaatca
3851 acgaccgcat cgggctggtg gatgatttgg gctttaccag caagcgcagc
3901 cgcaacgcgc aaaccggcga actcaacccc gccgaacagg tgctgaccgt
3951 cggcaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtccgtc aaactgattt accggctgac ccgcgccata
4051 caggcggttg cccgtatcgg cagccgttcg tcgggcggcg agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacgcaaa agggaaataa

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This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

g285.pep

```

1  MDTTPTDTD PTENGTRKMP SEHRPAPPAK KRRPLLKLSA ALLSVLILAV
51  CFLGWIAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPELMM RRSIHITDIS AGDIAIVTKP TPPKEERPPQ
151 GLPDSIDLPA AVYLDREFETG KISMGTDFDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGFEGE TIHSTARLSG
251 SLKDVRAELT IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFs DGIALEGLSD LENTKAGFAD RNGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFTK RLDGSIGIGG TTASPKISWQ LGTGTARTDG SLPIASDPAN
451 EQRKLVFDTV NISAGEGSLT AQGYLELFKD RLLKLDIRS AFDPSTRIDPQ
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIVKTDGGF GKKGDRLNLN ITAPDLRFSG FGLAGSLNVR
601 GHLSGDLGG IRTFETDLG TARNLHIGKA ADIRSLDFTL KGSPGTSRPM
651 RADIKGGRLS LSGGAADVDT AGLTLEGTGA QHRIRTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKSIGI LDIGGAFNLK LQNRMTLEAG AEHVAASAAN
751 WQAMGGSLNL QHFSWDRKTG ISAKGGARGL HIAELHNFFK PPFENLVLN
801 GDWDVAYGHN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLPA
901 AAQNITGSLN ASAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSD
951 TAPLGGRLNL TVADAEAFRN FLPVGTQVKG SLNAAVTLGG SIADPHLGGs
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 SMENSVPDGD IGAVFDKYRI LSRENRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAASLPVNMN LTLDLNDGIR
1151 FSGYGADVTI GGLTLTAQF GGNVRGVGTV RVIKGRYKAY QQDLDTKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSKED
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRLEFGSDKK DSAGNGKKG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

m285.seq

```

1  ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51  CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AACAGCCGCC
101 CGTTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTCCTGAT TTTGGCAGTA
151 TGTTTCCTCG GCTGGCTCGC CGGTACGGAA GCAGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTTCTCTC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAAT CAGCCGCTTC CGCTTCGCGT GGAACCCGTC
351 CGAACTGATG CGCCGCAGCC TGCACATTAC CGAAATTTCC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCCTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTTGACCTGA AGGCCGCCGA CACGCCGTGG AGCAGTTCGT CGGGGGCGGC
651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGCGGACT CGAAGGCAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG

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801	CCTCTCGGGA	AAATCCGTCA	TCCACCCGTT	TGCCGAATCA	TTGATAAAAA
851	CATTGGAAGA	AGTACTGGTC	AAAGGGTTCA	ACATCAATCC	GGCCGCCTTC
901	GTGCCTTCCC	TGCCCCGATG	CGGACTGAAT	TTCGACCTGA	CCGCCATCCC
951	GTCGTTTTCA	GACGGCATCG	CGCTGGAAGG	TTCGCTCGAT	TTGGAAAACA
1001	CCAAAGCCGG	CTTTGCCGAC	CGCAACGGCA	TCCCCGTCGG	TCAGGTTTTA
1051	GGCGGCTTTG	TCATCCGGCA	GGACGGCACG	GTGCATATCG	GCAATACGTC
1101	CGCCGCCCTG	CTCGGACGGG	GCGGCATCAG	GCTGTCGGGC	AAAATCGACA
1151	CCGAAAAAGA	CATCCTCGAT	TTAAATATAG	GCATCAACTC	CGTCGGCGCG
1201	GAAGACGTAC	TGCAAACCGC	GTTCAAAGGC	AGGTGGGACG	GCAGCATCGG
1251	CATCGGTGGC	ACGACCGCCT	CGCCCAAAT	CTCTTGCGAA	CTCGGCATCG
1301	GCACGGCGCG	CACGGACGGC	AGCCTCGCCA	TTGCAAGCGA	CCCAGCAAAC
1351	GGACAGCGGA	AACTGGTGCT	CGACACCGTC	AACATCGCCG	CCGGGCAAGG
1401	CAGCCTGACC	GCGCAAGGCT	ATCTCGAGCT	GTTTAAAGAC	CGCCTGCTCA
1451	AGCTGGACAT	CCGTTCCCGC	GCATTGACCC	CTTCGCGCAT	CGATCCGCAA
1501	CTTCCGGCAG	GCAATATCAA	CGGCTCAATA	AACCTTGCCG	GCGAACTGGC
1551	AAAAGAGAAA	TTCACAGGCA	AAATGCGGTT	TTTACCCGGC	ACGTTCAACG
1601	GCGTACCGAT	TGCCGGCAGT	GCCGACATTG	TTTACGAGTC	CCGCCACCTT
1651	CCGCGTGCCG	CCGTCGATTT	GCGGCTGGGG	CGGAACATTA	TTAAACACAGA
1701	CCGCGGCTTC	GGCAAAAAAG	GCGACCGGCT	TAACCTCAAT	ATCACCGCAC
1751	CCGATTATC	CCGTTTCGGT	TTCGGACTCG	CGGGGTCTTT	AAATGTACGC
1801	GGACACCTTT	CCGCTGATTT	GGACGCGCGC	ATCCGAACCT	TTGAAACCGA
1851	CCTTTCCGGC	GCGGCGCGCA	ACCTGCACAT	CGGCAAGGCG	GCAGACATCC
1901	GTTCGCTCGA	TTTCACGCTC	AAAGGTTGCG	CCGACACAAG	CCGCCCCGATA
1951	CGCGCCGACA	TCAAAGGCAG	CCGCCTTTCG	CTGTCGGGCG	GAGCGCGGGT
2001	TGTCGATACC	GCCGACCTGA	TGCTGGACGG	CACGGGCGTG	CAGCACCGCA
2051	TTCGCACACA	CGCCGCCATG	ACGCTGGATG	GCAAACCGTT	CAAATTTCGAT
2101	TTGGACGCTT	CAGGCGGCAT	CAACAGGGAA	CTTACCCGAT	GGAAAGGCGAG
2151	CATCGGCATC	CTCGACATCG	GCGGCGCATT	CAACCTCAAG	CTGCAAAACC
2201	GTATGACGCT	CGAAGCCGGT	GCGGAACGCG	TGGCGGCAAG	TGCGGCAAAT
2251	TGGCAGGCAA	TGGGCGGCAG	CCTCAACCTG	CAACACTTTT	CTTGGGATAA
2301	AAAAACCGGC	ATATCGGCAA	AAGCGGCGCG	ACACGGTCTG	CATATCGCCG
2351	AGTTGCACAA	TTTCTTCAAA	CCGCCCTTCG	AACACAATCT	GGTTTTAAAC
2401	GGCGACTGGG	ATGTCGCCTA	CGGGCGCAAC	GCGCGCGGCT	ACCTCAATAT
2451	CAGCCGGCAA	AGCGGCGATG	CCGTATTGCC	CGCGGGGCGAG	GCTTTGGGTT
2501	TGAACGCATT	TTCCCTGAAA	ACGCGCTTTC	AAAACGACCG	CATCGGAATC
2551	CTGCTTGACG	GCGGCGCGCG	TTTCGGGCGG	ATTAACGCCG	ATTTGGGCAT
2601	CGCCAACGCC	TTTCGGCGGCA	ATATGGCAAA	TGCACCGCTC	GGCGGCAGGA
2651	TTACCGCCTC	CCTTCCCGAC	TTGGGCGCAT	TGAAGCCCTT	TCTGCCCGCC
2701	GCCGCGCAAA	ACATTACCGG	CAGCCTGAAT	GCCGCGCGCG	AAATCGGCGG
2751	ACGGGTAGGC	TCTCCGTCCG	TCAATGCCGC	CGTCAACGGC	AGCAGCAACT
2801	ACGGGAAAAAT	CAACGGCAAC	ATCACCGTCG	GGCAAAGCCG	CTCTTTCGAT
2851	ACCGCGCCTT	TGGGCGGCAG	GCTCAACCTG	ACCGTTGCCG	ATGCCGAAGT
2901	ATTCCGCAAC	TTCTTACCGG	TCGGACAAAC	CGTCAAAGGC	AGCCTGAATG
2951	CCGCCGTAA	CCTCGGCGGC	AGCATCGCCG	ATCCGCACCT	GGGCGGCAGC
3001	ATCAACGGCG	ACAACTCTA	TTACCGCAAC	CAAACCCAAG	GCATCATCTT
3051	GGACAACGGC	TCGCTGCGTT	CGCATATCGC	GGGCAGGAAA	TGGGTAATCG
3101	ACAGCCTGAA	ATTCGGGCAC	GAAGGGACGG	CGGAACCTC	CGGTACGGTC
3151	GGTATGAAAA	ACAGCGGACC	CGATGTCGAT	ATCGGCGCGG	TGTTTCGACAA
3201	ATACCGCATC	CTGTCCCGCC	CCAACCGCCG	CCTGACGGTT	TCCGGCAACA
3251	CCCGCCTGCG	CTATTGCGCG	CAAAAAGGCA	TATCCGTTAC	CGGGATGATT
3301	AAAACGGATC	AGGGGCTGTT	CGGTTTCGAA	AAATCCTCGA	TGCCGTCCGT
3351	CGGCGACGAT	GTGTCGTAT	TAGGCGAAGT	CAAAAAGAG	GCGGCGGCAC
3401	CGTCCCCGT	CAATATGAAC	CTGACTTTAG	ACCTCAATGA	CGGCATCCGC
3451	TTCGCGCGCT	ACGGCGCGGA	CGTTACCATA	GCGGCGAAAC	TGACCTTGAC
3501	CGCCCAATCG	GGCGGAAGCG	TACGGGGCGT	GGGCACGGTC	CGCGTCATCA
3551	AAGGGCGTTA	TAAGGCATAC	GGGCAGGATT	TGGACATTAC	CAAAGGCACG
3601	GTCTCCTTTG	TCGGCCCGCT	CAACGATCCC	AACCTCAACA	TCCGCGCCGA
3651	ACGCCGCCTT	TCCCCCGTCG	GTGCGGGCGT	GGAAATATTG	GGCAGCCTCA
3701	ACAGCCCGCG	CATTACGCTG	ACGGCAAACG	AACCGATGAG	TGAAAAGAC
3751	AAGCTCTCTT	GGCTCATCCT	CAACCGCGCC	GGCAGCGGCA	GCAGCGGCGA
3801	CAATGCCGCC	CTGTCTGCAG	CCGCAGGTGC	GCTGCTTGCC	GGGCAATCA
3851	ACGACCGCAT	CGGGCTGGTG	GATGATTTGG	GCTTTACCAG	CAAGCGCAGC
3901	CGCAACGCGC	AAACCGGCGA	ACTCAACCCC	GCCGAACAGG	TGCTGACCGT
3951	CGGCAAAACA	CTGACCGGCA	AACTCTACAT	CGGCTACGAA	TACAGCATCT
4001	CCAGCGCGGA	ACAGTCCGTC	AAACTGATTT	ACCGGCTGAC	CCGCGCCATA
4051	CAGGCGGTTG	CCCGTATCGG	CAGCCGTTTCG	TGGGCGGCGG	AGCTGACATA

4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAAA GACTCCGCCG
 4151 GAAACGGCAA AGGAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

m285.pep
 1 MTDTAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
 51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
 101 EGADLKISRF RFAWKPELM RRSLLHITEIS AGDIAIVTKP TPPKEERPPL
 151 SLPDSIDLPA AVYLDRLFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
 201 LDLKAADTPW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
 251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPAAF
 301 VPSLPDAGLN FDLTAIPSF S DGIALEGLD LENTKAGFAD RINGIPVRQVL
 351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
 401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
 451 GQRKLVLDTV NIAAGQGSIT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
 501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
 551 PRAAVDLRLG RNIKTDDGGF GKKGDRNLN ITAPDLSRFG FGLAGSLNVR
 601 GHLSGDLDDG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
 651 RADIKGSRLS LSGGAADVDT ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
 701 LDASGGINRE LTRWKGSGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
 751 WQAMGGSNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFENLVLN
 801 GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDIRGI
 851 LLDGGARFGR INADLGIANA FGGNMANAPL GGRITASLPD LGALKPFLPA
 901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRFSD
 951 TAPLGGRLNL TVADAIEFRN FLPVGTQVKG SLNAAVTLGG SIADPHLGG
 1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
 1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
 1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAPLPVNMN LTLDLNDGIR
 1151 FAGYGADVTI GGKLTTLTAQS GGSVRGVGTV RVIKGRYKAY GQDLDTKGT
 1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSEKD
 1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
 1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
 1351 QAVARIGSRS SGGELTYTIR FDRFSGSKDK DSAGNGKKG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m285/g285 96.5% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
	:					
g285	MTDTTPTDPTENGTRKMPSEHRPAPPKRRPLLKLSAALLSVLILAVCFLGWIAGE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m285.pep	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRFAWKPELM					
g285	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRFAWKPELM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m285.pep	RRSLHITEISAGDIAIVTKPTTPKEERPPLSLPDSIDLPAAVYLDRLFETGKISMKGAFDK					
	: :					
g285	RRSLHITDISAGDIAIVTKPTTPKEERPQGLPDSIDLPAAVYLDRLFETGKISMGTDFDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
	: : :					
g285	QTVYLERLNAAYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGFEGE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m285.pep	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					

[illegible]

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|||||:|||||
g285 AAQNITGSLNASAQIGGRVGSPSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLN
      910      920      930      940      950      960

      970      980      990      1000      1010      1020
m285.pep TVADAEVFRNFLPVGQTVKGSLNAAVTLGGSADPHLGGSSINGDKLYYRNQTQGIILDNG
      |||||:|||||
g285 TVADAEAFRNFLPVGQTVKGSLNAAVTLGGSADPHLGGSSINGDKLYYRNQTQGIILDNG
      970      980      990      1000      1010      1020

      1030      1040      1050      1060      1070      1080
m285.pep SLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRLTV
      |||||:|||||
g285 SLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENSVDPVDIGAVFDKYRILSRPNRRLTV
      1030      1040      1050      1060      1070      1080

      1090      1100      1110      1120      1130      1140
m285.pep SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
      |||||:|||||
g285 SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAASLPVNMN
      1090      1100      1110      1120      1130      1140

      1150      1160      1170      1180      1190      1200
m285.pep LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLDTKGT
      |||||:|||||
g285 LTLDLNDGIRFSYGADVTIGGKLTTLTAQPGGNVRGVGTVRVIKGRYKAYGQDLDTKGT
      1150      1160      1170      1180      1190      1200

      1210      1220      1230      1240      1250      1260
m285.pep VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
      |||||:|||||
g285 VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
      1210      1220      1230      1240      1250      1260

      1270      1280      1290      1300      1310      1320
m285.pep GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ
      |||||:|||||
g285 GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTVGKQ
      1270      1280      1290      1300      1310      1320

      1330      1340      1350      1360      1370      1380
m285.pep LTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
      |||||:|||||
g285 LTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFSGSDKK
      1330      1340      1350      1360      1370      1380

      1390
m285.pep DSAGNGKGKX
      |||||
g285 DSAGNGKGKX

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1185>:

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a285.seq
1  ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51  CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCG
101 CGCTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTTCTGAT TTTGGCAGTA
151 TGTTTCCTCG GCTGGCTCGC CGGCACGGAA GCGGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTCCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGCGT GGAAACCGTC
351 CGAACTGATG CGCCGACGCC TGCACATTAC CGAAATTTCC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCCTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTCGACCTGA AGGCTGCCGA CACGCCGTGG AGCAGTTCGT CGGGGTCAGC

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651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
 701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
 751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG
 801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
 851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GTCCGCCTTC
 901 GTGCCTTCCC TGCCCGATGC CGGGCTGAAT TTCGACCTGA CCGCCATCCC
 951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG CTCGCTCGAT TTGGA AAAACA
 1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCCGTCCG TCAGGTTTTA
 1051 GGCAGCTTTG TCATCCGGCA GGACGGCAGC GTGCATATCG GCAATACGTC
 1101 CGTCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGGC AAAATCGACA
 1151 CCGAAAAAGA CATCCTCGAT TTAAATATAG GCATCAATC CGTCGGCGCG
 1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
 1251 CATCGGTGGC ACGACCGCT CGCCAAAAT CTCTTGCAA CTCGGCATCG
 1301 GCACGGCGCG CACGGACGGC AGCCTCGCA TTGCAAGCGA CCCC GCAAC
 1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
 1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
 1451 AGCTGGACAT CCGTTCCCGC GCATTTCGACC CTTCGCGCAT CGATCCGCAA
 1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAATGGC
 1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG
 1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
 1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAAACAGA
 1701 CGGCGGCTTC GGCAAAAAG GCGACCGGCT TAACCTCAAT ATCACC GCAC
 1751 CCGATTTATC CCGTTTCGGT TTCGGACTCG CGGGGTCTTT AAATGTACGC
 1801 GGACACCTTT CCGGCGATTT GGACGGTGGC ATCCGAACCT TTGAAACCGA
 1851 CCTTTCCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
 1901 GTTCGCTCGA TTTCACGCTC AAAGGTTGCG CCGACACAAG CCGCCGATA
 1951 CGCGCCGACA TCAAAGGCAG CCGCCTTTCG CTGTCGGGCG GAGCGGAGGT
 2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACC GCA
 2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
 2101 TTGGACGCTT CAGGCGGCAT CAACAGGGAA CTTACCCGAT GGAAAGGCAG
 2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
 2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TGCGGCAAA
 2251 TGAGAGGCAA TGGGCGGCGC CCTCAACCTG CAACACTTTT CTTGGGATAA
 2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
 2351 AGTTGCACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
 2401 GGCGACTGGG ATGTGCGCTA CGGGCGAAAC GCGGCGGGCT ACCTCAATAT
 2451 CAGCCGCGAA AGCGGCGATG CCGTATTGCC CGGCGGGCAG GCTTTGGGTT
 2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG TATCGGAATC
 2551 CTGCTTGACG GCGGCGCGCG TTTCGGGCGG ATTAACGCGG ATTTGGACAT
 2601 CGGCAACGCC TTCCGGCGCA ATATGGCAAA TGCACCGCTC GGCGGCAAGG
 2651 TTACCGCCTC CTTTCCCGAC TTGGGCACAT TGAAGCCCTT TCTGCCCGCC
 2701 GCCGCGCAAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGGCGG
 2751 ACGGGTCGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
 2801 ACGGGAAAAT CAACGGCAAC ATCACCCTCG GGCAAAGCCG CTCTTTCGAT
 2851 ACCGCGCCTT TGGGCGGCGC GCTCAACCTG ACCGTTGCCG ATGCCGAAGT
 2901 ATTCCGCAAC TTCTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
 2951 CCGCCGTAAC CCTCGGCGGC AGCATCGCCG ATCCGCACTT GGGCGG CAGC
 3001 ATCAACGGCG ACAAACCTA TTACCGCAAC CAAACCCAAG GCATCATCTT
 3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
 3101 ACAGCTGAA ATTCCGGCAC GAAGGGACGG CGGAACCTC CGGTACGGTC
 3151 GGTATGAAA ACAGCGGACC CGATGTCGAT ATCGGCGCGG GTTTCGACAA
 3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCTGACGGTT TCCGGCAACA
 3251 CCCGCTGCG CTATTCGCGC CAAAAAGGCA TATCCGTTAC CGGGATGATT
 3301 AAAACGATC AGGGGCTGTT CGGTTTCGCA AAATCCTCGA TGCCGTCCGT
 3351 CGGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC
 3401 CGCTCCCGT CAATATGAAC CTGACTTAG ACCTCAATGA CGGCATCCGC
 3451 TTCGCCGGCT ACGGCGCGGA CGTTACCATA GCGGCAAAAC TGACCCTGAC
 3501 CGCCCAATCG GGCGGAAGCG TGCGGGGCGT GGGCACGGTC CGCGTCATCA
 3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGACATTAC CAAAGGCACG
 3601 GTCTCTTTG TCGGCCGCT CAACGACCCC AACCTCAACA TCCGCGCCGA
 3651 ACGCCGCTT TCCCCGTCG GTGCGGGCGT GGAATATTG GGCAGCCTCA
 3701 ACAGTCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGAAAAAGAC
 3751 AAGCTCTCCT GGCTCATCCT CAACCGCGCC GGCAGTGGCA GCAGCGGCGA
 3801 CAATGCCGCC CTGTCCGAG CCGCCGGCGC GCTGCTTGCC GGGCAAATCA
 3851 ACGACCGCAT CGGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC
 3901 CGCAACGCGC AAACGGCGCA ACTCAACCCC GCCGAACAGG TGCTGACCGT

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3951 CGGCAAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AACTGATTT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTTG CCCGTATCGG CAGCCGTTCG TCGGGCGGCG AGCTGACATA
4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAAA GACTCCGCCG
4151 GAAACAGCAA AGGAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

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a285.pep
1  MTDAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
51  CFLGWLAGE AGLRFGlyQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSERM RRLSHITEIS AGDIAIVTKP TPPKEERPPL
151 SLPDSIDLPA AVYLDREFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
251 SLKDVRAELA IDGGNIRLSG KSVIHPPAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSF S DGIALEGLD LENTKAGFAD RRGIPVRQVL
351 GSFVIRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFTG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
451 GQRKLVLDTV NIAAGQGSIT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIKTDDGGF GKKGDRNLN ITAPDLSRFG FGLAGSLNVR
601 GHLSGDLDDG IRTFETDLGG AARNLHIGKA ADIRSLDFTL KGSPTDSRPI
651 RADIKGSRLS LSGGAEVVDI ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
701 LDASGGINRE LTRWKSGSIGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
751 WQAMGGSLNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFEHNLVLN
801 GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGLNAFLSK TRFQNDRIGI
851 LLDGGARFGR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFLPA
901 AAQNTGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVQSRSD
951 TAPLGGRLNL TVADAEVFRN FLPGVQTVKG SLNAAVTLGG SIADPHLGG
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAPLPVNMN LTLDLNDGIR
1151 FAGYGADVTI GGKLTILTAQS GGSVRGVGTV RVIKGRYKAY GQDLDTITKT
1201 VSFVGPLNDP NLNIRAERRL SPVAGVEIL GSINSPRITL TANEPMSKED
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGELTYTIR FDRFSGSDKK DSAGNSKKGK*

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m285/a285 99.4% identity in 1389 aa overlap

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          10      20      30      40      50      60
m285.pep  MTDAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
          |||
a285       MTDAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
          10      20      30      40      50      60

          70      80      90     100     110     120
m285.pep  AGLRFGlyQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPSERM
          |||
a285       AGLRFGlyQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPSERM
          70      80      90     100     110     120

          130     140     150     160     170     180
m285.pep  RRLSHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLDREFETGKISMKGAFDK
          |||
a285       RRLSHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLDREFETGKISMKGAFDK
          130     140     150     160     170     180

          190     200     210     220     230     240
m285.pep  QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK
          |||
a285       QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK
          190     200     210     220     230     240

          250     260     270     280     290     300
m285.pep  TIHSTARLSGSLKDVRAELIDGGNIRLSGKSVIHPPAESLDKTLEEVLVKGFNINPAAF
          |||

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a285	TIHSTARLSGSLKDVRAELAI	DGGNIRLSGKSVIHPFAESL	DKTLEEVLVKGFNINPSAF		
	250	260	270	280	290 300
	310	320	330	340	350 360
m285.pep	VPSLPDAGLNFDLTAIPSFSDGIALE	GSLENTKAGFADRNGIPVRQVLGGF	VIRQDGT		
a285	VPSLPDAGLNFDLTAIPSFSDGIALE	GSLENTKAGFADRNGIPVRQVLGSF	VIRQDGT		
	310	320	330	340	350 360
	370	380	390	400	410 420
m285.pep	VHIGNTSAALLGRGGIRLSGKIDTEK	DILDNLNIGINSVGAEDVLQTAFKGR	LDGSIGIGG		
a285	VHIGNTSAALLGRGGIRLSGKIDTEK	DILDNLNIGINSVGAEDVLQTAFKGR	LDGSIGIGG		
	370	380	390	400	410 420
	430	440	450	460	470 480
m285.pep	TTASPKISWQLGIGTARTDGS	LAIASDPANGQRKLVLDTVNIAAGQ	GS	LT	AQGYLELFKD
a285	TTASPKISWQLGIGTARTDGS	LAIASDPANGQRKLVLDTVNIAAGQ	GS	LT	AQGYLELFKD
	430	440	450	460	470 480
	490	500	510	520	530 540
m285.pep	RLKLDIRSRAFDPSRIDPQLPAGN	INGSINLAGELAKEKFTGKMRFLPG	T	FN	GVPIAGS
a285	RLKLDIRSRAFDPSRIDPQLPAGN	INGSINLAGELAKEKFTGKMRFLPG	T	FN	GVPIAGS
	490	500	510	520	530 540
	550	560	570	580	590 600
m285.pep	ADIVYESRHLPRAAVDLRLGRNI	IKTDGGFGKKGDRNLNITAPDL	SRFGFGLAGSLNVR		
a285	ADIVYESRHLPRAAVDLRLGRNI	IKTDGGFGKKGDRNLNITAPDL	SRFGFGLAGSLNVR		
	550	560	570	580	590 600
	610	620	630	640	650 660
m285.pep	GHLSGDLGGIRTFTDL	SGAARNLHIGKAADIRSLDFTLKG	SPDTSRPIRADIKGSRLS		
a285	GHLSGDLGGIRTFTDL	SGAARNLHIGKAADIRSLDFTLKG	SPDTSRPIRADIKGSRLS		
	610	620	630	640	650 660
	670	680	690	700	710 720
m285.pep	LSGGAAVVDTADLMLDGTGVQHR	IRTHAAMTLDGKPFKFDLDASGGIN	RELTRWKSIGI		
a285	LSGGAEVVDTADLMLDGTGVQHR	IRTHAAMTLDGKPFKFDLDASGGIN	RELTRWKSIGI		
	670	680	690	700	710 720
	730	740	750	760	770 780
m285.pep	LDIGGAFNLKLQNRMTLEAGAER	VAASAANWQAMGGSLNLQHFSW	DKKTGISAKGGAHGL		
a285	LDIGGAFNLKLQNRMTLEAGAER	VAASAANWQAMGGSLNLQHFSW	DKKTGISAKGGAHGL		
	730	740	750	760	770 780
	790	800	810	820	830 840
m285.pep	HIAELHNFFKPPFEHNLVLNGD	WDVAYGRNARGYLNISRQSGDAV	LPGGQALGLNAFSLK		
a285	HIAELHNFFKPPFEHNLVLNGD	WDVAYGRNARGYLNISRQSGDAV	LPGGQALGLNAFSLK		
	790	800	810	820	830 840
	850	860	870	880	890 900
m285.pep	TRFQNDRIGILLDGGARFGRINAD	LIGIANAFGGNMANAPLGGRITAS	LPDLGALKPFLPA		
a285	TRFQNDRIGILLDGGARFGRINAD	LIGIANAFGGNMANAPLGGRITAS	LPDLGALKPFLPA		
	850	860	870	880	890 900
	910	920	930	940	950 960
m285.pep	AAQNITGSLNAAAQIGGRVGS	PSVNAAVNGSSNYGKINGNITV	QSRSFDTAPLGGRNLN		

657

a285	AAQNITGSLNAAQIGGRVGSFSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLN
	910 920 930 940 950 960
	970 980 990 1000 1010 1020
m285.pep	TVADAEVFRNFLPVGQTVKGSLNAAVTLGGSIADPHLGGSSINGDKLYYRNQTQGIILDNG
a285	TVADAEVFRNFLPVGQTVKGSLNAAVTLGGSIADPHLGGSSINGDKLYYRNQTQGIILDNG
	970 980 990 1000 1010 1020
	1030 1040 1050 1060 1070 1080
m285.pep	SLRSHIAGRKWWIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRRLTV
a285	SLRSHIAGRKWWIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRRLTV
	1030 1040 1050 1060 1070 1080
	1090 1100 1110 1120 1130 1140
m285.pep	SGNTRLRYSPQKGISVTGMIKTDQGLFGSQSSMPSVGDDVVVLGEVKKEAAAPLPVNMN
a285	SGNTRLRYSPQKGISVTGMIKTDQGLFGSQSSMPSVGDDVVVLGEVKKEAAAPLPVNMN
	1090 1100 1110 1120 1130 1140
	1150 1160 1170 1180 1190 1200
m285.pep	LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLIDITKGT
a285	LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVRGVGTVRVIKGRYKAYGQDLIDITKGT
	1150 1160 1170 1180 1190 1200
	1210 1220 1230 1240 1250 1260
m285.pep	VSFVGPLNDPNLNIRAERRLSVPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
a285	VSFVGPLNDPNLNIRAERRLSVPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
	1210 1220 1230 1240 1250 1260
	1270 1280 1290 1300 1310 1320
m285.pep	GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTGKQ
a285	GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFTSKRSRNAQTGELNPAEQVLTGKQ
	1270 1280 1290 1300 1310 1320
	1330 1340 1350 1360 1370 1380
m285.pep	LTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRDFRFGSDKK
a285	LTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRDFRFGSDKK
	1330 1340 1350 1360 1370 1380
	1390
m285.pep	DSAGNGKGKX
a285	DSAGNSKGKX
	1390

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

```

1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51 CCTCGGCTGG ATCGCCGGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC CTGGTTCGGC GTAAACATTT CCTCCAAAA CCTCAAAGGC
151 ACACTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATCACCAGCA TCTCCGCCGG CGACATCGCC
301 ATCGTAACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CTCAAGGCCT
351 GCCCGACAGC ATAGACCTGC CCGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAACCTTTG ACAACAACAC CGTCTATCTC
451 GAACGCCTCA ACGCGGCATA CCGTTACGAC CGTAAAGGGC ACCGCCTCGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG

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551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGATTCGAAG GCGAAACCAT ACACAGTACG GCGCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGACGATCGA CGGCGGCAAT ATCCGCCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAAACATTG
751 GAAGAAGTAC TGGTCAAAGG ATTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTGGA CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTTGGA AAACACCAAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTACAG TTTTGGGCGG
951 CTTTGTGCATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCGG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CCGGCAAAAT CGACACCGAA
1051 AAAGACATCC TTGATTAAAT TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTGCTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GCGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CACCGGCACG
1201 GCACGCACGG ACGGCAGCCT cgcCATCGCA AGCGACCCCG CAAACGAACA
1251 GCGGAAACTG GTGTTTCGACA CCGTCAACAT CTCGCGCCGG GAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GCGCGCCGTC CCGCGCATTT CGACCCTTCG CGCATCGATC CGCAATTTC
1401 GGCAGGCGat atCAACGGTT CGATTATCTT TGCCGGTGAA CTGGCAAAAG
1451 AGAAATTTAC GGGCAAAATG CGTTTTTTGC CCGGTACGTT CAACGGCGTG
1501 CCGATTGCCG GCAGCGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 CGCGCCGCTC GATTTCGGT TGGGCGGAA CATCGTCAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGG GATTTCGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CGGGCACGGC GCGCAACTTA CACATCGGCA AAGCGGCAGA CATCCGTTTCG
1801 CTCGATTTTA CCCTCAAAGG CTCACCCGGC ACAAGCCGCC CGATGCGCGC
1851 CGATATCAAG GCGGCGCGCC TTTCCTGTG GCGCGCGCGG GCGGTTGTTCG
1901 ATACCGCCGG CCTGACGCTG GAAGGTACGG GCGCGCAGCA CCGCATCCGC
1951 ACACACGCGG CCATGACGCT GGACGGCAAA CCGTTCAAAC TCGATTTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACACGTGGCG GCAAGTGGG CAAATTGGCA
2151 GGCAATGGG GGCAGCCTCA ACCTGCAACA CTTTCTTGG GACAGGAAA
2201 CCGGCATATC GCGAAAAGGC GCGGCACGCG GCCTGCACAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGAAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC ACAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAGCGC CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAC GACCGCATCG GAATCCTGCT
2451 TGACGGCGGC GCGCTTTTCG GACGGATTAA CGCGGATTG GGCATCGGCA
2501 ACGCTTCGG CGGCAATATG GCAAATACAC CGCTCGCGCG CAGGATTACA
2551 GCCTCCCTTC CCGACTTGGG CGCATGAAG CCCTTTCTGC CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCTC CGCGCAAAAT GCGCGACGGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGTAGCAG CAACTACGGG
2701 AAAATCAACG GCAATATCAC CGTCGGGCAA AGCCGCTCCT TCGATACCGC
2751 ACCTTTGGG GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGCATTCC
2801 GCAACTTCCT ACCGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCG GCGGCAGCAT CGCCGACCCG CACTTGGGCG GCAGTATCAA
2901 CGGCACAAG CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGACA
2951 ACGGCTCGCT GCGTTCGCAT ATTGCAGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGCGA CGGTACGAT
3051 GGAAAACAGC GTGCCCGATG TCGATATCGG CGCGGTGTTC GACAAATACC
3101 GCATCTGTG CCGCCCAAC CGCCGCCTGA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGTA TGATTAATAA
3201 TGATCAGGG CTGTTTCGGT CGCAAAAATC CTCGATGCGG TCCGTCCGGC
3251 ACGATGTCTG CGTATTGGGC GAAGTCAAGA AAGAGGCGGC GGCATCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCTC
3351 CCGGTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCGC
3401 AACCGGGCGG AAATGTGCGT GGGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTACAAAG CATACGGGCA GGATTAGAC ATTACCAAAG GCACAGTCTC
3501 CTTTGTGCGC CCGCTCAACG ACCCAACCT GAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GCGGTGAAA TATTGGGCGC CCTCAACAGC
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTAAA AAGACAAGCT
3651 CTCCTGGCTC ATCCTCAACC GTGCCGGCAG CCGCAGCAGC GCGACAATG
3701 CCGCCCTGTC CGCAGCCGCA GGCGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAAAC GCGGAACTCA ACCCGCCGCA ACAGGTGCTG ACCGTCCGCA
3851 AACAACTGAC CGGCAAACTC TACATCGGCT ACGAATACGG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAAC TATTACCAGG CTGACCCGCG CCATACAGGC
3951 GGTTGCCCGT ATCGGCAGCC GTTCGTCCGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTCTTC GGTTCGGACA AAAAGACTC CGCAGGAAAC
4051 GGCAAAGGGA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1188; ORF 285-1.ng>:

g285-1.pep

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1  LKLSAALLSV LILAVCFLGW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITDISAGDIA
101 IVTKPTPPKE ERPPQGLPDS IDLPAVYLD RFETGKISMG KTFDKQTVYL
151 ERLNAARYRD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GFEGETIHST ARLSGSLKDV RAELTIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGTGT
401 ARTDGSIAIA SDPANEQRKL VFDTVNISAG EGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQFPAGD INGSIHLAGL LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLSG DLDGGIRTFE TDLSGTARNL HIGKAADIRS
601 LDFTLKGSPG TSRPMRADIK GGRSLSGGA AVVDTAGLTL EGTGAQHRI
651 THAAMTLDGK PFKLDDLASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAEHVA ASANWQAMG GSLNLQHFWS DRKTGISAKG GARGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGHNARGYL NISROSGDAV LPGGQALGLN
801 LKFRHEGTAE LSGTVSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
851 ASLPDLGALK PFLPAAQNI TGSLNASAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGQ SRSFDTAPLG GRLNLTVADA EAFRNFLPVG QTVKGS LNAA
951 VTLGGSIADP HLGGSINGDK LYRNTQTQGI ILDNGLSRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAASL
1101 PVNMNLTLDL NDGIRFSGYG ADVTIGGKLT LTAQPGGNVR GVGTVRVIKG
1151 RYKAYQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYGISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRLF GSDKKDSAGN
1351 GK GK*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCGGGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAC CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTTCCGCCGG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCCGCGT CTATCTCGAG CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAAAACAAC CGTCTATCTC
451 GAACGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTTGA
501 CCTGAAGGCC GCCGACACGC CGTGAGCAGC TTCGTCGGGG GCGGCCCTCG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCCTCT
701 CGGGAAAATC CGTCAATCCAC CCGTTTGCCG AATCATTTGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCGGGCGC CCTTCGTGCC
801 TTCCCTGCCC GATGCGGAC TGAATTTTGA CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGTTTCG TCGATTTTGA AAACACCAAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCGCTCAGG TTTTAGCGCG
951 CTTTGTTCAT CGGCGAGGAC GCACGGTGCA TATCGGCAAT ACGTCCGCGC
1001 CCTTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCACAGC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCAGC
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATTT CGACCTTCG CGCATCGATC CGCAACTTCC
1401 GGATCGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGGA CTGGCAAAAG
1451 AGAAATTCAC AGGCAAAATG CCGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCCG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCCGTC GATTGCGGCG TGGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCGGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGGT GATTGAGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGCGCGCGC GCGCAACCTG CACATCGGCA AGGCGGCAGA CATCCGTTCC
1801 CTCGATTTCG CGCTCAAAAG TTCGCCCAGC ACAAGCCGCC CGATACGCGC
1851 CGACATCAAA GGCAGCCGCC TTTCGCTGTC GGGCGGAGCG GCGGTTGTCG
1901 ATACCGCCCG CCTGATGCTG GACGGCACGG GCGTGCAGCA CCGCATCCGC
1951 ACACACGCCG CCATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACCTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGCGCGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGGTGCGCG GCAAGTCCGG CAAATTGGCA

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660

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2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAA
2201 CCGGCATATC GGCAAAAGGC GGCGCACACG GTCTGCATAT CGCCGAGTTG
2251 CACAAATTCT TCAAACCGCC CTTGCAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GCAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAAGCGG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAA
2401 GCATTTTCCC TGAAACGCGC CTTTCAAAAC GACCGCATCG GAATCCTGCT
2451 TGACGGCGGC GCGCGTTTCG GGCGGATTAA CGCCGATTTG GGCATCGCCA
2501 ACGCCTTCGG CGGCAATATG GCAAATGCAC CGCTCGGCGG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CGCATGGAAG CCCTTTCTGC CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAAATC GCGGACGCGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC CGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTTCG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CGGCGACAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGACA
2951 ACGGCTCGCT CGGCTCGCAT ATCGCGGCGA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGCGGAA CTCTCCGTA CGGTCCGGTAT
3051 GGAAACACAG GGACCCGATG TCGATATCGG CGCGGTGTTC GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCCGCTGA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAATAA
3201 GGATCAGGGG CTGTTCCGTT CGCAAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CCGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTACGG GGCGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATACGGGCA GGATTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTCCGG CCGCTCAACG ATCCCAACCT CAACATCCGC GCCGAACGCC
3551 CGCTTCCGCC CGTCCGTGCG GGCGTGGAAT TATTGGGCA CCTCAACAGC
3601 CCGCGCATTG CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCTTGGCTC ATCCTCAACC GCGCCGGCAG CGGCAGCAGC GGCACAAATG
3701 CCGCCCTGTC TGCAGCCGCA GGTGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAAAC GGCAGAACTC ACCCCGCCGA ACAGGTGCTG ACCGTCGGCA
3851 ACAAACGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTACCGG CTGACCCCGC CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCGGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAAC
4051 GGCAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1190; ORF 285-1>:

m285-1.pap

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1 LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51 TLLDGFDDN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPLSLPDS IDLPAAVYLD RFETGKISMV KAFDKQTVYL
151 ERLDASYRYD RKGHRLDLKA ADTPWSSSSG AASVGLKKPF ALDTAIYTKG
201 LEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPAAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGGGTTASP KISWQLGIGT
401 ARTDGLAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPN RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFLAG SLNVRGHLG DLDGGIRTFE TDLSGAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA AVVDTADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIG AFNLKLQNRN
701 TLEAGAERVA ASANWQAMG GSLNLQHFSW DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPPGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIANAFGGNM ANAPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSLNAAQI GGRVGSFSPV AAVNGSSNYG
901 KINGNITVGQ SRSFDTAPLG GRNLTVADA EVFRNFLPVG QTVKGSINAA
951 VTLGGSIA DP HLGGSSINGDK LYRNTQTQGI ILDNGLSLRH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PVNMNLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIK
1151 RYKAYGQDLD ITKGTVSFVG PLNDPNLNIR AERRLSVPGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRFS GSDKKDSAGN
1351 GK GK*

```

g285-1/m285-1 96.5% identity in 1354 aa overlap

10

20

30

40

50

60

g285-1.pep LKLSAALLSVLILAVCFLGWIAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN
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m285-1 LKLSAALLSVLILAVCFLGWLAGEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN
10 20 30 40 50 60

70 80 90 100 110 120
g285-1.pep WSIETEGADLKISRFRFAWKPSSELMRRSLHITDISAGDIAIVTKPTPKKEERPPQGLPDS
|||||:|||||:|||||
m285-1 WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPKKEERPPLSLPDS
70 80 90 100 110 120

130 140 150 160 170 180
g285-1.pep IDLPAAYLDRFETGKISMGKTFDKQTVYLERLNAAYRYDRKGHRDLKAADTPWSSSSG
|||||:|||||:|||||
m285-1 IDLPAAYLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRDLKAADTPWSSSSG
130 140 150 160 170 180

190 200 210 220 230 240
g285-1.pep SASVGLKKPFALDTAIYTKGGFEGETIHSTARLSGSLKDVRAELTIDGGNIRLSGKSVIH
:|||||:|||||:|||||:|||||
m285-1 AASVGLKKPFALDTAIYTKGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH
190 200 210 220 230 240

250 260 270 280 290 300
g285-1.pep PFAESLDKLTLEEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTK
|||||:|||||:|||||
m285-1 PFAESLDKLTLEEVLVKGFNINPAAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTK
250 260 270 280 290 300

310 320 330 340 350 360
g285-1.pep AGFADRNGIPVRQVLGGFVIRQDGTVHIGNTSAALLGRGGIRLSGKIDTEKDILDNLIGI
|||||:|||||:|||||
m285-1 AGFADRNGIPVRQVLGGFVIRQDGTVHIGNTSAALLGRGGIRLSGKIDTEKDILDNLIGI
310 320 330 340 350 360

370 380 390 400 410 420
g285-1.pep NSVGAEDVLQTAFAKGRLDGSGIGGTTASPKISWQLGTGTARTDGLAIASDPANEQRKL
|||||:|||||:|||||
m285-1 NSVGAEDVLQTAFAKGRLDGSGIGGTTASPKISWQLGIGTARTDGLAIASDPANGQRKL
370 380 390 400 410 420

430 440 450 460 470 480
g285-1.pep VFDTVNISAGEGSLTAQGYLELFKDRLLKLDIRSRAFDPSRIDPQFPAGDINGSIHLAGE
|:|||||:|||||:|||||:|||||:|||||
m285-1 VLDTVNIAAGQGSILTAQGYLELFKDRLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGE
430 440 450 460 470 480

490 500 510 520 530 540
g285-1.pep LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRRAVDLRLGRNIVKTDGGFGKKGD
|||||:|||||:|||||
m285-1 LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRRAVDLRLGRNIIKTDGGFGKKGD
490 500 510 520 530 540

550 560 570 580 590 600
g285-1.pep RLNLNITAPDLSRFGLAGSLNVRGHLSGDLGGIRTFTDLSGTARNLHIGKAADIRS
|||||:|||||:|||||
m285-1 RLNLNITAPDLSRFGLAGSLNVRGHLSGDLGGIRTFTDLSGAARNLHIGKAADIRS
550 560 570 580 590 600

610 620 630 640 650 660
g285-1.pep LDFTLKGSPTSRPMRADIKGGRSLSGGAADVDTAGLTLEGTGAQHRIRTHAAMTLDGK
|||||:|||||:|||||:|||||
m285-1 LDFTLKGSPTSRPIRADIKGGRSLSGGAADVDTADLMDGTGVQHRIRTHAAMTLDGK
610 620 630 640 650 660

670 680 690 700 710 720
g285-1.pep PFKLDLDASGGINRELTRWKGSGILDIGGAFNLKLQNRMTLEAGAETHVAASAANWQAMG
|||:|||||:|||||:|||||
m285-1 PFKFDLDASGGINRELTRWKGSGILDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMG
670 680 690 700 710 720

730 740 750 760 770 780
g285-1.pep GSLNLQHFSDRKTGISAKGGARGLHIAELHNFFKPPFEHNLVLNGDWDVAYGHNARGYL
|||||:|||||:|||||:|||||
m285-1 GSLNLQHFSDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL

	730	740	750	760	770	780
	790	800	810	820	830	840
g285-1.pep	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIGNAFGGNM					
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIANAFGGNM					
	790	800	810	820	830	840
	850	860	870	880	890	900
g285-1.pep	ANTPLGGRITASLPDLGALKPFLPAAAQNTGSLNAAQIGGRVGSPSVNAAVNGSSNYG					
m285-1	ANAPLGGRITASLPDLGALKPFLPAAAQNTGSLNAAQIGGRVGSPSVNAAVNGSSNYG					
	850	860	870	880	890	900
	910	920	930	940	950	960
g285-1.pep	KINGNITVGQSRSFDTAPLGGRLNLTVADAEAFRNFLPVGQTVKGSLSNAAVTLGGSIA DP					
m285-1	KINGNITVGQSRSFDTAPLGGRLNLTVADAEVFRNFLPVGQTVKGSLSNAAVTLGGSIA DP					
	910	920	930	940	950	960
	970	980	990	1000	1010	1020
g285-1.pep	HLGGSINGDKLYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
m285-1	HLGGSINGDKLYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
g285-1.pep	VPDVIDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP					
m285-1	GPDVIDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP					
	1030	1040	1050	1060	1070	1080
	1090	1100	1110	1120	1130	1140
g285-1.pep	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFSGYGADVTIGGKLTTLTAQPGGNVR					
m285-1	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVR					
	1090	1100	1110	1120	1130	1140
	1150	1160	1170	1180	1190	1200
g285-1.pep	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
m285-1	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
g285-1.pep	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
g285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYISSAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYISSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
g285-1.pep	IGSRSSGGELTYTIRFDRLFGSDKKDSAGNGK GK					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGK GKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1191>:

a285-1.seq

```

1 CTGAAGCTGT CGGCGGCACT GCTGTCTGTT CTGATTTTGG CAGTATGTTT
51 CCTCGGCTGG CTCGCCGCA CGGAAGCGGG TTGCGCTTC GGGCTGTACC
101 AAATCCCCTC TTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTTCCGCCG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAGAA GAACGCCCG CGCTCAGCCT
351 TCCCGACAGC ATAGACTCG CTGCCGCGT CTATCTGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTG ACAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTCGA

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGA CTGGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCGG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTCGA CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCAG
951 CTTTGTATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTCG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CCGATTGCCC ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCCG CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCGGG CAAGGCAGCC
1301 TCGCCGCTTG CCGATATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCCTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTCAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CGGATTGCCC CGAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCGGTC GATTTGCGGC TGGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGCGGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CTTTTCGGG GATTTGGACG GTGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGGCGGCAGA CATCCGTTCG
1801 CTCGATTTCG CGCTCAAAGG TTCGCCGAC ACAAGCCGCC CGATACGCGC
1851 CGACATCAAA GGCAGCCGCC TTTCGCTGTC GGGCGGAGCG GAGGTTGTCTG
1901 ATACCGCCGA CCGATGCTG GACGGCACGG GCGTGCAGCA CCGCATCCGC
1951 ACACACGCGC CCATGACGCT GGATGGCAAA CCGTTCAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGCGG CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAA
2201 CCGGCATATC GGCAAAAGGC GCGGCACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTCGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC CCTACGGGC GAAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAAGCG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAC GACCGTATCG GAATCCTGCT
2451 TGACGGCGGC GCGCGTTTCG GCGCGATTAA CGCCGATTTG GACATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAAATGCAC CGCTCGGCGC CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CACATTGAAG CCTTTCTGCG CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAAATC GCGGACGGG
2651 TCGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTTCG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGCGACAAA CTCTATTACC GCAACCAAC CCAAGGCATC ATCTTGACA
2951 ACGGCTCGCT CGGTTGCGAT ATCGCGGGA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGTA CGGTCGGTAT
3051 GGAAAACAGC GGACCCGATG TCGATATCGG CGCGGTGTTC GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCCGCTGA CGGTTCCGG CAACACCCGC
3151 CTGCGCTATT CCGCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAC
3201 GGATCAGGGG CTGTTGCGTT CGCAAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGTTTCGC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTGGCG GCGGTGGGCA CGGTCCGCGT CATCAAAGG
3451 CGTTATAAGG CATACGGGCA GGATTGAGC ATTACCAAAG GCACGGTCTC
3501 CTTTGTGCGG CGGCTCAACG ACCCAACCT CAACATCCGC GCCGAACGCC
3551 GCTTTTCCCC CCGTGGTGGC GGCGTGGAAT TATTGGGAG CCTCAACAGT
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCCTGGCTC ATCCTCAACC GCGCCGGCAG TGGCAGCAGC GGCAGCAATG
3701 CCGCCTGTCT CGCAGCCGCC GCGCGCTGCT TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAACC GCGGAACTCA ACCCGGCCGA ACAGGTGCTG ACCGTCGGCA
3851 ACAAACGAC CCGGAAACTC TACATCGGCT ACGAATACAG CATCTCAGC
3901 GCGGAACAGT CCGTCAAACCT GATTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTGGG CGCGGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAGACTC CGCCGGAAAC
4051 AGCAAAGGAA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:

a285-1.pep

```

1  LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPLSLPDS IDLPAAYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGSFVI RQDGTVHIGN TSVALLGRRG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGSIAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFIADG SLNVRGHLSG DLDGGIRTFE TDLGAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA EVVDTADLML DGTGVQHRIR
651 THAMTLDDGK PFKFDLDASG GINRELTRWK GSGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASAANWQAMG GSLNLQHFWS DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEL NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL DIGNAFGGNM ANAPLGGRIT
851 ASLPDLGTLK PFLPAAAQNI TGSLNAAAI GGRVGSPPSVN AAVNGSSNYG
901 KINGNITVGO SRSFDTAPLG GRLNLTADA EVFRNFLPVG QTVKGSNLAA
951 VTLLGSIADP HLGGSINGDK LYRNQQTQGI ILDNGSLRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PVNMNLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIKG
1151 RYKAYQDLDL ITKGTVSFVG PLNDPNLNIR AERRLSVPGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRFS GSDKKDSAGN
1351 SKGK*

```

a285-1/m285-1 99.3% identity in 1354 aa overlap

	10	20	30	40	50	60
a285-1.pep	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
m285-1						
	10	20	30	40	50	60
a285-1.pep	70	80	90	100	110	120
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS					
	70	80	90	100	110	120
a285-1.pep	130	140	150	160	170	180
m285-1	IDLPAAYLDLRFETGKISMKGAFDKQTVYLERLDASYRYDRKGHRDLKAADTPWSSSSG					
	130	140	150	160	170	180
a285-1.pep	190	200	210	220	230	240
m285-1	SASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
	190	200	210	220	230	240
a285-1.pep	250	260	270	280	290	300
m285-1	PFAESLDKTL EEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSIDLENTK					
	250	260	270	280	290	300
a285-1.pep	310	320	330	340	350	360
m285-1	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRRGIRLSGKIDTEKDILDLNIGI					
	310	320	330	340	350	360
a285-1.pep	370	380	390	400	410	420
m285-1	NSVGAEDVLQTAFKGRLDGSIGIGGTTASPKISWQLGIGTARTDGSIAIASDPANGQRKL					
	370	380	390	400	410	420
	430	440	450	460	470	480

665

a285-1.pep	VLDTVNIAAGQGSILTAQGYLELFKDRLLKLDIRSFADPSRIDPQLPAGNINGSINLAGE
m285-1	VLDTVNIAAGQGSILTAQGYLELFKDRLLKLDIRSFADPSRIDPQLPAGNINGSINLAGE
	430 440 450 460 470 480
a285-1.pep	490 500 510 520 530 540
m285-1	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGD
	490 500 510 520 530 540
a285-1.pep	550 560 570 580 590 600
m285-1	RLNLNITAPDLSRFGLAGSLNVRGHLSGDLGGIRTFTDLGAARNLHIGKAADIRS
	550 560 570 580 590 600
a285-1.pep	610 620 630 640 650 660
m285-1	LDFTLKGSPDTSRPIRADIKGSRLSLSGGAEVVDTADLMLDGTGVQHRIIRTHAAMTLDGK
	610 620 630 640 650 660
a285-1.pep	670 680 690 700 710 720
m285-1	PFKFDLDASGGINRELTRWKSGSIGILDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMG
	670 680 690 700 710 720
a285-1.pep	730 740 750 760 770 780
m285-1	GSLNLQHFSWDKKTGISAKGGAGHLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL
	730 740 750 760 770 780
a285-1.pep	790 800 810 820 830 840
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM
	790 800 810 820 830 840
a285-1.pep	850 860 870 880 890 900
m285-1	ANAPLGGRITASLPDLGTLKPFPLPAAQNITGSLNAAQIGGRVGSFVNAAVNGSSNYG
	850 860 870 880 890 900
a285-1.pep	910 920 930 940 950 960
m285-1	KINGNITVQSRSFDTAPLGGRNLTVADAEVFRNLPVGQTVKGSNAAVTLGGSADP
	910 920 930 940 950 960
a285-1.pep	970 980 990 1000 1010 1020
m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENS
	970 980 990 1000 1010 1020
a285-1.pep	1030 1040 1050 1060 1070 1080
m285-1	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQSSMP
	1030 1040 1050 1060 1070 1080
a285-1.pep	1090 1100 1110 1120 1130 1140
m285-1	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVR
	1090 1100 1110 1120 1130 1140
a285-1.pep	1150 1160 1170 1180 1190 1200
m285-1	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS
	1150 1160 1170 1180 1190 1200

666

	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
a285-1.pep	PRITLTANEP	MSEKDKLSW	LILNRAGSG	SSGDNAALS	SAAAGALLA	GQINDRIGLV
m285-1	PRITLTANEP	MSEKDKLSW	LILNRAGSG	SSGDNAALS	SAAAGALLA	GQINDRIGLV
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
a285-1.pep	TSKRSRNAQT	GELNP	AEQVLT	VGKQLTGK	LYIGYEYS	ISSAEQSVK
m285-1	TSKRSRNAQT	GELNP	AEQVLT	VGKQLTGK	LYIGYEYS	ISSAEQSVK
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
a285-1.pep	IGSRSSGGEL	TYTIRFDR	FSGSDKKD	SAGNSKGKX		
m285-1	IGSRSSGGEL	TYTIRFDR	FSGSDKKD	SAGNSKGKX		
	1330	1340	1350			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1193>:

g286.seq

```

1  atgcagaaca ccggtaccat gatgatcaaa ccgaccgccc tgctcctgcc
51  ggctttatth ttctttccgc acgcatacgc gcctgccgcc gacctttccg
101 aaaacaaggc ggcggttttc gcattgttca aaagcaaaag ccccgacacc
151 gaatcagtca aattaaaacc caaattcccc gtccgcateg acacgcagga
201 cagtgaatc aaagatatgg tcgaagaaca cctgccgctc atcacgcagc
251 agcaggaaga ggttttggat aaggaacaga cgggattcct tgccgaagaa
301 gcaccggaca acgttaaaac aatgctccgc agcaaaggct atttcagcag
351 caaggtcagc ctgacggaaa aagacggagc ttatacggtg cacatcacac
401 cgggcccgcg caccaaaatc gccaacgtcg gcgtcgccat cctcggcgac
451 atcctttcag acggcaacct cgccgaatac taccgcaacg cgctggaaaa
501 ctggcagcag ccggtaggca gcgatttcga tcaggacagt tgggaaaaca
551 gcaaaaacttc cgtcctcggc gcgtaacgc gcaaaggcta cccgcttgcc
601 aagctcggca acacccgggc ggccgtcaac cccgataccg ccaccgcca
651 tttgaacgtc gtcgtggaca gcggccgccc cattgccttc ggcgactttg
701 aaatcaccgg cacacagcgt taccggaac aaaccgtctc cggcctggcg
751 cgcttccaac cgggcacgcc ctacgacctc gacctgctgc tcgacttcca
801 acaggcgctc gaacaaaacg ggcatatttc cggcgcgtcc gtacaagccg
851 acttcgaccg cctcccaagg ggaccgcgtc cccgtcaaag tcagcgtaac
901 cgaggtcaaa cgccacaaac tcgaaaccgg catccgcctc gattcggaat
951 acggtttggg cggcaaaatc gcctacgact attacaacct cttcaacaaa
1001 ggctatatcg gctcggtcgt ctgggatatg gacaaatacg aaaccacgct
1051 tgccgccggc atcagccagc cgcgcaacta tcggggcaac tactggacaa
1101 gcaacgtttc ctacaaccgt tcgaccaccc aaaacctcga aaaacgcgcc
1151 ttctccggcg gcatctggtg tgtgcgcgac cgcgcgggca tcgatgccag
1201 gctggggggc gaatttctcg cagaaggccg gaaaatcccc ggctcggatg
1251 tcgatttggg caacagccac gccacgatgc tgaccgcctc ttggaaacgc
1301 cagctgctca acaacgtgct gcaccccgaa aacggccatt acctcgacgg
1351 caaaatcggg acgactttgg gcacattcct gtcctccacc gcgctaatec
1401 gcacctctgc ccgcgcaggt tatttcttca cgcccgaaaa caaaaaactc
1451 ggcacgttca tcatacggc acaagcgggt tacaccgttg cacgcgacaa
1501 tgccgatgtc ccctcggggc tgatgttccg cagcggcggc gcgtcttccg
1551 tcgcgggtta cgaacttga

```

This corresponds to the amino acid sequence <SEQ ID 1194; ORF 286.ng>:

g286.pep

```

1  MQNTGTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKSKSPDT
51  ESVKLPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGAYTV HITPGPRTKI ANVGVAIIGD
151 ILSDGNLAAY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKGYPLA
201 KLGNTAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQTVSGLA
251 RFQPGTPYDL DLLLDFQAL EQNGHYSAS VQADFRLPR GPRPRQSQRN
301 RQQTPTQTRN HPPRFGIRFG RQNRLRLQLP LQORLYRLGR LGYQIRNHA
351 CRRHQPAQQL SGQLLDKQRF LQPFDPKPR KTRLLRRHLV CARPRGHRQ
401 AGGGISRRRP ENPRLGCRFG QQPRHDADRL LETPAAQORA APRKRPLPRR

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667

451 QNRDDFGHIP VLHRANPHLC PRRFLHARK QKTRHVHHTR TSGLHRCTRQ
 501 CRCPLGADV PRRRVFRARL RT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

m286.seq

1	ATGCACGACA	CCCGTACCAT	GATGATCAAA	CCGACCGCCC	TGCTCCTGCC
51	GGCTTTATTT	TTCTTTCCGC	ACGCATACGC	GCCTGCCGCC	GACCTTTCCG
101	AAAACAAGGC	GGCGGGTTTC	GCATTGTTC	AAAACAAAAG	CCCCGACACC
151	GAATCAGTCA	AATTTAAACC	CAAATTCCTC	GTCTCATCG	ACACGCAGGA
201	CAGTGAAATC	AAAGATATGG	TGAAGAACA	CCTGCCGCTC	ATCACGCAGC
251	AGCAGGAAGA	AGTATTGGAC	AAGGAACAGA	CGGGCTTCCT	CGCCGAAGAA
301	GCGCCGGACA	ACGTATAAAC	GATGCTCCGC	AGCAAAGGCT	ATTTTCAGCAG
351	CAAAGTCAGC	CTGACGGAAA	AAGACGGAGC	TTATACGGTA	CACATCACAC
401	CGGGCCCGCG	CACCAAAATC	GCCAACGTCG	GCGTCGCCAT	CCTCGGCGAC
451	ATCCTTTCAG	ACGGCAACCT	CGCCGAATAC	TACCGCAACG	CGCTGGAAAA
501	CTGGCAGCAG	CCGGTAGGCA	GCGATTTCGA	TCAGGACAGT	TGGGAAAAACA
551	GCAAAACTTC	CGTCCTCGGC	GCGGTAACGC	GCAAAGCCTA	CCCGCTTGCC
601	AAGCTCGGCA	ATACGCAGGC	GGCCGTCAAC	CCCGATACCG	CCACCGCCGA
651	TTTGAACGTC	GTCGTGGACA	GCGGCCGCC	CATCGCCTTC	GGCGACTTTG
701	AAATCACCGG	CACACAGCGT	TACCCCGAAC	AAATCGTCTC	CGGCCTTGCG
751	CGTTTCCAGC	CCGGTATGCC	GTACGACCTC	GACCTGCTGC	TCGACTTCCA
801	ACAGGCGCTC	GAACAAAACG	GGCATTATTC	CGGCGCGTCC	GTACAAGCCG
851	ACTTCGACCG	CCTCCAAGGC	GACCGCGTCC	CCGTCAAAGT	CAGCGTAACC
901	GAGGTCAAAC	GCCACAAACT	CGAAACCGGC	ATCCGCTCTG	ATTCGGAATA
951	CGGTTTGGGC	GGCAAAATCG	CCTACGACTA	TTACAACCTC	TTCAACAAAG
1001	GCTATATCGG	TTCCGTCGTC	TGGGATATGG	ACAAATACGA	AACCACGCTT
1051	GCCGCCGGCA	TCAGCCAGCC	GCGCAACTAT	CGGGGCAACT	ACTGGACAAG
1101	CAACGTTTCC	TACAACCGTT	CGACCACCCA	AAACCTCGAA	AAACGCGCCT
1151	TCTCCGGCGG	CGTCTGGTAT	GTGCGCGACC	GCGCGGGCAT	CGATGCCAGG
1201	CTGGGGGCGG	AATTTCTCGC	AGAAGGCCGG	AAAATCCCCG	GCTCGGCTGT
1251	CGATTTGGGC	AACAGCCACG	CCACGATGCT	GACCGCCTCT	TGGAACGCC
1301	AGCTGCTCAA	CAACGTGCTG	CATCCCGAAA	ACGGCCATTA	CCTCGACGGC
1351	AAAATCGGTA	CGACTTTGGG	CACATTCTCG	TCCTCCACCG	CGCTGATCCG
1401	CACCTCTGCC	CGTGCAGGTT	ATTTCTTCAC	GCCCCAAAAC	AAAAAACTCG
1451	GCACGTTTCA	CATACGCGGA	CAAGCGGGTT	ACACCGTTGC	CCGCGACAAT
1501	GCCGACGTTT	CTTCAGGGCT	GATGTTCCGC	AGCGGCGGCG	CGTCTTCCGT
1551	GCGCGGTAC	GAATTCGACA	GCATCGGACT	TGCCGCGCCG	AACGGATCCG
1601	TCCTGCCCGA	ACGCGCCCTC	CTGGTGGGCA	GCCTGGAATA	CCAACGCGCG
1651	TTTACGCGCA	CCCTTTCCGG	CGCGGTGTTT	CACGATATGG	GCGATGCCGC
1701	CGCCAATTTC	AAACGTATGA	AGCTGAAACA	CGGTTCCGGA	CTGGGCGTGC
1751	GCTGGTTTCA	CCCGCTTGCG	CCGTTTTCCT	TCGACATCGC	CTACGGGCAC
1801	AGCGATAAGA	AAATCCGCTG	GCACATCAGC	TTGGGAACGC	GCTTCTAA

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

m286.pep

1	MHDTRTMMIK	PTALLLPALF	FFPHAYAPAA	DLSENKAAGF	ALFKNKSPDT
51	ESVKLKPKFP	VLIDTQDSEI	KDMVEEHLPL	ITQQQEEVLD	KEQTGFLEAE
101	APDNVKTMLR	SKGYFSSKVS	LTEKDGYTV	HITPGPRTKI	ANVGVAIGD
151	ILSDGNLAIE	YRNALENWQQ	PVGSDFDQDS	WENSKTSVLG	AVTRKAYPLA
201	KLGNLQAQVN	PDTATADLNV	VVDSGRPIAF	GDFEITGTQR	YPEQIVSGLA
251	RFQPGMPYDL	DLLEDFFQAL	EQNGHYSYGAS	VQADFDRLOQ	DRVPVKVSVT
301	EVKRHKLETG	IRLDSEYGLG	GKIAYDYNNL	FNKGYIGSVV	WDMKYEYTTL
351	AAGISQPRNY	RGNYWTSNVS	YNRSTQNL	KRAFSGGVWY	VRDRAGIDAR
401	LGAFLAEGR	KIPGSVDLG	NSHATMLTAS	WKRQLLNNVL	HPENGHYLDG
451	KIGTTLGTFL	SSTALIRTS	RAGYFFTPEN	KKLGTFLIRG	QAGYTVARDN
501	ADVPSGLMFR	SGGASSVRGY	ELDSIGLAGP	NGSVLPERAL	LVGSLEYQLP
551	FTRTLGAVF	HDMGDAAANF	KRMKLKHGSG	LGVRWFSPLA	PFSFDIAYGH
601	SDKKIRWHIS	LGTRF*			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap

668

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKPEP					
g286	MQNTGTMMIKPTALLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKPEP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m286.pep	VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
g286	VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m286.pep	LTEKDGAITVHITPGPRTKIANVGVAILGDILSDGNLAEEYRNALENWQQPVGSDFDQDS					
g286	LTEKDGAITVHITPGPRTKIANVGVAILGDILSDGNLAEEYRNALENWQQPVGSDFDQDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m286.pep	WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPDATADLNVVVDSEGRPIAFGDFEITGTQR					
g286	WENSKTSVLGAVTRKGYPLAKLGNTAAVNPDATADLNVVVDSEGRPIAFGDFEITGTQR					
	190	200	210	220	230	240
	250	260	270	280	290	299
m286.pep	YPEQIVSGLARFQPGMPYDLDLLDFQQALEQNGHYSGASVQADFRL-QGDRVPVKVSV					
g286	YPEQTVSGLARFQPGTPYDLDLLDFQQALEQNGHYSGASVQADFRLPRGPRPRQSQRN					
	250	260	270	280	290	300
	300	310	320	330	340	359
m286.pep	TEVKRHKLETGIRLDSEYGLGGKIAYDYNNLFNKGYIGSVVWMDKYETTLAAGISQPRN					
g286	RGQTPQTRNRHPPRFGRFRQNRRLRLQLPLQRLYRLGRLGYQIRNHACRRHQPAQAL					
	310	320	330	340	350	360

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1197>:

a286.seq

1	ATGCACGACA	CCCGTACCAT	GATGATTAAA	CCGACCGCCC	TGCTCCTGCC
51	GGCTTTATTT	TTCTTTCCGC	ACGCATACGC	GCCTGCCGCC	GACCTTTCCG
101	AAAACAAGGC	GGCGGGTTTC	GCATTGTTCA	AAAACAAAAG	CCCCGACACC
151	GAATCAGTTA	AATTAAAACC	CAAATTCCCC	GTCCGCATCG	ACACGCAGGA
201	TAGTGAAATC	AAAGATATGG	TCGAAGAACA	CCTGCCGCTC	ATCACGCAGC
251	AGCAGGAAGA	AGTATTGGAC	AAGGAACAGA	CGGGCTTCCT	CGCCGAAGAA
301	GCACCGGACA	ACGTTAAAAC	AATGCTCCGC	AGCAAAGGCT	ATTTCAGCAG
351	CAAAGTCAGC	CTGACGGAAA	AAGACGGAGC	TTATACGGTA	CACATCACAC
401	CGGGCCCGCG	CACCAAAATC	GCCAACGTCG	GCGTCGCCAT	CCTCGGCGAC
451	ATCCTTTCAG	ACGGCAACCT	CGCCGAATAC	TACCGCAACG	CGCTGGAAAA
501	CTGGCAGCAG	CCGGTAGGCA	GTGATTTCTGA	TCAGGACAGT	TGGGAAAAACA
551	GCAAAACTTC	CGTCCTCGGC	GCGGTAACGC	GCAAAGCCTA	CCCGCTTGCC
601	AAGCTCGGCA	ACACCCGGGC	GGCCGTCAAC	CCCGATACCG	CCACCGCCGA
651	TTTGAACGTC	GTCGTGGACA	GCGGCCGCCC	CATCGCCTTC	GGCGACTTTG
701	AAATTACCGG	CACGCAGCGT	TACCCCGAAC	AAATCGTCTC	CGGCTTGGCG
751	CGCTTCCAAC	CGGGCACGCC	CTACGACCTC	GACCTGCTGC	TCGACTTCCA
801	ACAGGCGCTC	GAACAAAACG	GGCATTATTTC	CGGCGCGTCC	GTACAAGCCG
851	ACTTCGACCG	CCTCCAAGGC	GACCGCGTCC	CCGTCAAAGT	CAGCGTAACC
901	GAGGTCAAAC	GCCACAAGCT	CGAAACCGGC	ATCCGCCTCG	ATTGCGAATA
951	CGGTTTGGGC	GGCAAAATCG	CCTACGACTA	TTACAACCTC	TTCAACAAAG
1001	GCTATATCGG	TTCGGTGCTC	TGGGATATGG	ACAAATACGA	AACCACGCTT
1051	GCCGCCGGCA	TCAGCCAGCC	GCGCAACTAT	CGGGGCAACT	ACTGGACAAG
1101	CAACGTTTCC	TACAACCGTT	CGACCACCCA	AAACCTCGAA	AAACGCGCCT
1151	TCTCCGGCGG	CATCTGGTAT	GTGCGCGACC	GCGCGGGCAT	CGATGCGAGG
1201	CTGGGGGCGG	AGTTTCTCGC	AGAAGGCCGG	AAAAATCCCCG	GCTCGGATAT
1251	CGATTTGGGC	AACAGCCACG	CCACGATGCT	GACCGCCTCT	TGGAAACGCC
1301	AGCTGCTCAA	CAACGTGCTG	CATCCCGAAA	ACGGCCATTA	CCTCGACGGC

```

1351 AAAATCGGTA CGACTTTGGG CGCATTCCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCAGGTT ATTTCTTCAC GCGCGAAAAC AAAAACTCG
1451 GCACGTTTCAT CACACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTC CTTCAGGGCT GATGTTCCGC AGCGCGGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCCA ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTCCGG CGCGGTGTTC CACGATATGG GCGACGCCGC
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTCGGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTCGCG CCGTTTTCCT TCGACATCGC CTACGGGCAC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

a286.pep

```

1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51 ESVKLPKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGAITV HITPGPRTKI ANVGVAI LGD
151 ILSDGNLA EY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLGNTRAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGTPYDL DLLLDFQQA LEQNGHYS GASVQADFRLQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKG YIGSVV WMDKYETTL
351 AAGISQPRNY RGNWTSNVS YNRSTQNL E KRAFSGGIWY VRDRAGIDAR
401 LGAEFLA EGR KIPGSDIDL G NSHATMLTAS WKRLNNVL HPENGYLDLG
451 KIGTTLGAFL SSTALIRTS A RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
501 ANVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRTL SGAVF HMDGDAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDDKIRWHIS LGTRF*

```

m286/a286 98.7% identity in 615 aa overlap

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKPKFP					
a286	MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKPKFP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m286.pep	VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
a286	VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m286.pep	LTEKDGAITVHITPGPRTKIANVGVAI LGDILSDGNLA EY YRNALENWQQPVGSDFDQDS					
a286	LTEKDGAITVHITPGPRTKIANVGVAI LGDILSDGNLA EY YRNALENWQQPVGSDFDQDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m286.pep	WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPDATADLNVVDSGRPIAFGDFEITGTQR					
a286	WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPDATADLNVVDSGRPIAFGDFEITGTQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m286.pep	YPEQIVSGLARFQPGMPYDL DLLLDFQQA LEQNGHYS GASVQADFRLQGDRVPVKVSVT					
a286	YPEQIVSGLARFQPGTPYDL DLLLDFQQA LEQNGHYS GASVQADFRLQGDRVPVKVSVT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m286.pep	EVKRHKLETGIRLDSEYGLGGKIAYDYNNL FNKG YIGSVVWMDKYETTLAAGISQPRNY					
a286	EVKRHKLETGIRLDSEYGLGGKIAYDYNNL FNKG YIGSVVWMDKYETTLAAGISQPRNY					
	310	320	330	340	350	360
	370	380	390	400	410	420

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m286.pep	RGNYWTSNVSYNRSTTQNLEKRAFSGGVWYVRDRAGIDARLGAEFLAEGRKIPGSAVDLG
a286	RGNYWTSNVSYNRSTTQNLEKRAFSGGIWYVRDRAGIDARLGAEFLAEGRKIPGSDIDLG
	370 380 390 400 410 420
m286.pep	NSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLGTFLSSTALIRTSARAGYFFTPEN
a286	NSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLGAFLSSTALIRTSARAGYFFTPEN
	430 440 450 460 470 480
m286.pep	KKLGTFIIRGQAGYTVARDNADVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
a286	KKLGTFIIRGQAGYTVARDNANVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
	490 500 510 520 530 540
m286.pep	LVGSLEYQLPFTRTLGSAVFHDMGDAAANFKRMKLKHGSGLGVRWFSPLAPFSFDIAYGH
a286	LVGSLEYQLPFTRTLGSAVFHDMGDAAANFKRMKLKHGSGLGVRWFSPLAPFSFDIAYGH
	550 560 570 580 590 600
m286.pep	SDKKIRWHISLGTREX
a286	SDKKIRWHISLGTREX
	610

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1199>:

g287.seq

1	atgtttaaac	gcagtgtgat	tgcaatggct	tgtatttttc	ccctttcagc
51	ctgtgggggc	ggcgggtggc	gatcgcccga	tgtcaagtcg	gcggacacgc
101	cgtcaaaacc	ggccgcccc	gttgttgctg	aaaatgccgg	ggaaggggtg
151	ctgccgaaag	aaaagaaaag	tgaggaggca	gcgggcggtg	cgccgcaagc
201	cgatacgag	gacgcaaccg	ccggagaagg	cagccaagat	atggcggcag
251	tttcggcaga	aaatacaggc	aatggcggtg	cggcaacaac	ggacaacccc
301	aaaaatgaag	acgcgggggc	gcaaaatgat	atgccgcaaa	atgccgcca
351	atccgcaa	aaacaggga	acaaccaacc	cgccggttct	tcagattccg
401	ccccgcgctc	aaacctgcc	cctgcgaatg	gcggtagcga	ttttggaagg
451	acgaacgtgg	gcaattctgt	tgtgattgac	ggaccgtcgc	aaaataaac
501	gttgaccac	tgtaaaggcg	attcttgtaa	tggtgataat	ttattggatg
551	aagaagcacc	gtcaaaatca	gaatttgaaa	aattaagtga	tgaagaaaaa
601	attaagcgat	ataaaaaaga	cgagcaacgg	gagaattttg	tcggtttggt
651	tgctgacagg	gtaaaaaagg	atggaactaa	caaatatata	atcttctata
701	cggacaaacc	acctactcgt	tctgcacggg	cgaggaggtc	gcttccggcc
751	gagattccgc	tgattcccg	caatcaggcc	gatacgtgta	ttgtggatgg
801	ggaagcggtc	agcctgacgg	ggcattccgg	caatatcttc	gcgccggaag
851	ggaattaccg	gtatctgact	tacggggcgg	aaaaattgcc	cgccggatcg
901	tatgccctcc	gtgtgcaagg	cgaaccggca	aaaggcgaaa	tgcttggttg
951	cacggccgtg	tacaacggcg	aagtgtctga	ttccatatg	gaaaacggcc
1001	gtccgtaccc	gtccggaggc	aggtttgccg	caaaagtcga	tttcggcagc
1051	aaatctgtgg	acggcattat	cgacagcggc	gatgatttgc	atatgggtac
1101	gcaaaaatc	aaagccgcca	tcgatggaaa	cggctttaag	gggacttggg
1151	cggaaaatgg	cggcggggat	gtttccggaa	ggttttacgg	cccggccggc
1201	gaggaagtgg	cgggaaaata	cagctatcgc	ccgacagatg	ctgaaaaggg
1251	cggattcggc	gtgtttgccg	gcaaaaaaga	tcgggattga	

This corresponds to the amino acid sequence <SEQ ID 1200; ORF 287.ng>:

g287.pep

1	MFKRSVIAMA	CIFPLSACGG	GGGGSPDVKS	ADTPSKPAAP	VVAENAGEGV
51	LPKEKKDEEA	AGGAPQADTQ	DATAGEGSQD	MAAVSAENTG	NGGAATTDNP
101	KNEDAGAQND	MPQNAAESAN	QTGNNQPAGS	SDSAPASNPA	PANGGSDFGR

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151  TNVGNVSVVID  GPSQNITLTH  CKGDSNCGDN  LLDEEAPSKS  EFEKLSDEEK
201  IKRYKKDEQR   ENFVGLVADR  VKKDGTNKYI  IFYTDKPPTR  SARSRRSLPA
251  EIPLIPVNQA   DTLIVDGEAV  SLTGHSGNIF  APEGNYRYLT  YGAEKLPGGS
301  YALRVQGEPA   KGEMLVGTAV  YNGEVLHFHM  ENGRPYPSGG  RFAAKVDFGS
351  KSVDDGIIDSG  DDLHMGTOKF  KAAIDGNFK  GTWTENGGGD  VSGRFYGPAG
401  EEVAGKYSYR   PTDAEKGFG  VFAGKKDRD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```

m287.seq
1   ATGTTTAAAC  GCAGCGTAAT  CGCAATGGCT  TGTATTTTGT  CCCTTTCAGC
51  CTGCGGGGGC  GCGGGTGGCG  GATCGCCCGA  TGTCAAGTCG  GCGGACACGC
101 TGTCAAACCC  TGCCGCCCTT  GTTGTTCCTG  AAAAAGAGAC  AGAGGCAAAG
151 GAAGATGCGC  CACAGGCAGG  TTCTCAAGGA  CAGGGCGCGC  CATCCGCACA
201 AGGCAGTCAA  GATATGGCGG  CGGTTTCGGA  AGAAAATACA  GGCAATGGCG
251 GTGCGGTAAC  AGCGGATAAT  CCCAAAATG   AAGACGAGGT  GGCACAAAAT
301 GATATGCCGC  AAAATGCCGC  CGGTACAGAT  AGTTCGACAC  CGAATCACAC
351 CCCGGATCCG  AATATGCTTG  CCGGAAATAT  GGAAAATCAA  GCAACGGATG
401 CCGGGGAATC  GTCTCAGCCG  GCAAACCAAC  CGGATATGGC  AAATGCGGCG
451 GACGGAATGC  AGGGGGACGA  TCCGTCGGCA  GCGGGGCAA  ATGCCGGCAA
501 TACGGCTGCC  CAAGGTGCAA  ATCAAGCCGG  AAACAATCAA  GCCGCCGGTT
551 CTTCAGATCC  CATCCCCGCG  TCAAACCTG   CACCTGCGAA  TGGCGGTAGC
601 AATTTTGGA  GGGTTGATTT  GGCTAATGGC  GTTTTGATTG  ACGGGCGTTC
651 GCAAAATATA  ACGTTGACCC  ACTGTAAAGG  CGATTCTTGT  AGTGGCAATA
701 ATTTCTTGA  TGAAGAAGTA  CAGCTAAAAT  CAGAATTGTA  AAAATTAAGT
751 GATGCAGACA  AAATAAGTAA  TTACAAGAAA  GATGGGAAGA  ATGATAAATT
801 TGTCGGTTTG  GTTGCCGATA  GTGTGCAGAT  GAAGGGAATC  AATCAATATA
851 TTATCTTTTA  TAAACCTAAA  CCCACTTCAT  TTGCGCGATT  TAGGCGTTCT
901 GCACGGTCGA  GCGGGTCGCT  TCCGGCCGAG  ATGCCGCTGA  TTCCCGTCAA
951 TCAGGCGGAT  ACGCTGATTG  TCGATGGGGA  AGCGGTACAG  CTGACGGGCG
1001 ATTCCGGCAA  TATCTTCGCG  CCCGAAGGGA  ATTACCGGTA  TCTGACTTAC
1051 GGGGCGGAAA  AATTGCCCGG  CGGATCGTAT  GCCCTTCGTG  TTCAAGGCGA
1101 ACCGGCAAAA  GCGGAAATGC  TTGCGGGCGC  GGCCGTGTAC  AACGGCGAAG
1151 TACTGCATTT  CCATACGGAA  AACGGCCGTC  CGTACCCGAC  CAGGGGACAG
1201 TTTGCCGCAA  AAGTCGATTT  CGGCAGCAAA  TCTGTGGACG  GCATTATCGA
1251 CAGCGGCGAT  GATTTCGATA  TGGGTACGCA  AAAATTCAAA  GCCGCCATCG
1301 ATGGAACGG  CTTTAAGGGG  ACTTGGACGG  AAAATGGCAG  CGGGGATGTT
1351 TCCGGAAGT  TTTACGGCCC  GGCCGGCGAG  GAAGTGGCGG  GAAAATACAG
1401 CTATCGCCCG  ACAGATGCGG  AAAAGGGCGG  ATTCGGCGTG  TTTGCCGGCA
1451 AAAAAGAGCA  GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```

m287.pep
1   MFKRSVIAMA  CIFALSACGG  GGGGSPDVKS  ADTLSKPAAP  VVSEKETEAK
51  EDAPQAGSQ  QGAPSAQGSQ  DMAAVSEENT  GNGGAVTADN  PKNEDEVAQN
101 DMPQNAAGTD  SSTPNHTPDP  NMLAGNMENQ  ATDAGESSQ  ANQPDMANAA
151 DGMQGDPSA  GGQNAAGTAA  QGANQAGNNQ  AAGSSDPIPA  SNPAPANGGS
201 NFGRVDLANG  VLIDGPSQNI  TLTHCKGDSC  SGNNFLDEEV  QLKSEFEKLS
251 DADKISNYKK  DGKNDKFVGL  VADSVQMKGI  NQYIIFYKPK  PTSFARFRRS
301 ARSRRSLPAE  MPLIPVNQAD  TLIVDGEAVS  LTGHSGNIFA  PEGNYRYLTY
351 GAEKLPGGSY  ALRVQGEPAK  GEMLAGAAVY  NGEVLHFHTE  NGRPYPTRGR
401 FAAKVDFGSK  SVDGIIDSGD  DLHMGTOKF  AAIDGNFGK  TWTENGSGDV
451 SGKFYGPAGE  EVAGKYSYRP  TDAEKGFGV  FAGKKEQD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

              10      20      30      40      49
m287.pep      MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSKPAAPVVSE-----KETEAK
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g287          MFKRSVIAMACIFPLSACGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPEKKDEEA
              10      20      30      40      50      60

```


a287.pep

1	MFKRSVIAMA	CIVALSACGG	GGGGSPDVKS	ADTLSPAAP	VVTEDVGEEV
51	LPKEKKDEEA	VSGAPQADTQ	DATAGKGGQD	MAAVSAENTG	NGGAATTDNP
101	ENKDEGPQND	MPQNAADTDS	STPNHTPAPN	MPTRDMGNQA	PDAGESAQPA
151	NQPDMANAAD	GMQGDDPSAG	ENAGNTADQA	ANQAENNQVG	GSQNPASSTN
201	PNATNGGSDF	GRINVANGIK	LDSGSENVTL	THCKDKVCDR	DFLDEEAPPK
251	SEFEKLSDEE	KINKYKKDEQ	RENFVGLVAD	RVEKNGTNKY	VIIYKDKSAS
301	SSSARFRRSA	RSRRSLPAEM	PLIPVQNAAD	LIVDGEAVSL	TGHSNFIAP
351	EGNYRYLTYS	AEKLSGGSYA	LSVQGEPAKG	EMLAGTAVYN	GEVLGHFMEN
401	GRPSPSGGRF	AAKVDFGSKS	VDGIIDSGDD	LHMQTKQFKA	VIDGNNGFKGT
451	WTENGGGDVS	GRFYGPAGEE	VAGKYSYRPT	DAEKGFGVF	AGKKEQD*

m287/a287 77.2% identity in 501 aa overlap

	10	20	30	40	49
m287.pep	MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSKPAAPVSE-----KETE				A
a287	MFKRSVIAMACIVALSACGGGGGSPDVKSADTLSKPAAPVVTE	DVGEEVL	PKEKKDEE		A
	10	20	30	40	60
	50	60	70	80	100
m287.pep	KEDAPQAGSQQGAPS	AQSQDMAAVSEENTGN	GGAVTADNPKN	EDEV	AQN
a287	VSGAPQADTQ--DATA	GKGQDMAAVSAENTGN	GGAATTDPNPK	DEGPQNDMP	QNAADT
	70	80	90	100	110
	110	120	130	140	160
m287.pep	DSSTPNHTPDPENMLAGNMENQATDAGESSQPANQPDMANAADGMQGD	DPSAGGQ	NAGNTA		
a287	DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADGMQGD	DPSAG-ENAGNTA			
	120	130	140	150	170
	170	180	190	200	220
m287.pep	AQQANQAGNNQAAGSSDPIPASNPAPANGGSNFGRVDLANGVLIDGPSQ	NITLTHCKGDS			
a287	DQAANQAENNQVGGSQNPASSTNPATNGGSDFGRINVANGIKLDSGSEN	VTLTHCKDKV			
	180	190	200	210	230
	230	240	250	260	280
m287.pep	CSGNNFLDEEVQLKSEFEKLSDADKISNYKKDGKNDKFVGLVADSVMK	GINQYIIFYKP			
a287	CD-RDFLDEEAPPKSEFEKLSDDEEKINKYKKDEQRENFVGLVADRVEK	NGTNTKYVIIYKD			
	240	250	260	270	290
	290	300	310	320	340
m287.pep	KP--TSFARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHS	GNIFAPEGNYRY			
a287	KSASSSSARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHS	GNIFAPEGNYRY			
	300	310	320	330	350

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	350	360	370	380	390	400
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF					
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF					
	360	370	380	390	400	410
	410	420	430	440	450	460
m287.pep	GSKSVDGIIDSGDDLHMGQTQKFKAAIDNGFNGFSGTWTENGSGDVSGKFYGPAGEEVAGKYS					
a287	GSKSVDGIIDSGDDLHMGQTQKFKAVIDNGFNGFSGTWTENGSGDVSGRFYGPAGEEVAGKYS					
	420	430	440	450	460	470
	470	480	489			
m287.pep	YRPTDAEKGFGVFAGKKEQDX					
a287	YRPTDAEKGFGVFAGKKEQDX					
	480	490				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1205>:

```

g288.seq
1  atgcacaccg gacaggcggg aagccggggt ctgtctcgga cagtcattcc
51  tctaggcata ccgttgccgg tatgctcaag caacctaccc gaacgctcgg
101 cgggcagcgt cattgcgttc tgtttggtct tgctccgaat ggggtttggc
151 ctgccgcata ttgttaccaa atgcgcgggtg cgcccttacc gcaccttttc
201 acccttgccg gtgctgccaa agcagccatc ggcggttttg ctttctgttc
251 cactttccgt cgcgttaccc cgcccggccg ttaaccggca ttctaccctg
301 cggagcccg cctttcctcc ccgtatgcct tacgcgatac gcggcgactg
351 tctgcccgtc ccgtgtgcgg cgcggttat aacacgaaac gcaaaaatgc
401 cgtctgaaac ggtacagggt tcagacggca tacagcctaa actacacacc
451 ctgtttcagg ctggcttcga tgaagccgtc caagtcgccc tccaatacgg
501 ctttgtggtt gccgacttcg tagcctgtac gcaagtcttt gatgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1206; ORF 288.ng>:

```

g288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHT
151 LFQAGFDEAV QVAVQYGFVV ADFVACTQVF DA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1207>:

```

m288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTACCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTCTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTACCT GTGCTGCCAA AGCAGCCATC GGCGGTTTTG CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC ACAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TGAAGCCGTC CAAGTCGCCA TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTAC GCAAGTCTTT GATACGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1208; ORF 288>:

```

m288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN TKMPSETVQV SDGIQPKLHA
151 LFQAGFDEAV QVAIQYGFVV ADFVACTQVF DT*

```

Computer analysis of this amino acid sequence gave the following results:

675

Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
g288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCPLV					
g288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCPLV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADVFVACTQVF					
	: : : :					
g288	PCAARIITRNAKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADVFVACTQVF					
	130	140	150	160	170	180
m288.pep	DTX					
	:					
g288	DAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

```

a288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTGCCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTGTTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTGCCCT GTGCTGCCAA AGCAGCCATC GGCGGTTTTC CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCCGGCCG TTAACGGCA TTCTACCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC GCAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TAAAGCCGTC CAAGTCGCCG TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTGC GCAAGTCTTT AATGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1210; ORF 288.a>:

```

a288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCPLV PCAARIITRN AKMPSETVQV SDGIQPKLHA
151 LFQAGFDKAV QVAVQYGFV ADFVACAQVF NA*

```

m288/a288 97.2% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
a288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCPLV					
a288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCPLV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADVFVACTQVF					
	: : : :					

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a288 PCAARIITRNAKMPSETVQVSDGIQPKLHALFQAGFDKAVQVAVQYGFVADFVACAQVF
 130 140 150 160 170 180

m288.pep DTX
 ::
 a288 NAX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1211>:

g290.seq
 1 atggcaaaaa tgatgaaatg ggcggctggt gcggcggtcg cggcggcagc
 51 ggtttggggc ggatggtctt atctgaagcc cgaaccgcag gctgcttata
 101 ttacggaagc ggtcaggcgc ggcgatatca gccggacggt ttccgcgacg
 151 ggcgagattt cgccgtccaa cctggtatcg gtcggcgcgc aggttcggg
 201 gcagattaaa aagctttatg tcaaactcgg gcaacaggtc aaaaagggcg
 251 atttgattgc ggaaatcaat tcgaccacgc agaccaacac gatcgatatg
 301 gaaaaatcca aattggaaac gtatcaggcg aagctggtgt ccgcacagat
 351 tgcatagggc agcgcggaaa aaaaatataa gcgtcaggcg gcgttggtga
 401 aggatgatgc gacctctaaa gaagatttgg aaagcgcgca ggatgcgctt
 451 gccgccgcca aagccaatgt tgccgagttg aaggctttaa tcagacagag
 501 caaaatttcc atcaataaccg ccgagtcgga tttgggctac acgcgcatta
 551 ccgcgacgat ggacggcacg gtggtggcga ttcccgtgga agaggggcag
 601 actgtgaacg cggcgacgac tacgccgacg attgtccaat tggcgaaatc
 651 ggatatgatg ttgaacaaaa tgcagattgc cgagggcgat attaccaagg
 701 tgaaggcggg gcaggatatt tcgtttacga ttttgtccga accggatacg
 751 ccgattaagg cgaagctcga cagcgtcgac cccgggctga ccacgatgtc
 801 gtcggcgggc tacaacagca gtacggatac ggcttccaat gcggtctatt
 851 attatgcccg ttcgtttgtg ccgaatccgg acggcaaact cgccacgggg
 901 atgacgacgc agaatacggg tgaatcgac ggtgtgaaaa atgtgttgct
 951 tattccgctg ctgaccgtga aaaaatcgcg cggaaggcg ttcgtacgcg
 1001 tgttgggtgc ggacggcaag gcagtggaac gcgaaatccg gaccggtatg
 1051 aaagacagta tgaataccga agtgaaaagc gggttgaaaag agggggacaa
 1101 agtggtcacg tccgaaataa ccgccgccga gcagcaggaa agcggcgaa
 1151 gcgccctagg cggcccgcgc cgccgataa

This corresponds to the amino acid sequence <SEQ ID 1212; ORF 290.ng>:

g290.pep
 1 MAKMMKWAIV AAVAAAAVWG GWSYLKPEPQ AAYITEAVRR GDISRTVSAT
 51 GEISPSNLVS VGAQASGQIK KLYVKLGQV KKGDLIAEIN STTQNTIDM
 101 ESKLETYQA KLVSAQIALG SAEKKYKQA ALWKDDATSK EDLESAQDAL
 151 AAKANVAEL KALIRQSKIS INTAESDLGY TRITATMDGT VVAIPVEEGQ
 201 TVNAAQSTPT IVQLANLDM LNKMQIAEGD ITKVKAGQDI SFTILSEPDT
 251 PIKAKLDSVD PGLTTMSSGG YNSSTDASN AVYYARSFV PNPDGKLATG
 301 MTTQNTVEID GVKNVLLIPS LTVKNRGGKA FVRVLGADGK AVEREIRTGM
 351 KDSMNTEVKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1213>:

m290.seq (partial)
 1 ..GTATCGGTCG GCGCGCAGGC ATCGGGGCAG ATTAAGATAC TTTATGTCAA
 51 ACTCGGGCAA CAGGTTAAAA AGGCGGATT GATTGCGGAA ATCAATTCTGA
 101 CCTCGCAGAC CAATACGCTC AATACGAAA AATCCAAGTT GGAAACGTAT
 151 CAGGCGAAGC TGGTGTCCGC ACAGATTGCA TTGGGCAGCG CGGAGAAGAA
 201 ATATAAGCGT CAGGCGGCGT TATGGAAGGA AAACGCGACT TCCAAAGAGG
 251 ATTTGGAAAG CGCGCAGGAT GCGTTTGCCG CCGCCAAAGC CAATGTTGCC
 301 GAGCTGAAGG CTTTAATCAG ACAGAGCAA ATTTCCATCA ATACCGCCGA
 351 GTCGGAATTG GGCTACACGC GCATTACCGC AACGATGGAC GGCACGGTGG
 401 TGGCGATTCT CGTGGAAGAG GGGCAGACTG TGAACGCGGC GCAGTCTACG
 451 CCGACGATTG TCCAATTGGC GAATCTGGAT ATGATGTTGA ACAAATGCA
 501 GATTGCCGAG GGCGATATTA CCAAGGTGAA GGCGGGGCAG GATATTTCTG
 551 TTACGATTTT GTCCGAACCG GATACGCCGA TTAAGGCGAA GCTCGACAGC
 601 GTCGACCCCG GGCTGACCAC GATGTCGTCG GGCGGTTACA ACAGCAGTAC
 651 GGATACGGCT TCCAATGCGG TCTACTATTA TGCCCGTTTCG TTTGTGCCGA

```
m290.pep (partial)
  1  ..VSVGAAQASGQ IKILYVKLGQ QVKKGDLIAE INSTSQNTNL NTEKSKLETY
 51  QAKLVSAQIA LGSAEKKYKR QAALWKENAT SKEDLESAQD AFAAAKANVA
101  ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAAILVEE GQTVNAAQST
151  PTIVQLANLD MMLNKMQUIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201  VDPGLTMTSS GGYNSSTDITA SNAVYYIARS FVPNPDGKLA TGMTTQNTVE
251  IDGVKNVLII PSLTVKNRGG KAFVRVLGAD GKAAEREIRT GMRDSMNTVE
301  KSGLKEGDKV VISEITAAEQ QESGERALGG PPRR*
```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m290.pep					10	20	30
					VSVGAQASGQIKILYVKLGQQVKKGDLIAE		
g290					PQAAYITEAVRRGDISRTVSATGEISPSNLVSVGAQASGQIKKLYVKLGQQVKKGDLIAE		
		30	40	50	60	70	80
m290.pep			40	50	60	70	80
			INSTSQNTNLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD				90
				:		:	
g290			INSTTQTNTIDMEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATSKEDLESAQD				140
		90	100	110	120	130	140
m290.pep			100	110	120	130	150
			AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST				
			:		:		
g290			ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVAIPVEEGQTVNAAQST				
		150	160	170	180	190	200
m290.pep			160	170	180	190	210
			PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS				
g290			PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS				
		210	220	230	240	250	260
m290.pep			220	230	240	250	270
			GGYNSSTD TASNAVYYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG				
g290			GGYNSSTD TASNAVYYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLLIIPSLTVKNRGG				
		270	280	290	300	310	320
m290.pep			280	290	300	310	330
			KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVI SEITAAEQQESGERALGG				
g290			KAFVRVLGADGKAVEREIRTGMKDSMNTEVKSGLKEGDKVVI SEITAAEQQESGERALGG				
		330	340	350	360	370	380
m290.pep			P	P	R	R	X
g290			P	P	R	R	X
			390				

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1215>:

```
a290.seq
1   ATGGCAAAAA TGATGAAATG GGCGGCTGTT GCGGCGGTCG CCGCGGCAGC
51  GGTTCGGGGC GGATGGTCTT ATCTGAAGCC CGAGCCGCAG GCTGCTTATA
101 TTACGGAAAC GGTTCAGGCGC GGCGACATCA GCCGACGGT TTCTGCAACA
151 GGGGAGATTT CGCCGTCCAA CCTGGTATCG GTCGGCGCGC AGGCATCGGG
201 GCAGATTAAG AAACCTTTATG TCAAACTCGG GCAACAGGTT AAAAAGGGCG
251 ATTTGATTGC GGAAATCAAT TCGACCTCGC AGACCAATAC GCTCAATACG
301 GAAAAATCCA AATTGGAAC GTATCAGGCG AAGCTGGTGT CGGCACAGAT
351 TGCATTGGGC AGCGCGGAGA AGAAATATAA GCGTCAGGCG GCGTTGTGGA
401 AGGATGATGC GACCGCTAAA GAAGATTGTT AAAGCGCACA GGATGCGCTT
451 GCCGCCGCCA AAGCCAATGT TGCCGAGCTG AAGGCTCTAA TCAGACAGAG
501 CAAAATTTCC ATCAATACCG CCGAGTCGGA ATTGGGCTAC ACGCGCATTA
551 CCGCAACGAT GGACGGCAGC GTGGTGGCGA TTCTCGTGGA AGAGGGGCAG
601 ACTGTGAACG CGGCGCAGTC TACGCCGACG ATTGTCCAAT TGGCGAATCT
651 GGATATGATG TTGAACAAAA TGCAGATTGC CGAGGGCGAT ATTACCAAGG
701 TGAAGGCGGG GCAGGATATT TCGTTTACGA TTTTGTCCGA ACCGGATACG
751 CCGATTAAGG CGAAGCTCGA CAGCGTCGAC CCCGGGCTGA CCACGATGTC
801 GTCGGGCGGC TACAACAGCA GTACGGATAC GGCTTCCAAT GCGGTCTACT
851 ATTATGCCCG TTCGTTTGTG CCGAATCCGG ACGGCAAACG CGCCACGGGG
901 ATGACGACGC AGAATACGGT TGAAATCGAC GGTGTGAAAA ATGTGCTGAT
951 TATTCCGTCG CTGACCGTGA AAAATCGCGG CGGCAGGGCG TTTGTGCGCG
1001 TGTTGGGTGC AGACGGCAAG GCGGCGGAAC GCGAAATCCG GACCGGTATG
1051 AGAGACAGTA TGAATACCGA AGTAAAAAGC GGGTTGAAAG AGGGGGACAA
1101 AGTGGTCATC TCCGAAATAA CCGCCGCCGA GCAGCAGGAA AGCGGCGAAC
1151 GCGCCCTAGG CGGCCGCCG CGCCGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1216; ORF 290.a>:

```
a290.pep
1   MAKMMKWAAY AAVAAAAVWG GWSYKPEPQ AAYITETVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQV KKGDLIAEIN STSQNTLNLT
101 ESKLETYQA KLVSAQIALG SAEKKYKQQA ALWKDDATAK EDLESAQDAL
151 AAKANVAEL KALIRQSKIS INTAESELGY TRITATMDGT VVAILVEEGQ
201 TVNAAQSTPT IVQLANLDM LNMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSG YNSSTDASN AVYYYARFV PNPDKLATG
301 MTTQNTVEID GVKNVLIIPS LTVKNRGGRA FVRVLGADGK AAEREIRTM
351 RDSMNTVEKS GLKEGDKVVI SEITAEQQE SGERALGGPP RR*

m290/a290 98.2% identity in 334 aa overlap

m290.pep
10 20 30
VSVGAQASGQIKILYVKLGQVKKGDLIAE
|||||

a290
30 40 50 60 70 80
PQAAYITETVRRGDISRTVSATGEISPSNLVS VQAQASGQIKKLYVKLGQVKKGDLIAE

m290.pep
40 50 60 70 80 90
INSTSQNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKQQAALWKENATSKEDLESAQD
|||||

a290
90 100 110 120 130 140
INSTSQNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKQQAALWKDDATAKEDLESAQD

m290.pep
100 110 120 130 140 150
AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
|:|||||

a290
150 160 170 180 190 200
ALAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST

m290.pep
160 170 180 190 200 210
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
|||||

a290
210 220 230 240 250 260
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS

220 230 240 250 260 270
```

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```

m290.pep      GGYNSSTD TASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
              |||||||
a290          GGYNSSTD TASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
              270      280      290      300      310      320

              280      290      300      310      320      330
m290.pep      KAFVRVLGADGKAAEREIRTGM RDSMNTEVKSGLKEGDKVVIS EITAAEQQESGERALGG
              :|||||
a290          RAFVRVLGADGKAAEREIRTGM RDSMNTEVKSGLKEGDKVVIS EITAAEQQESGERALGG
              330      340      350      360      370      380

m290.pep      PPRRX
              |||||
a290          PPRRX
              390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1  atgaaaacca agttaatcaa aatcttgacc ccctttaccg tcctgccgct
51 gctggcttgc gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcg
151 ttggaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgccgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgccgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttggacaa agccatcaaa gaagtacg
401 gcaacggcaa gctgaaagtc gccgtcttct ccgaccccca ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaatctt atggtgtcag cccgaccgtg ccaaagcgtg gacggattgg
601 atgcgtaaag gcaaatcccc ggtcggcggc agcatctg
651 cgcgaaacc acttccttgg gcgaacagtt cggttcaac ggacgcccga
701 cccttcgtct tccccaacgg gcgcacccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaac cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pep
1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA ESAVKAESAG KSAASLKAR
51 LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTD AEG GYMFGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPAET TSLGEQFGFN GTPTLRLPQR AHPKRLQPPA
251 PTGGNHPQKP AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1  ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51 GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCTCTTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTGGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGC
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTC
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATTG CCGGCCTGCA CCCCAGTGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTCAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAATCCC GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAAAT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCAACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCCC

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751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

This corresponds to the amino acid sequence <SEQ ID 1220; ORF 292>:

```

m292.pep
  1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVAAASLKAR
 51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101  IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151  CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201  MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251  QLEEIIRKNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m292/g292 98.7% identity in 238 aa overlap

	10	20	30	40	50	60
m292.pep	MKTKLIKILTPFTVLPLLACGQTPVSNANAEP	AVKAESAGKSVAAASLKARLEKTYSAQDL				
g292	MKTKLIKILTPFTVLPLLACGQTPVSNANAESA	VAESAGKSVAAASLKARLEKTYSAQDL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m292.pep	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGY	MFVGELINIDTRKNLTEERAADLNKIDF				
g292	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGY	MFVGELINIDTRKNLTEERAADLNKIDF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m292.pep	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCK	RLEHEFEKMTDVTVYSFMMPIAGLHPDA				
g292	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCK	RLEHEFEKMTDVTVYSFMMPIAGLHPDA				
	130	140	150	160	170	180
	190	200	210	220	230	240
m292.pep	ARKAQILWCQPDRAKAWTDWMRKGKFPVGG	SICDNPVAETTSLGEQFGFNGTPTLVFPNG				
g292	ARKAQILWCQPDRAKAWTDWMRKGKFPVGG	SICDNPVAETTSLGEQFGFNGTPTLRPQR				
	190	200	210	220	230	240
	250	260				
m292.pep	RSQSGYSPMPQLEEIIRKNQX					
g292	AHPKRLQPDAPTGGNHPQKPAVNPQX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1221>:

```

a292.seq
  1  ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
 51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101  TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151  TTGGAAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTTGA GCGTCAGCGA
201  AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251  TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301  ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351  AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGC GCG
401  GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451  TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTA
501  CAGCTTTATG ATGCCCATG CCGGCCTGCA CCCCAGTGCC GCGCGCAAGG
551  CGCAAATCTT ATGGTGTCAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601  ATGCGTAAAG GCAAATTCCC GGTCGGCGGC AGCATCTGCG ACAATCCCGT
651  CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701  CCCTCGTCTT CCCCAACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCCC
751  CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292.pep
  1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVAAASLKAR
 51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSG RQIIYTDAEG GYMFVGELIN
101  IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGLKV AVFSDPDCPF
151  CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201  MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251  QLEEIIRKNQ *

m292/a292    100.0% identity in 260 aa overlap

              10      20      30      40      50      60
m292.pep     MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVAAASLKAR LEKTYSAQDL
              |||||
a292          MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVAAASLKAR LEKTYSAQDL
              10      20      30      40      50      60

              70      80      90     100     110     120
m292.pep     KVLVSSETPV KGIYEVVVSG RQIIYTDAEG GYMFVGELIN IDTRKNLTEE RAADLNKIDF
              |||||
a292          KVLVSSETPV KGIYEVVVSG RQIIYTDAEG GYMFVGELIN IDTRKNLTEE RAADLNKIDF
              70      80      90     100     110     120

              130     140     150     160     170     180
m292.pep     ASLPLDKAI KEVRGNGLKV AVFSDPDCPF CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA
              |||||
a292          ASLPLDKAI KEVRGNGLKV AVFSDPDCPF CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA
              130     140     150     160     170     180

              190     200     210     220     230     240
m292.pep     ARKAQILWCQ PDRAKAWTDW MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG
              |||||
a292          ARKAQILWCQ PDRAKAWTDW MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG
              190     200     210     220     230     240

              250     260
m292.pep     RSQSGYSPMP QLEEIIRKNQX
              |||||
a292          RSQSGYSPMP QLEEIIRKNQX
              250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
  1  atgcgtatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtctggtc
 51  gggtcgggct gtcagaacat catcgaaaccg ctttcctgcg gcgttacgac
101  gatattcggc ttttcgacct acaatttttc cgaagcctgc cggcacgcct
151  tggcatcggg tgcggcgggt caagtcgaat cggcggacgc gtggcgtgaa
201  gccgttgaaa aaaccttata tggcgagggg ggcggaatgc agatgcaggc
251  gcgcgtggag ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301  ccgaggcggt gcgggaagcg gtatgcggac atcgggggcg atagtgtatc
351  aatccgtatc cgagttttcc ggttgagca tcgtatgagt atttatgccg
401  tcgcgcacat catccacctg tattgcgcca ccgcctttgt cggcggcgtg
451  ttttttgaag tgctggtttt gtccgtcctg catacgggac ggggtgtcgcg
501  cgaggcgcgg cgcgaaagtgg aaaaggcaat gtcttaccgc gccgtcaggg
551  tgatgccgtt tgcggtcggg ctgctgttcg ccagggaac tctagagtcg
601  actgcagcag catgccctc...

```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
  1  MRITCAPMSL LSAAVWSVRA VRTSSNRFP A LRRYSAPFR TIFPKPAGTP
 51  WHRVRRFKSN RTRGVKPLK KPYLARGAEC RCRRRAWTALS HNIAERARES
101  PRRCGKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVGGV
151  FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMPPFVAVG LLFARGTLES
201  TAAACP....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

682

m294.seq
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
 51 GATTTCGGGT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCGCAC
 101 GATATTCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT
 151 TGGCATCGGG TGCGGCGGTT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA
 201 GCCGTTGAAA AAACCTTATC GTCCGAGGGG GGGGGGATGC AGATGCAGGC
 251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
 301 CCGAGGCGGT GCGGGAAGCG GTATGCGGAT ATCGGGGGCG ATAGTGATAC
 351 AATCCGTATC CGAGTTTTC GTTTGGAGCA TCGTATGAGT ATTTATGCCG
 401 TCGCGCACAT CGTTCATCTG TATTGCGCTA TTGCCTTTGT CGGCGGCGTG
 451 TTTTGTGAAG TGCTGGTTT GTCCGTCCTG CATACGGGAC GGGTGTCGCG
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTCAGGG
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTC CCAGCGGCAT CGTGATGGCG
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTA TTGGCGCACT
 701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC GGTGCGTTGG
 751 TCGAAATACA TACACGCGT CGTCTTACC CATATGCTGC TGATTGCTCT
 801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1226; ORF 294>:

m294.pep
 1 MRITCAPMSL LSAAVWSIRV VRTSSNRFP AFRRYSAFQP TIFPKPADTP
 51 WHRVRRFKN RMRGGKPLK KPYRPRGGC RCRRWTALS HNIAERARES
 101 PRRCCKRYAD IGGDSITRI RVFRLEHRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMFVVG LLFASGIVMA
 201 ANRYSILGE PFATSFMTL TLKILLAFSV LAHFAIAVVK MARSTLTVGW
 251 SKYIHAVVET HMLLIVELAK AMFYISW*

g294/m294 92.3% identity in 196 aa overlap

	10	20	30	40	50	60
g294.pep	MRITCAPMSLLSAAVWSVRAVRTSSNRFPALRRYSAFRPTIFPKPAGTPWHRVRRFKN					
	: : : : :					
m294	MRITCAPMSLLSAAVWSIRVVRTSSNRFPALRRYSAFQPTIFPKPADTPWHRVRRFKN					
	10	20	30	40	50	60
	70	80	90	100	110	120
g294.pep	RRTRGVKPLKPYLARGAECRCRRWTALSHNIAERARESPRRCCKRYADIGGDSITRI					
	: : : : :					
m294	RRMRGGKPLKPYRPRGGCRCRRWTALSHNIAERARESPRRCCKRYADIGGDSITRI					
	70	80	90	100	110	120
	130	140	150	160	170	180
g294.pep	RVFRLEHRMSIYAVAHIIHLYCATAFVGGVFFEVVLVLSVLHTGRVSREARREVEKAMSYR					
	: : : : :					
m294	RVFRLEHRMSIYAVAHIVHLYCAIAFVGGVFFEVVLVLSVLHTGRVSREARREVEKAMSYR					
	130	140	150	160	170	180
	190	200				
g294.pep	AVRVMFVAVGLLFARGTLESTAAACP					
	:					
m294	AVRVMFVAVGLLFASGIVMAANRYSILGEPFATSFMTLTLKILLAFSVLAHFAIAVVK					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1227>:

a294.seq
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
 51 GATTTCGGGT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCGCAC
 101 GATATTCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT
 151 TGGCATCGGG TGCGGCGGTT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA
 201 GCCGTTGAAA AAACCTTATC GTCCGAGGAG GCGGGAATGC AGATGCAGGC
 251 GCGCGCGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
 301 CCGAGGCGGT ACGGGAAGCG GTATGCGGAC ATCGGGGACG ATAGTGATAC
 351 AATCCGTATC CGAGTTTTC GGTGAGTA CCGTATGAGT ATTTATGCCG
 401 TCGCGCACAT CGTCCACCTG TATTGCGCCA TCGCCTTTGT CGGCGGCGTG
 451 TTTTGTGAAG TGCTGGTTT GTCCGTCCTG CATACGGGAC GGGTGTCGCG
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTCAGGG
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTC CCAGCGGCAT CGTGATGGCG
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTG TTGGCGCACT

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